



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 179999

TO: Sheela Huff
Location: rem/3A15/3C18
Art Unit: 1643
Monday, February 27, 2006
Case Serial Number: 10/723872

From: Kristine Hensle
Location: Biotech-Chem Library
REM-1B69
Phone: (571) 272-4161

Kristine.Hensle@uspto.gov

Search Notes

Examiner Huff,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle
Librarian
STIC Biotech/Chem Library
(571)272-4161

For scanning.
Search Notes

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STIC-Biotech/ChemLib

179999

Me

From: Huff, Sheela
Sent: Tuesday, February 21, 2006 5:32 AM
To: STIC-Biotech/ChemLib
Subject: search request for 10723872

Please search and interference search SEQ ID NO. 12, 14, 16,18, 20, 22, 24 and 26. All are polypeptides.

Thanks-

Sheela Huff
Art Unit 1643
571-272-0834
Remsen 3A15
mailbox Remsen 3C18

RECEIVED
FEB 21 2006
STIC

Searcher:_____
Searcher Phone:_____
Date Searcher Picked up:_____
Date completed:_____
Searcher Prep Time:_____
Online Time:_____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 09:13:28 ; Search time 135.298 Seconds
(without alignments)
457.897 Million cell updates/sec

Title: US-10-723-872-12
Perfect score: 755
Sequence: 1 MVLQTVFISLLWISGAYG.....TFVYFVDMGRGTPVTVSS 141

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003s.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 755 | 100.0 | 141 | 2 | Aar70192 Humanized |
| 2 | 755 | 100.0 | 141 | 2 | Aay23770 Heavy cha |
| 3 | 755 | 100.0 | 141 | 2 | Aay18117 Heavy cha |
| 4 | 663 | 87.8 | 141 | 2 | Aar70191 Chimeric |
| 5 | 663 | 87.8 | 141 | 2 | Aay23769 Heavy cha |
| 6 | 663 | 87.8 | 141 | 2 | Aay18125 Chimeric |
| 7 | 577 | 76.4 | 140 | 2 | Aar70190 Mouse Mab |
| 8 | 577 | 76.4 | 140 | 2 | Aay23768 Heavy cha |
| 9 | 577 | 76.4 | 140 | 2 | Aay18121 Heavy cha |
| 10 | 553 | 73.2 | 121 | 2 | Aay23780 Heavy cha |
| 11 | 553 | 73.2 | 121 | 2 | Aay18122 Heavy cha |
| 12 | 551 | 73.0 | 472 | 6 | Abp58289 Humanised |
| 13 | 549.5 | 72.8 | 139 | 5 | Abg31445 Amino aci |
| 14 | 546.5 | 72.4 | 118 | 8 | Adf71905 Hu3G8VH-1 |
| 15 | 546.5 | 72.4 | 448 | 8 | Adf71908 Hu3G8VH-1 |
| 16 | 544.5 | 72.1 | 450 | 5 | Abp66590 Human RSV |
| 17 | 544.5 | 72.1 | 450 | 5 | Abp66588 Human RSV |
| 18 | 544.5 | 72.1 | 450 | 5 | Abp66586 Human RSV |
| 19 | 544.5 | 72.1 | 450 | 6 | Abu69451 Respirato |
| 20 | 544.5 | 72.1 | 450 | 6 | Abu69453 Respirato |
| 21 | 544.5 | 72.1 | 450 | 6 | Abu69449 Respirato |
| 22 | 544.5 | 72.1 | 450 | 7 | Adf35948 SYNAGIS a |
| 23 | 544.5 | 72.1 | 450 | 7 | Adf35946 SYNAGIS a |
| 24 | 544.5 | 72.1 | 450 | 7 | Adf35944 SYNAGIS a |

| | | | | | |
|----|-------|------|-----|---|--------------------|
| 25 | 544.5 | 72.1 | 450 | 9 | Adw20090 RSV antig |
| 26 | 544.5 | 72.1 | 450 | 9 | Adw20086 RSV antig |
| 27 | 544.5 | 72.1 | 450 | 9 | Adw20088 RSV-speci |
| 28 | 544.5 | 72.1 | 450 | 9 | Aeb07072 RSV-speci |
| 29 | 544.5 | 72.1 | 450 | 9 | Aeb07068 RSV-speci |
| 30 | 544.5 | 72.1 | 450 | 9 | Aeb07070 RSV-speci |
| 31 | 542.5 | 71.9 | 118 | 8 | Adf71910 Hu3G8VH-5 |
| 32 | 542.5 | 71.9 | 120 | 5 | Abp66409 Human RSV |
| 33 | 542.5 | 71.9 | 120 | 5 | Aae28064 Human mod |
| 34 | 542.5 | 71.9 | 120 | 6 | Abu69272 Respirato |
| 35 | 542.5 | 71.9 | 120 | 7 | Adf35767 SYNAGIS a |
| 36 | 542.5 | 71.9 | 120 | 8 | Adf56929 RSV antib |
| 37 | 542.5 | 71.9 | 120 | 8 | Adt89252 Humanised |
| 38 | 542.5 | 71.9 | 120 | 9 | Adw19909 RSV antig |
| 39 | 542.5 | 71.9 | 120 | 9 | Aeb06891 RSV-speci |
| 40 | 542.5 | 71.9 | 448 | 8 | Adf71916 Hu3G8VH-2 |
| 41 | 542.5 | 71.9 | 448 | 8 | Adf71912 Hu3G8VH-5 |
| 42 | 541.5 | 71.7 | 120 | 5 | Abp66405 Human RSV |
| 43 | 541.5 | 71.7 | 120 | 5 | Aae28060 Human mod |
| 44 | 541.5 | 71.7 | 120 | 6 | Abu69268 Respirato |
| 45 | 541.5 | 71.7 | 120 | 7 | Adf35763 SYNAGIS a |

ALIGNMENTS

RESULT 1
AAR70192
ID AAR70192 standard; protein; 141 AA.
XX AAR70192;
AC AC
XX 25-MAR-2003 (revised)
DT 20-SEP-1995 (first entry)
XX Humanized antibody 3B9 heavy chain.
XX Humanized antibody; antibody engineering; monoclonal antibody; MAb;
KW interleukin-4; IL-4; allergy.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..19
FT /label= Sig_peptide
FT Region 51..57
FT /label= CDR
FT /note= "complementarity determining region"
FT Region 72..87
FT /label= CDR
FT /note= "complementarity determining region"
FT Region 120..130
FT /label= CDR
FT /note= "complementarity determining region"
XX WO9507301-A1.
XX 16-MAR-1995.
XX 07-SEP-1994; 94WO-US010308.
XX 07-SEP-1993; 93US-00117366.
PR 14-OCT-1993; 93US-00136783.
XX (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX Holmes S, Gross MS, Sylvester DR;
PI WPI; 1995-123387/16.
XX N-PSDB; AAQ83493.
XX Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from

PT high affinity mAbs - useful in treatment of IL-4-mediated and IgE-mediated allergic conditions.

XX Disclosure; Fig 4; 97pp; English.

XX A humanized antibody heavy chain variable region and signal sequence is given in AAR70192. The signal sequence is also provided in AAR70193. The CDR sequences of the construct are identical to the native CDRs of mouse anti-human IL-4 MAB 3B9 (AAR70198-200). (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 141 AA;

XX Query Match 100.0%; Score 755; DB 2; Length 141;

XX Best Local Similarity 100.0%; Pred. No. 1.2e-62;

XX Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVLQTVFISLLWISGAYGVTLRESGPALVKPTQTLLTCTFSGFSLSTSGMGVSWIR 60

Db 1 MVLQTVFISLLWISGAYGVTLRESGPALVKPTQTLLTCTFSGFSLSTSGMGVSWIR 60

Qy 61 QPPGKGLEWLAHIYWDKRYNPSLKSRLTISKDTSRNQVLTMTNMDPVDVTATYYCARR 120

Db 61 QPPGKGLEWLAHIYWDKRYNPSLKSRLTISKDTSRNQVLTMTNMDPVDVTATYYCARR 120

Qy 121 ETVFYWYFDVWGRGTPVTVSS 141

Db 121 ETVFYWYFDVWGRGTPVTVSS 141

RESULT 2

AAAY23770

ID AAY23770 standard; protein; 141 AA.

XX AC AAY23770;

XX DT 13-SEP-1999 (first entry)

XX Heavy chain variable region of humanised murine IL-4 antibody 3B9.

XX Heavy chain variable region; interleukin-4; IL-4; antibody 3B9;

XX Chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;

XX Immunoglobulin E-mediated allergic reaction; allergic rhinitis;

XX conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;

XX rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.

XX Synthetic.

XX Mus sp.

XX Homo sapiens.

XX US5928904-A.

XX 27-JUL-1999.

XX 07-JUN-1995; 95US-00483632.

XX 07-SEP-1993; 93US-00117366.

XX 14-OCT-1993; 93US-00136783.

XX 07-SEP-1994; 94WO-US010308.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Holmes SD, Sylvester DR, Gross MS;

XX WPI; 1999-429500/36.

XX N-PSDB; AAX85887.

XX New DNA molecules encoding recombinant antibodies useful for treating IL4-mediated conditions.

XX Example 3; Fig 4; 50pp; English.

CC The present sequence represents the heavy chain variable region of a humanised murine interleukin-4 (IL-4) antibody 3B9. The specification describes chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host -versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans

XX Sequence 141 AA;

XX Query Match 100.0%; Score 755; DB 2; Length 141;

XX Best Local Similarity 100.0%; Pred. No. 1.2e-62;

XX Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVLQTVFISLLWISGAYGVTLRESGPALVKPTQTLLTCTFSGFSLSTSGMGVSWIR 60

Db 1 MVLQTVFISLLWISGAYGVTLRESGPALVKPTQTLLTCTFSGFSLSTSGMGVSWIR 60

Qy 61 QPPGKGLEWLAHIYWDKRYNPSLKSRLTISKDTSRNQVLTMTNMDPVDVTATYYCARR 120

Db 61 QPPGKGLEWLAHIYWDKRYNPSLKSRLTISKDTSRNQVLTMTNMDPVDVTATYYCARR 120

Qy 121 ETVFYWYFDVWGRGTPVTVSS 141

Db 121 ETVFYWYFDVWGRGTPVTVSS 141

RESULT 3

AAAY18117

ID AAY18117 standard; protein; 141 AA.

XX AC AAY18117;

XX DT 11-AUG-1999 (first entry)

XX Heavy chain sequence for humanised 3B9 antibody.

XX Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;

XX allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;

XX atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;

XX autoimmune disease; graft versus host disease.

XX Synthetic.

XX US5914110-A.

XX 22-JUN-1999.

XX 07-JUN-1995; 95US-00483636.

XX 07-SEP-1993; 93US-00117366.

XX 14-OCT-1993; 93US-00136783.

XX 07-SEP-1994; 94WO-US010308.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Sylvester DR, Holmes SD, Gross MS;

XX WPI; 1999-370482/31.

XX N-PSDB; AAX79516.

XX Recombinant IL4 antibodies useful for treatment of allergic rhinitis,

XX atopic asthma and anaphylactic shock.

XX Claim 15; Fig 4; 50pp; English.

XX This sequence represents the heavy chain of the humanised 3B9 antibody of the invention. The antibody is a chimeric or humanised interleukin-4

CC (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE)
 CC mediated diseases. The antibodies are useful for the treatment of
 CC allergic disorders such as allergic rhinitis, conjunctivitis, atopic
 CC dermatitis, atopic asthma and anaphylactic shock. The antibodies are also
 CC useful for regulating B and T cell proliferation and as such are useful
 CC in the treatment of autoimmune diseases and graft versus host disease

XX Sequence 141 AA;

Query Match 100.0%; Score 755; DB 2; Length 141;
 Best Local Similarity 100.0%; Pred. No. 1.2e-62; Indels 0; Gaps 0;
 Matches 141; Conservative 0; Mismatches 0;
 QY 1 MVLQTVFISLLWISGAYGVTLRESGPALVKPTQTLTLCTFGSFLSTSGMGVSWIR 60
 DB 1 MVLQTVFISLLWISGAYGVTLRESGPALVKPTQTLTLCTFGSFLSTSGMGVSWIR 60
 QY 61 QPQKGLWLAHIYWDKRYNPSLSKRLTISKOTSRNQVLTMTNMDPVDATYYCARR 120
 DB 61 QPQKGLWLAHIYWDKRYNPSLSKRLTISKOTSRNQVLTMTNMDPVDATYYCARR 120
 QY 121 ETVFYWYFDVWGRGTPVTVSS 141
 DB 121 ETVFYWYFDVWGRGTPVTVSS 141

RESULT 4

AAR70191
 ID AAR70191 standard; protein; 141 AA.

XX AAR70191;

XX 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 20-SEP-1995 (first entry)

DE Chimeric antibody 3B9 heavy chain.

XX Chimeric antibody; antibody engineering; monoclonal antibody; Mab;
 KW interleukin-4; IL-4; allergy.

XX Homo sapiens.
 OS Mus sp.

Key Location/Qualifiers
 FT Peptide 1..19
 FT Region 51..57
 FT /label= Sig_peptide
 FT /note= "complementarity determining region"
 FT Region 72..87
 FT /label= CDR
 FT /note= "complementarity determining region"
 FT Peptide 120..130
 FT /label= CDR
 FT /note= "complementarity determining region"

PN WO9507301-A1.

XX 16-MAR-1995.

XX 07-SEP-1994; 94WO-US010308.

XX 07-SEP-1993; 93US-00117366.

XX 14-OCT-1993; 93US-00136783.

XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.

XX Holmes S, Gross MS, Sylvester DR;

XX WPI; 1995-123387/16.

DR N-PSDB; AAQ83492.

XX

Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from
 high affinity mAb - useful in treatment of IL-4-mediated and IgE-
 mediated allergic conditions.

PS Disclosure; Fig 3; 97pp; English.

XX A human/mouse chimeric antibody heavy chain variable region was
 CC constructed (given in AAR70191) that contained the mouse anti-human IL-4
 CC Mab 3B9 variable region including 3 CDRs (AAR70198-200) and a human
 CC antibody signal peptide (AAR70193). The construct was used for humanized
 CC antibody production. (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 141 AA;

Query Match 87.8%; Score 663; DB 2; Length 141;
 Best Local Similarity 86.5%; Pred. No. 4.9e-54; Indels 0; Gaps 0;
 Matches 122; Conservative 10; Mismatches 9;
 QY 1 MVLQTVFISLLWISGAYGVTLRESGPALVKPTQTLTLCTFGSFLSTSGMGVSWIR 60
 DB 1 MVLQTVFISLLWISGAYGVTLRESGPALVKPTQTLTLCTFGSFLSTSGMGVSWIR 60
 QY 61 QPQKGLWLAHIYWDKRYNPSLSKRLTISKOTSRNQVLTMTNMDPVDATYYCARR 120
 DB 61 QPQKGLWLAHIYWDKRYNPSLSKRLTISKOTSRNQVLTMTNMDPVDATYYCARR 120
 QY 121 ETVFYWYFDVWGRGTPVTVSS 141
 DB 121 ETVFYWYFDVWGRGTPVTVSS 141

RESULT 5

AA23769

ID AA23769 standard; protein; 141 AA.

XX AA23769;

XX 17-OCT-2003 (revised)

DT 13-SEP-1999 (first entry)

XX Heavy chain variable region of murine/human chimeric antibody 3B9.

XX Heavy chain variable region; interleukin-4; IL-4; antibody 3B9;
 KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
 KW Immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.

XX Mus sp.

OS Homo sapiens.

OS Chimeric.

PN US5928904-A.

XX 27-JUL-1999.

XX 07-JUN-1995; 95US-00483632.

XX 07-SEP-1993; 93US-00117366.

PR 14-OCT-1993; 93US-00136783.

PR 07-SEP-1994; 94WO-US010308.

XX (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX Holmes SD, Sylvester DR, Gross MS;

XX WPI; 1999-429500/36.

DR N-PSDB; AA85886.

XX New DNA molecules encoding recombinant antibodies useful for treating IL4

XX WPI; 1995-123387/16.
 DR N-PSDB; AAQ83491.
 XX
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from
 PT high affinity mAbs - useful in treatment of IL-4-mediated and IgE-
 PT mediated allergic conditions.
 XX
 XX Disclosure; Fig 2; 97pp; English.
 XX
 CC Spleen cells from mice immunized with human IL-4 were used to prepare
 CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only clone
 CC 3B9 was positive. cDNA clones of the 3B9 light and heavy chains were
 CC cloned into pGEM7f+ and transformed into E. coli DH5-alpha. The clones
 CC were sequenced (AAQ83490-91), and used for antibody engineering. (Updated
 CC on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 140 AA;
 SQ

Query Match 76.4%; Score 577; DB 2; Length 140;
 Best Local Similarity 81.3%; Pred. No. 5.4e-46;
 Matches 109; Conservative 10; Mismatches 13; Indels 2; Gaps 1;
 10 SLLLLWISGAY--GQVTLRSGPALVKTPTLTCTFSGFSLSTSGMGVSWIRQPSGKGL 67
 7 SLLLLIVPAYVLSQVTLKESGPGILQPSQTLSTCSFGSFLSTSGMGVSWIRQPSGKGL 66
 68 EWLAIHYWDDDKRYNPSLKSRLTISKDTSRNOVLTMTNMDPVDATATYTCARRETVFYWY 127
 67 EWLAIHYWDDDKRYNPSLKSRLTISKDTSRNOVLTMTNMDPVDATATYTCARRETVFYWY 126
 128 FDVWGRGTPVTVSS 141
 127 FDVWGAGTTVTVSS 140

RESULT 8
 AAY23768
 ID AAY23768 standard; protein; 140 AA.
 XX
 AC AAY23768;
 XX
 DT 13-SEP-1999 (first entry)
 XX
 DE Heavy chain variable region of murine IL-4 antibody 3B9.
 XX
 KW Heavy chain variable region; interleukin-4; IL-4; antibody 3B9;
 KW Chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
 KW Immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.
 XX
 OS Mus sp.
 XX
 XX US5928904-A.
 XX
 XX 27-JUL-1999.
 XX
 XX 07-JUN-1995; 95US-00483632.
 XX
 XX 07-SEP-1993; 93US-00117366.
 XX 14-OCT-1993; 93US-00136783.
 XX 07-SEP-1994; 94WO-US010308.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PA
 XX Holmes SD, Sylvestre DR, Gross MS;
 XX
 XX WPI; 1999-429500/36.
 DR N-PSDB; AAX85885.
 XX
 PT New DNA molecules encoding recombinant antibodies useful for treating IL4

PT -mediated conditions.
 XX
 XX Example 3; Fig 2; 50pp; English.
 XX
 CC The present sequence represents the heavy chain variable region of murine
 CC interleukin-4 (IL-4) antibody 3B9. The sequences are used in the
 CC production chimeric and humanised IL-4 monoclonal antibodies. The
 CC antibodies of the invention are used in therapeutic and pharmaceutical
 CC compositions for treating IL-4 mediated and immunoglobulin E-mediated
 CC allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic
 CC dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host
 CC versus-graft disease and renal disease. They are also useful in the
 CC diagnosis of an allergy or condition associated with excess IL-4
 CC production through the measurement e.g. by ELISA of circulating
 CC endogenous IL-4 levels in humans
 XX
 XX Sequence 140 AA;
 SQ

Query Match 76.4%; Score 577; DB 2; Length 140;
 Best Local Similarity 81.3%; Pred. No. 5.4e-46;
 Matches 109; Conservative 10; Mismatches 13; Indels 2; Gaps 1;
 10 SLLLLWISGAY--GQVTLRSGPALVKTPTLTCTFSGFSLSTSGMGVSWIRQPSGKGL 67
 7 SLLLLIVPAYVLSQVTLKESGPGILQPSQTLSTCSFGSFLSTSGMGVSWIRQPSGKGL 66
 68 EWLAIHYWDDDKRYNPSLKSRLTISKDTSRNOVLTMTNMDPVDATATYTCARRETVFYWY 127
 67 EWLAIHYWDDDKRYNPSLKSRLTISKDTSRNOVLTMTNMDPVDATATYTCARRETVFYWY 126
 128 FDVWGRGTPVTVSS 141
 127 FDVWGAGTTVTVSS 140

RESULT 9
 AAY18121
 ID AAY18121 standard; protein; 140 AA.
 XX
 AC AAY18121;
 XX
 DT 11-AUG-1999 (first entry)
 XX
 DE Heavy chain sequence for murine 3B9 antibody.
 XX
 KW Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;
 KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
 KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
 KW autoimmune disease; graft versus host disease.
 XX
 OS Mus sp.
 XX
 XX US5914110-A.
 XX
 XX 22-JUN-1999.
 XX
 XX 07-JUN-1995; 95US-00483636.
 XX
 XX 07-SEP-1993; 93US-00117366.
 XX 14-OCT-1993; 93US-00136783.
 XX 07-SEP-1994; 94WO-US010308.
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA
 XX Sylvestre DR, Holmes SD, Gross MS;
 XX
 XX WPI; 1999-370482/31.
 DR N-PSDB; AAX79520.
 XX
 XX Recombinant IL4 antibodies useful for treatment of allergic rhinitis,
 PT atopic asthma and anaphylactic shock.
 XX

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PS Claim 24; Fig 2; 50pp; English.
XX
CC This sequence represents the heavy chain of the murine 3B9 antibody of
CC the invention. The antibody is a chimeric or humanised interleukin-4
CC (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE)
CC mediated diseases. The antibodies are useful for the treatment of
CC allergic disorders such as allergic rhinitis, conjunctivitis, atopic
CC dermatitis, atopic asthma and anaphylactic shock. The antibodies are also
CC useful for regulating B and T cell proliferation and as such are useful
CC in the treatment of autoimmune diseases and graft versus host disease
XX
SQ Sequence 140 AA;

Query Match      76.4%; Score 577; DB 2; Length 140;
Best Local Similarity 81.3%; Pred. No. 5.4e-46;
Matches 109; Conservative 10; Mismatches 13; Indels 2; Gaps 1;

QY 10 SILLWISGAY--GOVTLRESGPALVKPTQTLTLCTSFSGFSLSTSGMGVSWIRQPPGKGL 67
DB 7 SLLLLIVPAYVLQSQVTLKESGPGILQPSQTLSTLCTSFSGFSLSTSGMGVSWIRQPSGKGL 66

QY 68 EWLAIHYWDDDKRYNPSLKSRLTISKDTSRNQVVLTMNMDPVDATATYTCARRETFFVY 127
DB 67 EWLAIHYWDDDKRYNPSLKSRLTISKDTSRNQVFLKITSVDTADTATYTCARRETFFVY 126

QY 128 FDVWGRGTPVTVSS 141
DB 127 FDVWAGAGTTVTVSS 140

RESULT 10
AAV23780
ID AAV23780 standard; protein; 121 AA.
XX
AC AAV23780;
XX
DT 13-SEP-1999 (first entry)
XX
DE Heavy chain variable region of Ig NEW.
XX
KW Light chain variable region; interleukin-4; IL-4; antibody 3B9;
KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;
KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy;
KW Ig NEW.
XX
OS Synthetic.
XX
FN US5928904-A.
XX
PD 27-JUL-1999.
XX
PF 07-JUN-1995; 95US-00483632.
XX
PR 07-SEP-1993; 93US-00117366.
PR 14-OCT-1993; 93US-00136783.
PR 07-SEP-1994; 94WO-US010308.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Holmes SD, Sylvester DR, Gross MS;
XX
XX WPI; 1999-429500/36.
DR N-PSDB; AAX85929.
XX
XX New DNA molecules encoding recombinant antibodies useful for treating IL4
PT -mediated conditions.
XX
PS Disclosure; Col 65-66; 50pp; English.
XX
XX The specification describes chimeric and humanised IL-4 monoclonal
CC
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```
CC antibodies. The antibodies of the invention are used in therapeutic and
CC pharmaceutical compositions for treating IL-4 mediated and immunoglobulin
CC E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis,
CC atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid
CC arthritis, host-versus-graft disease and renal disease. They are also
CC useful in the diagnosis of an allergy or condition associated with excess
CC IL-4 production through the measurement e.g. by ELISA of circulating
CC endogenous IL-4 levels in humans. The present sequence represents the
CC heavy chain variable region of Ig NEW, and is used in the course of the
XX invention
XX
SQ Sequence 121 AA;

Query Match      73.2%; Score 553; DB 2; Length 121;
Best Local Similarity 81.8%; Pred. No. 8e-44;
Matches 99; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 21 QVTLRESGPALVKPTQTLTLCTSFSGFSLSTSGMGVSWIRQPPGKLEWLAHIYWDDDKR 80
DB 1 QVQLQESGPGILVRFPSQTLSTLCTSFSGFSLSTSGMGVSWIRQPPGKLEWLAHIYWDDDKR 60

QY 81 YNPSLKSRLTISKDTSRNQVVLTMNMDPVDATATYTCARRETFFVYFDVWGRGTPVTVS 140
DB 61 YNPSLKSRLTILKDTSKNQVSLRSLSSVTADTATYTCARRETFFVYFDVWGGQTTVTS 120

QY 141 S 141
DB 121 S 121

RESULT 11
AAV18122
ID AAV18122 standard; protein; 121 AA.
XX
AC AAV18122;
XX
DT 11-AUG-1999 (first entry)
XX
DE Heavy chain sequence for humanised 3B9 antibody.
XX
KW Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;
KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
KW autoimmune disease; graft versus host disease.
XX
OS Synthetic.
XX
FN US5914110-A.
XX
PD 22-JUN-1999.
XX
PF 07-JUN-1995; 95US-00483636.
XX
PR 07-SEP-1993; 93US-00117366.
PR 14-OCT-1993; 93US-00136783.
PR 07-SEP-1994; 94WO-US010308.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI Sylvester DR, Holmes SD, Gross MS;
XX
XX WPI; 1999-370482/31.
DR N-PSDB; AAX79527.
XX
XX Recombinant IL4 antibodies useful for treatment of allergic rhinitis,
PT atopic asthma and anaphylactic shock.
XX
PS Example 3; Col 65-66; 50pp; English.
XX
XX This sequence represents the heavy chain of the humanised 3B9 antibody of
CC the invention. The antibody is a chimeric or humanised interleukin-4
CC (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE)
```


CC mediated diseases. The antibodies are useful for the treatment of
CC allergic disorders such as allergic rhinitis, conjunctivitis, atopic
CC dermatitis, atopic asthma and anaphylactic shock. The antibodies are also
CC useful for regulating B and T cell proliferation and as such are useful
XX in the treatment of autoimmune diseases and graft versus host disease
XX
SQ Sequence 121 AA;
SQ

| | |
|-----------|---|
| XX | New humanized 10D5 antibody, useful for the manufacture of a medicament for treating Down's syndrome, clinical or pre-clinical Alzheimer's disease or cerebral amyloid angiopathy. |
| XX | Disclosure; Page 13-15; 52pp; English. |
| XX | The present sequence is the protein sequence of the heavy chain of a humanised antibody of the present invention. In the variable portion, the complementarity determining regions (CDRs) originate from murine monoclonal antibody 10D5 and the framework region originates from human germline VH segment DP-28 and J segment JH4. Novel humanised antibodies of the invention have CDRs from 10D5 and human framework sequences. These humanised antibodies have binding affinities (affinity and epitope location) approximately the same as those of the mouse 10D5 antibody. The invention includes antibodies, single chain antibodies, and their fragments, as well as nucleotide sequences, vectors, transformed host cells, and methods of using the humanised antibody to treat, prevent, alleviate, reverse or otherwise ameliorate symptoms and/or pathology associated with Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise OS field) |
| XX | Sequence 472 AA; |
| SQ | Query Match 73.0%; Score 551; DB 6; Length 472; Best Local Similarity 80.9%; Pred. No. 5 5e-43; Matches 110; Conservative 5; Mismatches 17; Indels 4; Gaps 2; |
| QY | 10 SLLLTWISGAY--GGVTLRSGPALVKPTQLTLCITFSGFSLSGTSGMGVSWIRQPFGKGL 67 |
| DB | 7 SFELLIVPAYVLSSQVTLKESGPVLKPTETLTLCTCFSGFSLSGTSGMGVSWIRQPFGKAL 66 |
| QY | 68 EWLAHIYWDDDKRYNPSLSRLTSIKDTSRNQVLTMTNMDPVDATYYICARR--ETVPFY 125 |
| DB | 67 EWLAHIYWDDDKRYNPSLSRLTSIKDTSKSVLTMTNMDPVDATYYICVRRPITPVLV 126 |
| QY | 126 WYFDVMVGRGFPVTVSS 141 |
| DB | 127 DAMDYWGQGTLTVSS 142 |
| RESULT 13 | |
| ABG31445 | |
| ID | ABG31445 standard; protein; 139 AA. |
| XX | ABG31445; |
| AC | |
| XX | |
| DT | 29-NOV-2002 (first entry) |
| XX | |
| DE | Amino acid sequence for humanised antibody 1129 VH. |
| XX | |
| KW | Human-murine chimeric antibody; humanised antibody; CDR; |
| KM | complementarity determining region; variable heavy chain; VH; |
| KW | variable light chain; VL; monoclonal antibody; MAb; RSV infection; |
| KW | respiratory syncytial virus infection; virucide; 1129 VH; mutant; mutein. |
| XX | |
| OS | Homo sapiens. |
| OS | Mus sp. |
| OS | Synthetic. |
| OS | Chimeric. |
| XX | |
| PN | US2002102257-A1. |
| XX | |
| PD | 01-AUG-2002. |
| XX | |
| PF | 21-SEP-1998; 98US-00158120. |
| XX | |
| PR | 21-SEP-1998; 98US-00158120. |
| XX | |
| PA | (JOHN/) JOHNSON L S. |
| XX | |

immune response; haemostatic; antirheumatic; antiarthritic;
 dermatological; immunosuppressive; antiinflammatory; antianaemic;
 vasotropic; nephrotropic; neuroprotective; antipsoriatic; uropathic;
 ophthalmological; antiaesthetic; inflammatory response;
 autoimmune disease; idiopathic thrombocytopenic purpura;
 rheumatoid arthritis; systemic lupus erythematosus;
 autoimmune haemolytic anaemia; scleroderma;
 autoantibody triggered urticaria; pemphigus; vasculitis syndrome;
 systemic vasculitis; Goodpasture's syndrome; multiple sclerosis;
 psoriatic arthritis; ankylosing spondylitis; Sjogren's syndrome;
 Reiter's syndrome; Kawasaki's disease; polymyositis; dermatomyositis;
 allergic asthma.

XX
 OS Synthetic.
 OS Mus sp.
 OS Homo sapiens.
 XX
 PN WO2003101485-A1.
 XX
 PD 11-DEC-2003.
 XX
 XX 29-MAY-2003; 2003WO-US017111.
 XX
 XX 30-MAY-2002; 2002US-0384689P.
 PR 10-JAN-2003; 2003US-0439320P.
 XX
 XX (MACR-) MACROGENICS INC.
 XX
 PI Johnson LS, Huang L, Li H, Tuallon N;
 XX
 XX WPI; 2004-042985/04.
 XX
 XX Novel anti-CD16A antibody comprising complementarity determining regions
 PT derived from mouse 3G8 antibody and humanized anti-CD16A antibody that
 PT lacks effector function, useful for treating deleterious immune response.
 XX
 PS Disclosure; SEQ ID NO 107; 103pp; English.
 XX
 XX The present invention describes an anti-CD16A antibody (I) comprising a
 CC VH domain comprising complementarity determining regions (CDRs) derived
 CC from the mouse 3G8 antibody heavy chain and a VL domain comprising CDRs
 CC derived from the mouse 3G8 antibody light chain or a humanised anti-CD16A
 CC antibody (II) that lacks effector function and comprises all six CDRs of
 CC mouse antibody 3G8. Also described is a method (M1) for reducing a
 CC deleterious immune response in a mammal in need of such reduction, which
 CC involves administering to the mammal a CD16A binding protein comprising
 CC an Fc region derived from a human IgG heavy chain, where the Fc region
 CC lacks effector function or is modified to reduce binding to an Fc
 CC effector ligand. (I) and (II) have haemostatic, antirheumatic,
 CC antiarthritic, dermatological, immunosuppressive, antiinflammatory,
 CC antianaemic, vasotropic, nephrotropic, neuroprotective, antipsoriatic,
 CC uropathic, ophthalmological and antiaesthetic activities. (I) or (II) is
 CC useful for reducing a deleterious immune response in a mammal which
 CC involves administering to the mammal (I) or (II). The deleterious immune
 CC response is an inflammatory response caused by autoimmune disease such as
 CC idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA),
 CC systemic lupus erythematosus (SLE), autoimmune haemolytic anaemia (AHA),
 CC scleroderma, autoantibody triggered urticaria, pemphigus, vasculitis
 CC syndrome, systemic vasculitis, Goodpasture's syndrome, multiple sclerosis
 CC (MS), psoriatic arthritis, ankylosing spondylitis, Sjogren's syndrome,
 CC Reiter's syndrome, Kawasaki's disease, polymyositis and dermatomyositis
 CC and also for treating diseases susceptible to treatment with intravenous
 CC immunoglobulin (IVIg) therapy e.g., allergic asthma. The present sequence
 CC is used in the exemplification of the present invention.
 XX
 SQ Sequence 448 AA;

Query Match 72.4%; Score 546.5; DB 8; Length 448;
 Best Local Similarity 86.0%; Pred. No. 1.4e-42;
 Matches 104; Conservative 6; Mismatches 8; Indels 3; Gaps 1;

QY 21 QVTLRESGPAVKPTQTTLTCTTSGFSLSTSGMGVMIROPPGKALEWLAHIWDDDKR 80
 |||||

Db 1 QVTLRESGPAVKPTQTTLTCTTSGFSLSTSGMGVMIROPPGKALEWLAHIWDDDKR 60
 QY 81 YNPISLKSRLTISKDTSRNOVLTMNMDPVDATATYTCARRETVFYWYFDVWGRGTPVTYS 140
 Db 61 YNPALKSRLLTISKDTSRNOVLTMNMDPVDATATYTCARINPAWFAY---WGQGLTVTVS 117
 QY 141 S 141
 Db 118 S 118

Search completed: February 23, 2006, 09:18:03
 Job time : 137.298 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 09:18:23 ; Search time 24.8824 Seconds
(without alignments)
545.228 Million cell updates/sec

Title: US-10-723-872-12
Perfect score: 755
Sequence: 1 MVLPQVFIISLLWISGAYG.....TVFYWYFDWGRGTPVTVS 141

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | ID | Description |
|------------|-------|-------|--------|----------|--------------------|
| 1 | 523.5 | 69.3 | 138 | 2 S31513 | Ig heavy chain - h |
| 2 | 515.5 | 68.3 | 124 | 2 A49002 | Ig heavy chain v r |
| 3 | 509 | 67.4 | 121 | 2 A36005 | Ig heavy chain v r |
| 4 | 498.5 | 66.0 | 120 | 1 G1HUCO | Ig heavy chain v-I |
| 5 | 493.5 | 65.4 | 143 | 2 PT0174 | Ig heavy chain pre |
| 6 | 492.5 | 65.2 | 122 | 2 S11740 | Ig heavy chain v r |
| 7 | 484.5 | 64.2 | 119 | 2 S18555 | Ig heavy chain v r |
| 8 | 483.5 | 64.0 | 374 | 2 S69339 | Ig heavy chain v r |
| 9 | 476 | 63.0 | 125 | 1 MHHUMC | Ig heavy chain v-I |
| 10 | 460 | 60.9 | 121 | 1 G1HUHE | Ig heavy chain v-I |
| 11 | 458.5 | 60.7 | 113 | 2 S26465 | Ig heavy chain v r |
| 12 | 458 | 60.7 | 118 | 2 S18556 | Ig heavy chain v r |
| 13 | 455 | 60.3 | 147 | 1 G2HUCS | Ig heavy chain pre |
| 14 | 448 | 59.3 | 96 | 2 S26923 | Ig heavy chain v r |
| 15 | 448 | 59.3 | 96 | 2 S26924 | Ig heavy chain v r |
| 16 | 445.5 | 59.0 | 116 | 2 S26328 | Ig heavy chain v r |
| 17 | 433 | 57.4 | 121 | 2 S09959 | Ig heavy chain v r |
| 18 | 425.5 | 56.4 | 126 | 1 MHHUOU | Ig heavy chain v-I |
| 19 | 423 | 56.0 | 107 | 2 A49442 | Ig heavy chain v r |
| 20 | 417 | 55.2 | 96 | 2 S26922 | Ig heavy chain v r |
| 21 | 413 | 54.7 | 119 | 1 G1HUDW | Ig heavy chain v-I |
| 22 | 396 | 52.5 | 103 | 2 B25913 | Ig heavy chain pre |
| 23 | 379 | 50.2 | 146 | 2 S09711 | Ig heavy chain v r |
| 24 | 378.5 | 50.1 | 130 | 2 S31690 | Ig heavy chain v r |
| 25 | 375.5 | 49.7 | 140 | 2 I37782 | Ig variable region |
| 26 | 370.5 | 49.1 | 147 | 2 S13519 | Ig heavy chain v r |
| 27 | 370.5 | 49.1 | 155 | 2 S31511 | Ig heavy chain - h |
| 28 | 368.5 | 48.8 | 155 | 2 S31512 | Ig heavy chain - h |
| 29 | 368 | 48.7 | 128 | 2 S31514 | Ig heavy chain - h |

| | | | | | |
|----|-------|------|-----|----------|--------------------|
| 30 | 368 | 48.7 | 231 | 2 PC4155 | Ig gamma-2b chain |
| 31 | 366.5 | 48.5 | 130 | 2 S30534 | Ig heavy chain v r |
| 32 | 365.5 | 48.4 | 139 | 2 A32456 | Ig heavy chain pre |
| 33 | 365 | 48.3 | 139 | 2 A41287 | Ig heavy chain pre |
| 34 | 356.5 | 47.2 | 135 | 2 PL0100 | Ig heavy chain pre |
| 35 | 355 | 47.0 | 123 | 2 S30530 | Ig heavy chain v r |
| 36 | 355 | 47.0 | 144 | 1 G2MS14 | Ig heavy chain pre |
| 37 | 355 | 47.0 | 145 | 2 S78055 | Ig heavy chain pre |
| 38 | 354.5 | 47.0 | 129 | 2 S44114 | Ig heavy chain v r |
| 39 | 354 | 46.9 | 137 | 2 S31676 | Ig heavy chain v r |
| 40 | 353.5 | 46.8 | 122 | 2 S20809 | Ig heavy chain v r |
| 41 | 353.5 | 46.8 | 121 | 2 S54226 | Ig mu heavy chain |
| 42 | 352.5 | 46.7 | 135 | 2 S78051 | Ig heavy chain pre |
| 43 | 352 | 46.6 | 121 | 2 S44113 | Ig heavy chain v r |
| 44 | 351.5 | 46.6 | 146 | 2 S09710 | Ig heavy chain v r |
| 45 | 351 | 46.5 | 78 | 2 S46461 | Ig heavy chain v r |

ALIGNMENTS

RESULT 1

S31513

Ig heavy chain - human

C:Species: Homo sapiens (man)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C:Accession: S31513

R:Chastagner, P.; Demaison, C.; These, J.; Zouali, M.

submitted to the EMBL Data Library, December 1992.

A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto

A:Reference number: S31509

A:Accession: S31513

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-138 <CHA>

A:Cross-references: UNIPARC:UPI00001160FA; EMBL:X69861; NID:g33084; PIDN:CAA49495.1. PII

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:30-114/Domain: immunoglobulin homology <IMM>

Query Match 69.3%; Score 523.5; DB 2; Length 138;

Best Local Similarity 72.9%; Pred. No. 1.3e-39;

Matches 102; Conservative 13; Mismatches 20; Indels 5; Gaps 2;

QY 3 LQTVFISLLWISGAYGQVTLRESGPAVKPTQTLTCTFSGSLSTSGMGVSIROP 62

Db 1 LSTLLLPSPVW---LSQITLKESGPTLVKPTQTLTCTFSGSLSTSGMGVSIROP 57

QY 63 PGKGLEWLAHIYDDDKRYNPSLKRITISKDTSRNQVLTMTNMDPVDATYTCARRE- 121

Db 58 PGKTTLEWLAHIYDDDKRYNPSLKRITISKDTSRNQVLTMTNMDPVDATYTCARPG 117

QY 122 -TVFYWYFDWGRGTPVTVS 140

Db 118 IAVTGNFDYWGQGLTVTS 137

RESULT 2

A49002

Ig heavy chain V region, rheumatoid factor RF antibody - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999

C:Accession: A49002

R:Stuber, F.; Lee, S.K.; Bridges Jr., S.L.; Koopman, W.J.; Schroeder, H.W.J.; Gaskin, F.

Arthritis Rheum. 35, 900-904, 1992

A:Title: A rheumatoid factor from a normal individual encoded by VH2 and V kappa II gene

A:Reference number: A49002; MUID:92352481; PMID:1322670

A:Accession: A49002

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-124 <STUS>

A:Cross-references: UNIPARC:UPI0000176978; GB:M90808; NID:g185515; PIDN:AAAS2989.1; PID

A:Experimental source: EBV-transformed lymphoblastoid cell line S8H23

A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: UNIPARC:UPI0000176F24; EMBL:X81695
R:Khamlinchi, A.A.
submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140,'C','142-374 <KH2>
A:Cross-references: UNIPARC:UPI0000176F25; EMBL:X81695
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 64.0%; Score 483.5; DB 2; Length 374;
Best Local Similarity 64.3%; Pred.No.1.3e-35;
Matches 92; Conservative 21; Mismatches 25; Indels 5; Gaps 2

QY 1 MYLQTQVTSLLMIWISGAYGVQLRRSGPALVKPTQLTLTCTPSGSLSTSGMGVSWIR 60
DB : : : : :
3 ILCSLTLLLTIPSFW--LSQIFLKESGPLVKPTQLTLTCTPSGSLSKSGVGWGVR 59
QY 61 QPBGKGLEWLHIYDDDKRYNPSLKSRLTISKDTSNOVLTMNDPVDVTATYYCARR 120
DB : : : : :
60 QPPGOALEWLALIFDWDKKRYSPLRLTITKDTSKNQVLTMNVDPADTATYYCGYS 119
QY 121 ETVF--YWYFDVMGRGTPVTSS 141
DB : : : : :
120 VEGYGQGYRFHSGQGTLTVSS 142

RESULT 9
MHMUMC
Ig heavy chain V-II region (McE) - human
C:Species: Homo sapiens (man)
C>Date: 14-Nov-1983 #sequence_revision 22-Nov-1983 #text_change 09-Jul-2004
C:Accession: A02092
R:Gerber-Jenson, B.; Kazin, A.; Kehoe, J.M.; Scheffel, C.; Erickson, B.W.; Litt,
J. Immunol. 126, 1212-1216, 1981
A:Title: Molecular basis for the temperature-dependent insolubility of cryoglobulin
A:Reference number: A02092; MUID:8118242; PMID:6780622
A:Accession: A02092
A:Molecule type: protein
A:Residues: 1-125 <GER>
A:Cross-references: UNIPROT:P01817; UNIPARC:UPI000012CEED
A>Note: This chain was derived from a monoclonal IgM cryoimmunoglobulin
C:Genetics:
A:Gene: GDB:IGHV@
A:Cross-references: GDB:128528; OMIM:147070
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F:15-99/Domain: immunoglobulin homology <IMW>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 63.0%; Score 476; DB 1; Length 125;
Best Local Similarity 71.9%; Pred.No.1.9e-35;
Matches 92; Conservative 11; Mismatches 15; Indels 10; Gaps 2

QY 21 QVTLRESGPALKVPTQLTLTCTPSGSLSTSGMGVSWIRPPGKGLEWLAIHYDDDKR 80
DB : : : : :
1 QITLKESGPLVKPTETLTITCTPSGSLSTSGVGWIRQRPCKALEWLAFINWDDNR 60
QY 81 YNPSSLKRLTISKDTSRNQVLTMNDPVDVTATYYCARRETFYKY-----FDWGR 133
DB : : : : :
61 YSPSLSRLTGTGKDTSRNQVLITNMNDPVDSGTYFCARPPP---WRFTGNLGGFDFXWQ 117
QY 134 GTPTVSS 141
DB 118 GLTLTVSS 125

RESULT 10

GIHUHE
Ig heavy chain V-II region (He) - human
C:Species: Homo sapiens (man)
C>Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 09-Jul-2004
C:Accession: A02093
R:Cunningham, B.A.; Pflumm, M.N.; Rutishauser, U.; Edelman, G.M.
Proc. Natl. Acad. Sci. U.S.A. 64, 997-1003, 1969
A>Title: Subgroups of amino acid sequences in the variable regions of immunoglobulin heavy chain locus: cl
A:Reference number: A02093; MUID:70114712; PMID:5264153
A:Accession: A02093
A:Molecule type: protein
A:Residues: 1-121 <CUN>
A:CROSS-references: UNIPROT:P01818; UNIPARC:UPI000012CBEF
C:Comment: This gamma-1 chain was isolated from a myeloma protein.
C:Genetics:
A:Gene: GDB:IGHV@
A:CROSS-references: GDB:128528; OMIM:147070
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: blocked amino end; heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>
F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status
Query Match 60.9%; Score 460; DB 1; Length 121;
Best Local Similarity 71.0%; Pred. No. 4.9e-34;
Matches 88; Conservative 15; Mismatches 15; Indels 6; Gaps 3;
QY 21 QVTLRESGPAIVKPTQTLLTCTFSGFSLSGSGVSWIRPPGKGLEWLAH-IYWDGDK 79
Db 1 QVTLKENGPTLVKPTETLLTCTLSGLSLTTDGVAVGIRQPGRALEWLAHLLYWDGDK 60
QY 80 RYNPSLKRLTISKDTSRNOVLTMTNMDPVDATYTCARR--ETVFWYFDVWGRGPTV 137
Db 61 RFPSPSKSLRTVTRDTSKNQVLTMTNMDPVDATYTCVHRHPTL---AFDVWGQGTKV 117
QY 138 TVSS 141
Db 118 AVSS 121
RESULT 11
S26465
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S26465
R:Kavaler, J.
submitted to the EMBL Data Library, April 1991
A:Reference number: S26459
A:Accession: S26465
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <KAV>
A:CROSS-references: UNIPARC:UPI0000115P69; EMBL:X59115; NID:g51928; PIDN:CAA41841.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:6-90/Domain: immunoglobulin homology <IMM>
Query Match 60.7%; Score 458.5; DB 2; Length 113;
Best Local Similarity 75.9%; Pred. No. 6.2e-34;
Matches 85; Conservative 11; Mismatches 13; Indels 3; Gaps 1;
QY 31 LVKPTQTLLTCTFSGFSLSGSGVSWIRPPGKGLEWLAHIYWDGDKRYPNPSLSKRLT 90
Db 2 ILKPSQTLSTCTFSGFSLSGSGVSWIRQPSGKGLEWLAHIWDDDKYYPNPSLSKSLT 61
QY 91 ISKDTSRNOVLTMTNMDPVDATYTCARR---TVFWYFDVWGRGPTV 139
Db 62 ISKDTSRNQVFLKITSVTDATYTCARRAGGYGNYGWYFDVWGAGTTVT 113
RESULT 12
S18556

Ig heavy chain V region precursor (VII-5b) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C:Accession: S18556
R:Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; I
EMBO J. 10, 3641-3645, 1991
A>Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A:Reference number: S18551; MUID:92037524; PMID:1935893
A:Accession: S18556
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-118 <SHI>
A:CROSS-references: UNIPARC:UPI0000115FEC; EMBL:X62108; NID:g37840; PIDN:CAA44018.1; PID
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-118/Product: Ig heavy chain V region (VII-5b) #status predicted <MAT>
F:34-116/Domain: immunoglobulin homology <IMM>
Query Match 60.7%; Score 458; DB 2; Length 118;
Best Local Similarity 75.9%; Pred. No. 7.2e-34;
Matches 88; Conservative 10; Mismatches 14; Indels 4; Gaps 2;
QY 5 TQVFISLLWTSYGAYGQVTLRESGPAIVKPTQTLLTCTFSGFSLSGSGVSWIRQPPG 64
Db 7 TLLLTTPISW---LSQITLKESGPTLVKPTQTLLTCTFSGFSLSGSGVSWIRQPPG 62
QY 65 KGLEWLAHIYWDGDKRYPNPSLSKRLTISKDTSRNOVLTMTNMDPVDATYTCARR 120
Db 63 KALEWLAHIYWDGDKRYPNPSLSKRLTISKDTSRNOVLTMTNMDPVDATYTCARR 118
RESULT 13
G2HUCS
Ig heavy chain precursor V-II region (Cess) - human
C:Species: Homo sapiens (man)
C>Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C:Accession: A02090
R:Takahashi, N.; Noma, T.; Honjo, T.
Proc. Natl. Acad. Sci. U.S.A. 81, 5194-5198, 1984
A>Title: Rearranged immunoglobulin heavy chain variable region (V-H) pseudogene that del
A:Reference number: A02090; MUID:84298107; PMID:6089186
A:Accession: A02090
A:Molecule type: mRNA
A:Residues: 1-147 <TAK>
A:CROSS-references: UNIPROT:P04438; UNIPARC:UPI0000012CEFO
A>Note: the sequence was determined from the differentiated gene
A>Note: the authors translated the codon GGG for residue 16 as Trp, TGG for residue 142
as Ser, and CAG for residue 147 as Ser
C:Genetics:
A:Gene: GDB:IGHV@
A:CROSS-references: GDB:128528; OMIM:147070
A:Map position: 14q32.33-14q32.33
A:Introns: 15/3
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-147/Product: Ig heavy chain V-II region (Cess) #status predicted <MAT>
F:34-118/Domain: immunoglobulin homology <IMM>
F:119-132/Region: D segment
F:133-147/Region: J segment
Query Match 60.3%; Score 455; DB 1; Length 147;
Best Local Similarity 67.7%; Pred. No. 1.7e-33;
Matches 90; Conservative 10; Mismatches 25; Indels 8; Gaps 2;
QY 11 LLLMTI-SGAYGQVTLRESGPAIVKPTQTLLTCTFSGFSLSGSGVSWIRQPPGKGLEW 69
Db 9 LLLTVPSGVLSQVNLRESGPAIVKATHTLLTCTFSGFSLSGSGVSWIRQPPGKALEW 68

Search completed: February 23, 2006, 09:23:57
Job time : 25.8824 secs

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| Result No. | Query | | | DB | ID | Description |
|------------|-------|-------|--------|----|--------------|---------------------|
| | Score | Match | Length | | | |
| 1 | 523.5 | 69.3 | 493 | 2 | Q569J1_HUMAN | Q569j1 homo sapien |
| 2 | 515 | 68.2 | 121 | 2 | Q9UL96_HUMAN | Q9ul96 homo sapien |
| 3 | 508.5 | 67.4 | 617 | 2 | Q598B3_RAT | Q598b3 rattus norv |
| 4 | 501.5 | 66.4 | 485 | 2 | Q56IM5_MOUSE | Q56im5 mus musculus |
| 5 | 498.5 | 66.0 | 120 | 1 | HV2B_HUMAN | P01815 homo sapien |
| 6 | 476 | 63.0 | 125 | 1 | HV2D_HUMAN | P01817 homo sapien |
| 7 | 460.5 | 61.0 | 118 | 2 | Q81IU5_MOUSE | Q81iu5 mus musculus |
| 8 | 460 | 60.9 | 121 | 1 | HV2B_HUMAN | P01818 homo sapien |
| 9 | 455 | 60.3 | 147 | 1 | HV2H_HUMAN | P04438 homo sapien |
| 10 | 445 | 58.9 | 485 | 2 | Q58E54_MOUSE | Q58e54 mus musculus |
| 11 | 442 | 58.5 | 487 | 2 | Q58E53_MOUSE | Q58e53 mus musculus |
| 12 | 438.5 | 58.1 | 482 | 2 | Q5VLR6_RAT | Q5v1r6 rattus norv |
| 13 | 425.5 | 56.4 | 126 | 1 | HV2A_HUMAN | P01814 homo sapien |
| 14 | 422 | 55.9 | 97 | 2 | Q43234_HUMAN | Q43234 homo sapien |
| 15 | 413 | 54.7 | 119 | 1 | HV2C_HUMAN | P01816 homo sapien |
| 16 | 367 | 48.6 | 477 | 2 | Q510J1_RAT | Q510j1 rattus norv |
| 17 | 366 | 48.5 | 576 | 2 | Q6P418_HUMAN | Q6p418 homo sapien |
| 18 | 365.5 | 48.4 | 476 | 2 | Q6GMX1_HUMAN | Q6gmx1 homo sapien |
| 19 | 362.5 | 48.0 | 483 | 2 | Q5U413_MOUSE | Q5u413 mus musculus |
| 20 | 361.5 | 47.9 | 492 | 2 | Q72374_HUMAN | Q72374 homo sapien |
| 21 | 360 | 47.7 | 465 | 2 | Q6GMX6_HUMAN | Q6gmx6 homo sapien |
| 22 | 358 | 47.4 | 119 | 2 | Q9UL73_HUMAN | Q9ul73 homo sapien |
| 23 | 356 | 47.2 | 469 | 2 | Q5W839_RAT | Q5w839 rattus norv |
| 24 | 355 | 47.0 | 144 | 1 | HV43_MOUSE | P01819 mus musculus |
| 25 | 350.5 | 46.4 | 121 | 2 | Q99NG4_MOUSE | Q99ng4 mus musculus |
| 26 | 346 | 45.8 | 478 | 2 | Q72379_HUMAN | Q72379 homo sapien |
| 27 | 345.5 | 45.8 | 591 | 2 | Q510L9_RAT | Q510l9 rattus norv |
| 28 | 343.5 | 45.5 | 482 | 2 | Q91X92_MOUSE | Q91x92 mus musculus |
| 29 | 342 | 45.3 | 137 | 1 | HV46_MOUSE | P01822 mus musculus |
| 30 | 342 | 45.3 | 458 | 2 | Q5W842_RAT | Q5w842 rattus norv |
| 31 | 341.5 | 45.2 | 484 | 2 | Q5U472_MOUSE | Q5u472 mus musculus |

```
QY 65 KGLEWLAHIYWDKRYNPSLSKSLRTISKDTSRNOQVLTMTNMDPVDATYYCARRETVF 124
Db 64 KALEWLAHIYWNDDKRHRPSLSKSLRTITKDTSKNQVLTMTNMDPVDATYYCAHKYSGS 123
QY 125 YWYFDVWGRGTPVTVSS 141
Db 124 WNAFDWQGTMTVTVSS 140

RESULT 2
Q9UL96 HUMAN
ID Q9UL96_1 HUMAN PRELIMINARY; PRT; 121 AA.
AC Q9UL96_1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
D# Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF05018; AAD56254.1; -; mRNA.
DR HSSP; P01820; 1A7N.
DR SMR; Q9UL96; 1-121.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13695 MW; D502D450596BDD35 CRC64;

Query Match 68.2%; Score 515; DB 2; Length 121;
Best Local Similarity 80.2%; Pred. NO. 4.2e-44;
Matches 97; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 21 QVTLRESGALVKPTQTTLTCTFSGSLSTSGMGVSWIROPPGKLEWLAHIYWDKDR 80
Db 1 QITLKESGTLVKPTQTTLTCTFSGSLSTSGMGVSWIROPPGKLEWLAHIYWDKDR 60
QY 81 YNPSLSKSLRTISKDTSRNOQVLTMTNMDPVDATYYCARRETVFYWYFDVWGRGTPVTVS 140
Db 61 YSPSLKSLRTITKDTSKNQVLTMTFMDPMDATYYCAHKSGDGYFYDYWGQGLTVTVS 120
QY 141 S 141
Db 121 S 121

RESULT 3
Q569B3 RAT
ID Q569B3_RAT PRELIMINARY; PRT; 617 AA.
AC Q569B3;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE LOC314521 protein.
GN Name=LOC314521;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
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OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T.I., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McQuinn P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.N.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC092586; AA92586.1; -; mRNA.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG ci.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 4.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00407; IGci; 4.
DR PROSITE; PS50835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 617 AA; 68362 MW; 5943B1AFDD14C460 CRC64;

Query Match 67.4%; Score 508.5; DB 2; Length 617;
Best Local Similarity 72.6%; Pred. No. 1.2e-42;
Matches 98; Conservative 12; Mismatches 22; Indels 3; Gaps 2;

QY 10 SLLLIWISGAY--GQVTLRESGALVKPTQTTLTCTFSGSLSTSGMGVSWIROPPGKGL 67
Db 7 SFLLLIYPAYVLVSQVTLKESGPGILQPSQTLTCTFSGSLSTSGMGVSWIROPPGKGL 66
QY 68 EWLAIHWDDDKRYNPSLSKSLRTISKDTSRNOQVLTMTNMDPVDATYYCARRETV-FYW 126
Db 67 EWLAIHWDDDKRYNPSLSKSLRTISKDTSRNOQVLTMTNMDPVDATYYCARIATGYW 126
QY 127 YFDVWGRGTPVTVSS 141
Db 127 YFDVWGRGTPVTVSS 141

RESULT 4
Q561M5 MOUSE
ID Q561M5_MOUSE PRELIMINARY; PRT; 485 AA.
AC Q561M5;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE LOC238447 protein (Fragment).
GN Name=LOC238447;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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DE DE Ig heavy chain V-II region COR.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=70258837; PubMed=5449120;
RA Press E.M., Hogg N.M.;
RT "The amino acid sequences of the Fd fragments of two human gamma-1
RT heavy chains."
RL Biochem. J. 117:641-660(1970).
CC -I- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
CC protein.
CC -I- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC
DR PIR; A02089; GIHUCO.
DR HSSP; P01820; IAYN.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS08335; IG_LIKE; 1.
DR Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 110
FT MOD_RES 1 1 Ig-like.
FT CARBOHYD 62 62 Pyrrolidone carboxylic acid.
FT DISULFID 22 94 N-linked (GlcNAc. .).
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13226 MW; 158A8B29AE7EEB98 CRC64;

Query Match 66.0%; Score 498.5; DB 1; Length 120;
Best Local Similarity 81.3%; Pred. No. 2e-42;
Matches 100; Conservative 5; Mismatches 13; Indels 5; Gaps 2;

Qy 21 QVTLRESGPAVKPTQTLLTCTFSGFSLSTSGMGYSWIRQPPGKGLEWLAHYWDDDKR 80
Db 1 QVTLRESGPAVKPTQTLLTCTFSGFSLSTSGMGYSWIRQPPGKGLEWLAHYWDDDKY 60

Qy 81 YNPGLSKRLTISKDTSRNQVLTMTNMNDPVDVTATYYCARRET--FYWFDVMGRGTPVT 138
Db 61 YNTSLTSLTISKDTSRNQVLT--MDPVDVTATYYCARITVTPAPAGYMDVWGRGTPVT 117

Qy 139 VSS 141
Db 118 VSS 120

RESULT 6
HV2D_HUMAN STANDARD; PRT; 125 AA.
AC P0187;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-II region NCE.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.

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RX MEDLINE=81118242; PubMed=6780622;
RA Gerber-Jenson B., Kazin A., Kehoe J.M., Scheffel C., Erickson B.W.,
RA Litman G.W.;
RT "Molecular basis for the temperature-dependent insolubility of
RT cryoglobulins. X. The amino acid sequence of the heavy chain variable
RT region of MCG."
RL J. Immunol. 126:1212-1216(1981).
CC -!- MISCELLANEOUS: This chain was derived from a monoclonal IgM
CC cryoglobulin.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC removed.
CC
CC PIR: A02092; MHUMC.
DR HSSP; P01820; 1A7N.
DR SMR; P01817; 1-125.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 113
FT MOD_RES 1 125
FT NON_TER 125 125 Pyrrolidone carboxylic acid.
FT SEQUENCE 125 AA; 13785 MW; 7A1ADF4C40F47BB5 CRC64;
SQ
Query Match 63.0%; Score 476; DB 1; Length 125;
Best Local Similarity 71.9%; Pred. No. 3.9e-40;
Matches 92; Conservative 11; Mismatches 15; Indels 10; Gaps 2;
QY 21 QVTLRESGPALVKPTQTTLTCTFSGFSLSGTSGMGVSWIRQPPGKLEWLAHIYWDGDKR 80
Db 1 QITLKESGPTLVKPTETLTCTFSGFSLSGTSGMGVSWIRQPPGKLEWLAFINWDDNR 60
QY 81 YNPSLKSLRTISKDTSRNOVLMTNMDPVDATATYCCARRETVFYVY-----FDWGR 133
Db 61 YSPSLRSLTGKDTSRNOVLMTNMDPVDTSGTFFCAHRPP---WRFTGNLGGFDXWQ 117
QY 134 GTPVTSS 141
Db 118 GTLVTVSS 125
RESULT 7
ID Q811U5 MOUSE PRELIMINARY; PRT; 118 AA.
AC Q811U5
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-human Fc gamma receptor III 3G8 gamma heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BA15/c;
RX PubMed=15059139; DOI=10.1111/j.1365-2141.2004.04893.x;
RA Bruenke J., Fischer B., Barbin K., Schreiter K., Wachter Y., Mahr K.,
RA Titzgmeier F., Niederweis M., Peipp M., Zunino S.J., Repp R.,
RA Valerius T., Fey G.H.;
RT "A recombinant bispecific single-chain Fv antibody against HLA class
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RT II and Fc gammaRIII (CD16) triggers effective lysis of lymphoma
RT cells."
RL Br. J. Haematol. 125:167-179(2004).
DR EMBL; AY173025; AA018227.1; -, mRNA.
DR HSSP; P01820; 1A7N.
DR SMR; Q811U5; 1-118.
DR Ensembl; ENSMUSG000000057010; Mus musculus.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 118 118
FT SEQUENCE 118 AA; 12979 MW; F57BB07033742E99 CRC64;
SQ
Query Match 61.0%; Score 460.5; DB 2; Length 118;
Best Local Similarity 70.2%; Pred. No. 1.3e-38;
Matches 85; Conservative 17; Mismatches 16; Indels 3; Gaps 1;
QY 21 QVTLRESGPALVKPTQTTLTCTFSGFSLSGTSGMGVSWIRQPPGKLEWLAHIYWDGDKR 80
Db 1 QVTLKESGPTLVKPTETLTCTFSGFSLSGTSGMGVSWIRQPPGKLEWLAHIWDDDKR 60
QY 81 YNPSLKSLRTISKDTSRNOVLMTNMDPVDATATYCCARRETVFYVYFDWGRGTPVTVS 140
Db 61 YNPALKSLRTISKDTSRNOVLKIASVDATATYCAINPAWFAY---WGQGLTVTVS 117
QY 141 S 141
Db 118 A 118
RESULT 8
ID HV2E_HUMAN STANDARD; PRT; 121 AA.
AC P01818;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-II region HE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=70114712; PubMed=5264153;
RA Cunningham B.A., Pflumm M.N., Rutishauser U., Edelman G.M.;
RT "Subgroups of amino acid sequences in the variable regions of
RT immunoglobulin heavy chains."
RL Proc. Natl. Acad. Sci. U.S.A. 64:997-1003(1969).
CC -!- MISCELLANEOUS: This gamma-1 chain was isolated from a myeloma
CC protein.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; A02093; G1HUHE.
DR HSSP; P01820; 1A7N.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
```

KW Direct protein sequencing; Immunoglobulin domain;
 KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
 FT DOMAIN 1 120 Ig-like.
 FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
 FT NON_TER 121 121
 SQ SEQUENCE 121 AA; 13483 MW; 88A5082C273753B4 CRC64;

Query Match 60.9%; Score 460; DB 1; Length 121;
 Best Local Similarity 71.0%; Pred. No. 1.6e-38;
 Matches 88; Conservative 15; Mismatches 15; Indels 6; Gaps 3;

QY 21 QVTLRESGALVKPTQTTLTCTFSGSLSTGSGVSWIRPPCKGLEWLAH-IYWDDDK 79
 DB 1 QVTLKENGTLVKPTETLTCTLSGLSLTDTGAVGIRQCGRALEWLAWLLYWDDDK 60
 QY 80 RYNPSLKSRLTISKTSRQVLTNTNMDPVDATYICARR--ETVYFYFVWVGRTGPV 137
 DB 61 RSPSLKSLTWTSDTSKNQVLTNTNMDPVDATYICVHRHPTL---AFDVGQGTQV 117
 QY 138 TVSS 141
 DB 118 AVSS 121

RESULT 9

HV2H HUMAN STANDARD; PRT; 147 AA.
 AC P04438;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig heavy chain V-II region SESS precursor.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=84298107; PubMed=6089186;
 RA Takahashi N., Noma T., Honjo T.;
 RT Rearranged immunoglobulin heavy chain variable region (VH) pseudogene
 RT that deletes the second complementarity-determining region."
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5194-5198(1984).
 CC -----
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 CC -----
 DR PIR; A02090; G2HUCS.
 DR HSP; P01820; IG7I.
 DR GO; GO:0005576; C:extracellular region; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin domain; Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 147 Ig heavy chain V-II region SESS.
 FT REGION 20 118 V segment.
 FT REGION 119 132 D segment.
 FT REGION 133 147 J segment.
 FT NON_TER 147 147
 SQ SEQUENCE 147 AA; 16323 MW; FCBCDB3D00FB6666 CRC64;

Query Match 60.3%; Score 455; DB 1; Length 147;
 Best Local Similarity 67.7%; Pred. No. 6.3e-38;
 Matches 90; Conservative 10; Mismatches 25; Indels 8; Gaps 2;

QY 11 LLLWI-SGAYGVTLRESGALVKPTQTTLTCTFSGSLSTGSGVSWIRPPCKGLEW 69
 DB 9 LLLTPSGVLSQLNRESGALVKATHTLTCTFSGLSVNTRGMSVSWIRPPCKALEW 68
 QY 70 LAHIYWDGDKRYNPSLKSRLTISKTSRQVLTNTNMDPVDATYICARRTFVFW--- 126
 DB 69 LARIDWDDDDKYGTSLTSLTSLTSLTSLTSLTSLTSLTSLTSLTSLTSLTSLTSLT 128
 QY 127 ----YFDVWVGRT 135
 DB 129 ITSNAPDIWGQST 141

RESULT 10

Q58E54 MOUSE PRELIMINARY; PRT; 485 AA.
 AC Q58E54;
 DT 10-MAY-2005 (TREMBLrel. 30, Created)
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
 DE LOC544903 protein.
 GN Name=LOC544903;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RG NIH MGC Project;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC092065; AAH92065.1; -; mRNA.
 DR GO; GO:0003823; F:antigen binding; IEA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; Cl-set; 2.
 DR SMART; SM00409; IG; 3.
 DR SMART; SM00407; IGcl; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
 SQ SEQUENCE 485 AA; 52383 MW; 44087147CB49A50B CRC64;

Query Match 58.9%; Score 445; DB 2; Length 485;
 Best Local Similarity 64.9%; Pred. No. 2.5e-36;


```

RN RP NUCLEOTIDE SEQUENCE.
RA Borreszen M., Natvig J.B., Thompson K.M.;
RT "Heterogenous RP structures between and within healthy individuals are
RL not related to HLA DRB1*0401.";
DR Mol. Immunol. 0:0-0(1997).
DR EMBL; AF035802; AAB88534.1; -; mRNA.
DR HSSP; P01820; 1G7I.
DR SNR; O43234; 1-96.
DR Ensemble1; ENSG00000196662; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 97
FT NON_TER 97
SQ SEQUENCE 97 AA; 10748 MW; DDC0BF47B9AA812D CRC64;

Query Match 55.9%; Score 422; DB 2; Length 97;
Best Local Similarity 81.4%; Pred. No. 8.5e-35;
Matches 79; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 23 TLRESGPAIVKPTQTLTCTCTSGFSLSGCVSWIROPFGKLEWLAHIYDDDKRYN 82.
DB 1 TLKESGPAIVKPTETLTLTCTVSGFSLSNRMGVSWIROPFGKAVEWLAHIFANDEKSYS 60

QY 83 PSLKSLTISKDTSRNOQVLTWNMDPDTATYYCAR 119
DB 61 TSLKSLTISKDTSKQVLTWNMDPDTATYYCAR 97

RESULT 15
HV2C_HUMAN STANDARD; PRT; 119 AA.
ID HV2C_HUMAN
AC P01816;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-II region DAW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
[1]
RN RP PROTEIN SEQUENCE.
RX MEDLINE=70258837; PubMed=5449120;
RA Press E.M., Hogg N.M.;
RT "The amino acid sequences of the Fd fragments of two human gamma-1
RL heavy chains.";
RL Biochem. J. 117:641-660(1970).
CC -1- MISCELLANEOUS: This chain was obtained from IgG1 isolated from the
CC serum of a patient with hypergammaglobulinemia.
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A02091; GIHUDW.
DR HSSP; P01820; 1A7N.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
DR Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Pyrolydione carboxylic acid.
FT DOMAIN 1 113
FT DOMAIN 1 113

```

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FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13045 MW; 4E13E00214BAD789 CRC64;

Query Match      54.7%; Score 413; DB 1; Length 119;
Best Local Similarity 68.5%; Pred. No. 8.8e-34;
Matches 85; Conservative 11; Mismatches 20; Indels 8; Gaps 3;

Qy 21 QVTLRESGPAVKPTQTTLTCTFSGFSLSTSGMGVSWIRQPPGKGLEWLAHIYWD---D 77
Db 1 QVTLRESGPAVKPTQTTLTCTFSGFSLSTSGMGVSWIRQPPGKGLEWLAHIYWD---D 77

Qy 78 DKRYNPGLKSLTISKDTSRQVLTMTMDPDVDTATYYCARRETVFYFYEDVWGRGTPV 137
Db 58 DKYYGASLETRLAVSKDTSRQVLTMTMDPDVDTATYYCARRETVFYFYEDVWGRGTPV 137

Qy 138 TVSS 141
Db 116 TVSS 119
```

Search completed: February 23, 2006, 09:23:05
Job time : 155.441 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 09:13:28 ; Search time 125.702 Seconds
(without alignments)
457.897 Million cell updates/sec

Title: US-10-723-872-14

Perfect score: 687

Sequence: 1 MGWSCIIPLVATATGVHSD.....QQSNEDPRFGGKTVEIKR 131

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 43937871 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|---------------------|
| 1 | 687 | 100.0 | 131 | 2 | Aar75355 Humanized |
| 2 | 687 | 100.0 | 131 | 2 | Aay23771 Light cha |
| 3 | 687 | 100.0 | 131 | 2 | Aay18118 Light cha |
| 4 | 681 | 99.1 | 131 | 2 | Aar70202 Humanized |
| 5 | 681 | 99.1 | 131 | 2 | Aay23779 Light cha |
| 6 | 681 | 99.1 | 131 | 2 | Aay18126 Light cha |
| 7 | 572.5 | 83.3 | 238 | 6 | Ada47339 TRX1 light |
| 8 | 572.5 | 83.3 | 238 | 6 | Ada47330 TRX1 light |
| 9 | 572.5 | 83.3 | 238 | 6 | Ada47338 TRX1 light |
| 10 | 572.5 | 83.3 | 238 | 6 | Ada47332 TRX1 light |
| 11 | 572.5 | 83.3 | 238 | 8 | Adp88434 Antibody |
| 12 | 572.5 | 83.3 | 238 | 8 | Adp88442 Antibody |
| 13 | 572.5 | 83.3 | 238 | 8 | Adp88450 Antibody |
| 14 | 572.5 | 83.3 | 238 | 8 | Adp88426 Antibody |
| 15 | 572.5 | 83.3 | 238 | 8 | Adq87972 Light cha |
| 16 | 572.5 | 83.3 | 238 | 8 | Adq87976 Light cha |
| 17 | 572.5 | 83.3 | 238 | 8 | Adq87964 Light cha |
| 18 | 572.5 | 83.3 | 238 | 8 | Adg87968 Light cha |
| 19 | 564 | 82.1 | 218 | 8 | Adp88435 Antibody |
| 20 | 564 | 82.1 | 218 | 8 | Adp88427 Antibody |
| 21 | 564 | 82.1 | 218 | 8 | Adp88451 Antibody |
| 22 | 564 | 82.1 | 218 | 8 | Adp88443 Antibody |
| 23 | 543 | 79.0 | 111 | 8 | Aeb13680 Human vlik |
| 24 | 543 | 79.0 | 218 | 8 | Adf71899 Hu3G8VL-1 |

| | | | | | | |
|----|-------|------|-----|---|----------|--------------------|
| 25 | 539 | 78.5 | 531 | 3 | AAV43749 | Aay43749 Amino aci |
| 26 | 538 | 78.3 | 111 | 8 | Adf71897 | Adf71897 Hu3G8VL-1 |
| 27 | 535 | 77.9 | 237 | 2 | AAW73873 | AAW73873 Human ant |
| 28 | 532.5 | 77.5 | 238 | 8 | ADL23055 | ADL23055 Humanised |
| 29 | 532.5 | 77.5 | 238 | 8 | ADS88804 | ADS88804 Humanised |
| 30 | 532 | 77.4 | 218 | 8 | Adf71920 | Adf71920 Hu3G8VL-2 |
| 31 | 531 | 77.3 | 111 | 9 | AEb13684 | AEb13684 Human ant |
| 32 | 530 | 77.1 | 218 | 8 | Adf71903 | Adf71903 Hu3G8VL-4 |
| 33 | 530 | 77.1 | 240 | 2 | AAW73875 | AAW73875 Human ant |
| 34 | 527 | 76.7 | 111 | 8 | Adf71919 | Adf71919 Hu3G8VL-2 |
| 35 | 525 | 76.4 | 111 | 8 | Adf71901 | Adf71901 Hu3G8VL-4 |
| 36 | 523.5 | 76.2 | 132 | 2 | AAW70189 | AAW70189 Mouse MAb |
| 37 | 523.5 | 76.2 | 132 | 2 | AAy23767 | AAy23767 Light cha |
| 38 | 523.5 | 76.2 | 132 | 2 | AAy18120 | AAy18120 Light cha |
| 39 | 523 | 76.1 | 218 | 9 | AEb13693 | AEb13693 Human ant |
| 40 | 521 | 75.8 | 112 | 9 | AEb21493 | AEb21493 Anti-IL13 |
| 41 | 521 | 75.8 | 112 | 9 | AEb21495 | AEb21495 Anti-IL13 |
| 42 | 521 | 75.8 | 112 | 9 | AEb31253 | AEb31253 Antibody |
| 43 | 521 | 75.8 | 112 | 9 | AEb31251 | AEb31251 Antibody |
| 44 | 520 | 75.7 | 112 | 9 | AEb21446 | AEb21446 Anti-IL13 |
| 45 | 520 | 75.7 | 112 | 9 | AEb21501 | AEb21501 Anti-IL13 |

ALIGNMENTS

RESULT 1

AAW75355

ID AAR75355 standard; protein; 131 AA.

XX

AC AAR75355;

XX

DT 25-MAR-2003 (revised)

DT 20-SEP-1995 (first entry)

XX

DE Humanized antibody 3B9 light chain.

XX

KW Humanized antibody; antibody engineering; monoclonal antibody; MAb;
interleukin-4; IL-4; allergy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1..20

FT Region /label= Sig_peptide

FT Region 43..57

FT /label= CDR

FT /note= "complementarity determining region"

FT Region 73..79

FT /label= CDR

FT /note= "complementarity determining region"

FT Region 112..120

FT /label= CDR

FT /note= "complementarity determining region"

XX WO9507301-A1.

XX

PD 16-MAR-1995.

XX

PD 07-SEP-1994; 94WO-US010308.

XX

PD 07-SEP-1993; 93US-00117366.

XX

PD 14-OCT-1993; 93US-00136783.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Holmes S, Gross MS, Sylvester DR;

XX

DR WPI, 1995-123387/16.

XX

DR N-PSDB; AAQ73986.

XX

PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from

PT high affinity mAbs - useful in treatment of IL-4-mediated and IgE-mediated allergic conditions.

XX Disclosure; Fig 5; 97pp; English.

CC A humanized antibody light chain variable region and signal sequence is given in AAR75355. The signal sequence is also provided in AAR70194. The sequences of the first 2 CDRs are identical to mouse anti-human IL-4 Mab 3B9 light chain CDRs (given in AAR70195-96), but the third (AAR70201) differs by a single amino acid from the native mouse CDR (AAR70197).
(Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 131 AA;

Query Match 100.0%; Score 687; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 5.7e-42;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSYVDYDGSYMNWYQ 60
DB 1 MGWSCIILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSYVDYDGSYMNWYQ 60

QY 61 QKPGOPPKLLIYAASNLSEGVDPDRFSGSGGTDFLTITSSLOAEDVAVVYCCQSNEDPPR 120
DB 61 QKPGOPPKLLIYAASNLSEGVDPDRFSGSGGTDFLTITSSLOAEDVAVVYCCQSNEDPPR 120

QY 121 FGGGTKVEIKR 131
DB 121 FGGGTKVEIKR 131

RESULT 2

AAV23771
ID AAV23771 standard; protein; 131 AA.

AC AAV23771;

DT 13-SEP-1999 (first entry)

DE Light chain variable region of humanised murine IL-4 antibody 3B9.

XX Light chain variable region; interleukin-4; IL-4; antibody 3B9;
KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;
KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.

OS Synthetic.

OS Mus sp.

OS Homo sapiens.

XX US5928904-A.

XX 27-JUL-1999.

XX 07-JUN-1995; 95US-00483632.

XX 07-SEP-1993; 93US-00117366.

PR 14-OCT-1993; 93US-00136783.

PR 07-SEP-1994; 94WO-US010308.

XX (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX Holmes SD, Sylvester DR, Gross MS;

XX WPI; 1999-429500/36.

DR N-PSDB; AAX85888.

XX New DNA molecules encoding recombinant antibodies useful for treating IL4-mediated conditions.

XX Example 3; Fig 5; 50pp; English.

XX The present sequence represents the light chain variable region of a humanised murine interleukin-4 (IL-4) antibody 3B9. The specification describes chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host-versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans

XX Sequence 131 AA;

Query Match 100.0%; Score 687; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 5.7e-42;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSYVDYDGSYMNWYQ 60
DB 1 MGWSCIILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSYVDYDGSYMNWYQ 60

QY 61 QKPGOPPKLLIYAASNLSEGVDPDRFSGSGGTDFLTITSSLOAEDVAVVYCCQSNEDPPR 120
DB 61 QKPGOPPKLLIYAASNLSEGVDPDRFSGSGGTDFLTITSSLOAEDVAVVYCCQSNEDPPR 120

QY 121 FGGGTKVEIKR 131
DB 121 FGGGTKVEIKR 131

RESULT 3

AAV18118

ID AAV18118 standard; protein; 131 AA.

XX AAV18118;

DT 11-AUG-1999 (first entry)

DE Light chain sequence for humanised 3B9 antibody.

XX Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;
KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
KW autoimmune disease; graft versus host disease.

OS Synthetic.

XX US5914110-A.

XX 22-JUN-1999.

XX 07-JUN-1995; 95US-00483636.

XX 07-SEP-1993; 93US-00117366.

PR 14-OCT-1993; 93US-00136783.

PR 07-SEP-1994; 94WO-US010308.

XX (SMIK) SMITHKLINE BEECHAM PLC.

PA (SMIK) SMITHKLINE BEECHAM CORP.

XX Sylvester DR, Holmes SD, Gross MS;

XX WPI; 1999-370482/31.

DR N-PSDB; AAX79517.

XX Recombinant IL4 antibodies useful for treatment of allergic rhinitis,
PT atopic asthma and anaphylactic shock.

XX Claim 16; Fig 5; 50pp; English.

XX This sequence represents the light chain of the humanised 3B9 antibody of

CC the invention. The antibody is a chimeric or humanised interleukin-4
 CC (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE)
 CC mediated diseases. The antibodies are useful for the treatment of
 CC allergic disorders such as allergic rhinitis, conjunctivitis, atopic
 CC dermatitis, atopic asthma and anaphylactic shock. The antibodies are also
 CC useful for regulating B and T cell proliferation and as such are useful
 CC in the treatment of autoimmune diseases and graft versus host disease
 XX
 SQ Sequence 131 AA;

Query Match 100.0%; Score 687; DB 2; Length 131;
 Best Local Similarity 100.0%; Pred. No. 5.7e-42; Indels 0; Gaps 0;
 Matches 131; Conservative 0; Mismatches 0;
 QY 1 MGVSCIIILFLVATATGVHSDIVMTQSPDLSAVSLGERATINCKASQSDVDYDGDSYNNWYQ 60
 DB 1 MGVSCIIILFLVATATGVHSDIVMTQSPDLSAVSLGERATINCKASQSDVDYDGDSYNNWYQ 60
 QY 61 QKPGOPPPLLIIYAASNLSEGVDPDRFSGSGGTDFLTITSSLOAEDVAVVYCOQSNEDPPR 120
 DB 61 QKPGOPPPLLIIYAASNLSEGVDPDRFSGSGGTDFLTITSSLOAEDVAVVYCOQSNEDPPR 120
 QY 121 FGGGTTKVEIKR 131
 DB 121 FGGGTTKVEIKR 131

RESULT 4
 AAR70202
 ID AAR70202 standard; protein; 131 AA.
 AC AAR70202;
 DT 25-MAR-2003 (revised)
 DT 20-SEP-1995 (first entry)
 XX Humanized antibody 3B9 light chain.
 DE Humanized antibody; antibody engineering; monoclonal antibody; Mab;
 KW interleukin-4; IL-4; allergy.
 XX Homo sapiens.
 OS WO9507301-A1.
 PN 16-MAR-1995.
 PD 07-SEP-1994; 94WO-US010308.
 PF 07-SEP-1993; 93US-00117366.
 PR 14-OCT-1993; 93US-00136783.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX Holmes S, Gross MS, Sylvester DR;
 PI WPI; 1995-123387/16.
 DR N-PSDB; AAQ83520.
 XX Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from
 PT high affinity mAbs - useful in treatment of IL-4-mediated and IGE-
 PT mediated allergic conditions.
 XX Disclosure; Page 71-72; 97pp; English.

XX A humanized antibody light chain variable region and signal sequence is
 CC given in AAR75355. The signal sequence is also provided in AAR70194. The
 CC sequences of the 3 CDRs are identical to mouse anti-human IL-4 Mab 3B9
 CC light chain CDRs (given in AAR70195-97). (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX Sequence 131 AA;

Query Match 99.1%; Score 681; DB 2; Length 131;
 Best Local Similarity 99.2%; Pred. No. 1.5e-41;
 Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MGVSCIIILFLVATATGVHSDIVMTQSPDLSAVSLGERATINCKASQSDVDYDGDSYNNWYQ 60
 DB 1 MGVSCIIILFLVATATGVHSDIVMTQSPDLSAVSLGERATINCKASQSDVDYDGDSYNNWYQ 60
 QY 61 QKPGOPPPLLIIYAASNLSEGVDPDRFSGSGGTDFLTITSSLOAEDVAVVYCOQSNEDPPR 120
 DB 61 QKPGOPPPLLIIYAASNLSEGVDPDRFSGSGGTDFLTITSSLOAEDVAVVYCOQSNEDPPR 120
 QY 121 FGGGTTKVEIKR 131
 DB 121 FGGGTTKVEIKR 131

RESULT 5
 AAY23779
 ID AAY23779 standard; protein; 131 AA.
 AC AAY23779;
 XX 13-SEP-1999 (first entry)
 DE Light chain variable region of humanised murine IL-4 antibody 3B9.
 XX Light chain variable region; interleukin-4; IL-4; antibody 3B9;
 KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
 KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.
 XX Synthetic.
 OS Mus sp.
 OS Homo sapiens.
 XX US5928904-A.
 PN 27-JUL-1999.
 PD 07-JUN-1995; 95US-00483632.
 PF 07-SEP-1993; 93US-00117366.
 PR 14-OCT-1993; 93US-00136783.
 PR 07-SEP-1994; 94WO-US010308.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX Holmes SD, Sylvester DR, Gross MS;
 PI WPI; 1999-429500/36.
 DR N-PSDB; AAX85924.
 XX New DNA molecules encoding recombinant antibodies useful for treating IL4
 PT -mediated conditions.
 XX Disclosure; Col 61-62; 50pp; English.
 XX The present sequence represents the light chain variable region of a
 CC humanised murine interleukin-4 (IL-4) antibody 3B9. The specification
 CC describes chimeric and humanised IL-4 monoclonal antibodies. The
 CC antibodies of the invention are used in therapeutic and pharmaceutical
 CC compositions for treating IL-4 mediated and immunoglobulin E-mediated
 CC allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic
 CC dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host
 CC -versus-graft disease and renal disease. They are also useful in the
 CC diagnosis of an allergy or condition associated with excess IL-4
 CC production through the measurement e.g. by ELISA of circulating
 CC endogenous IL-4 levels in humans
 XX

SQ Sequence 131 AA;

Query Match 99.1%; Score 681; DB 2; Length 131;
 Best Local Similarity 99.2%; Pred. No. 1.5e-41;
 Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVATATGVHSDIVMTQSPDLSAVSLGERATINCKASQSVYDGDSDYMNWYQ 60
 DB 1 MGWSCIILFLVATATGVHSDIVMTQSPDLSAVSLGERATINCKASQSVYDGDSDYMNWYQ 60

QY 61 QKPGOPKLLIYAASNLSEGVDPDRFSGSGGTDTFTLTSSLOAEDVAVVYCCQSNEDPPT 120
 DB 61 QKPGOPKLLIYAASNLSEGVDPDRFSGSGGTDTFTLTSSLOAEDVAVVYCCQSNEDPPT 120

QY 121 FGGGKVEIKR 131
 DB 121 FGGGKVEIKR 131

RESULT 7
 ADA47339
 ID ADA47339 standard; protein; 238 AA.
 XX
 AC ADA47339;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE TRX1 light chain amino acid sequence #SEQ ID 14.
 XX
 KW Antibody; TRX1; immunosuppressive; immunomodulator; vaccine; antigen;
 KW graft rejection; autoimmune disease; humanised.
 XX
 OS Homo sapiens.
 XX
 EH Key Location/Qualifiers
 FT Peptide 1..20
 FT /label= leader peptide
 FT Region 44..58
 FT /label= CDR
 FT Region 74..80
 FT /label= CDR
 FT Region 113..121
 FT /label= CDR
 XX
 PN WO2002102853-A2.
 XX
 PD 27-DEC-2002.
 XX
 PF 14-JUN-2002; 2002WO-GB002796.
 XX
 PR 14-JUN-2001; 2001GB-00014517.
 PR 20-SEP-2001; 2001GB-00022724.
 PR 19-OCT-2001; 2001US-0345194P.
 PR 18-APR-2002; 2002US-0373470P.
 PR 18-APR-2002; 2002US-0373471P.
 XX
 PA (ISIS-) ISIS INNOVATION LTD.
 PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
 PA (TOLE-) TOLERRX INC.
 XX
 PI Frewin M, Waldmann H, Gorman S, Hale G, Rao P, Kornaga T;
 PI Ringler D, Cobbold S, Winsor-Hines D;
 XX
 WPI; 2003-175228/17.
 XX
 DR Treating a primate to induce tolerance to at least one antigen, useful
 PT for inhibiting graft rejection or treating an autoimmune disease,
 PT comprises administering a TRX1 antibody to reduce the amount of CD4+
 PT CD25+ cells produced.
 XX
 PS Claim 30; Fig 2C; 131pp; English.
 XX
 CC The invention relates to a method for treating a primate to induce
 CC tolerance to at least one antigen. The method of the invention comprises
 CC administering at least one compound which when in a primary mixed
 CC lymphocyte reaction in vitro reduces the amount of CD4+ CD25+ cells
 CC produced. The preferred compound is a humanised antibody or its fragment,
 CC that does not bind to the Fc receptor, and includes CDRs that are free of

SQ Sequence 131 AA;

Query Match 99.1%; Score 681; DB 2; Length 131;
 Best Local Similarity 99.2%; Pred. No. 1.5e-41;
 Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVATATGVHSDIVMTQSPDLSAVSLGERATINCKASQSVYDGDSDYMNWYQ 60
 DB 1 MGWSCIILFLVATATGVHSDIVMTQSPDLSAVSLGERATINCKASQSVYDGDSDYMNWYQ 60

QY 61 QKPGOPKLLIYAASNLSEGVDPDRFSGSGGTDTFTLTSSLOAEDVAVVYCCQSNEDPPT 120
 DB 61 QKPGOPKLLIYAASNLSEGVDPDRFSGSGGTDTFTLTSSLOAEDVAVVYCCQSNEDPPT 120

QY 121 FGGGKVEIKR 131
 DB 121 FGGGKVEIKR 131

RESULT 6
 AAY18126
 ID AAY18126 standard; protein; 131 AA.
 XX
 AC AAY18126;
 XX
 DT 11-AUG-1999 (first entry)
 XX
 DE Light chain sequence for humanised 3B9 antibody.
 XX
 KW Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;
 KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
 KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
 KW autoimmune disease; graft versus host disease.
 XX
 OS Synthetic.
 XX
 PN US5914110-A.
 XX
 PD 22-JUN-1999.
 XX
 PF 07-JUN-1995; 95US-00483636.
 XX
 PR 07-SEP-1993; 93US-00117366.
 PR 14-OCT-1993; 93US-00136783.
 PR 07-SEP-1994; 94WO-US010308.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 PI Sylvester DR, Holmes SD, Gross MS;
 XX
 WPI; 1999-370482/31.
 DR N-PSDB; AAX79543.
 XX
 PT Recombinant IL4 antibodies useful for treatment of allergic rhinitis,
 PT atopic asthma and anaphylactic shock.
 XX
 PS Disclosure; Col 59-62; 50pp; English.
 XX
 CC This sequence represents the light chain of the humanised 3B9 antibody of
 CC the invention. The antibody is a chimeric or humanised interleukin-4
 CC (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE)
 CC mediated diseases. The antibodies are useful for the treatment of
 CC allergic disorders such as allergic rhinitis, conjunctivitis, atopic
 CC dermatitis, atopic asthma and anaphylactic shock. The antibodies are also
 CC useful for regulating B and T cell proliferation and as such are useful
 CC in the treatment of autoimmune diseases and graft versus host disease

SQ Sequence 131 AA;

Query Match 99.1%; Score 681; DB 2; Length 131;
 Best Local Similarity 99.2%; Pred. No. 1.5e-41;
 Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

PR 09-DEC-2002; 2002US-0431839P.
XX (TOLE-) TOLERRX INC.
PA Windsor-Hines D, Rao P, Ringler DJ;
PI WPI; 2004-468712/44.
XX DR N-PSDB; ADP88433, ADP88432.
DR
XX
PT Treating a primate to induce tolerance to at least one antigen comprises
PT administering at least one anti-CD4 antibody or its fragment in an
PT initial dose of at least 40 mg/kg and at least one compound that inhibits
PT CD8+ T cells.
XX
PS Example 3; SEQ ID NO 11; 113pp; English.
XX
CC The present invention relates to a process of treating a primate to
CC induce tolerance to at least one antigen, which comprises administering
CC to the primate at least one anti-CD4 antibody or its fragment in an
CC initial dose of at least 40 mg/kg and at least one compound that inhibits
CC CD8+ T cells, where the anti-CD4 antibody or its fragment is present in
CC the primate when the antigen is present in the primate. The method is
CC useful in treating a primate to induce tolerance to at least one foreign
CC antigen to prevent transplant rejection. The present sequence is an
CC antibody fragment used in the exemplification of the invention.
XX
SQ Sequence 238 AA;
Query Match 83.3%; Score 572.5; DB 8; Length 238;
Best Local Similarity 88.9%; Pred. No. 1.7e-33;
Matches 112; Conservative 4; Mismatches 7; Indels 3; Gaps 1;
QY 6 IILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSDVDYDGSYMNWYQOKPGQ 65
DB 10 VLLWVPGSTG---DIVMTQSPDSLAVSLGERATINCKASQSDVDYDGSYMNWYQOKPGQ 66
QY 66 PPKLIYVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSDVDYDGSYMNWYQOKPGQ 125
DB 67 PPKLIYVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSDVDYDGSYMNWYQOKPGQ 126
QY 126 KVEIKR 131
DB 127 KVEIKR 132
RESULT 12
ADP88442
ID ADP88442 standard; protein; 238 AA.
XX
AC ADP88442;
XX
DT 09-SEP-2004 (first entry)
XX
DE Antibody TRX1 light chain with leader sequence SEQ ID NO: 19.
XX immunosuppressive; transplant rejection; antigen tolerance; antibody;
KW TRX1.
XX Unidentified.
OS
XX WO2004052398-A1.
PN
XX 24-JUN-2004.
PD
XX 09-DEC-2003; 2003WO-US039165.
PP
XX 09-DEC-2002; 2002US-0431839P.
PR
XX (TOLE-) TOLERRX INC.
PA Windsor-Hines D, Rao P, Ringler DJ;
PI WPI; 2004-468712/44.
XX

DR N-PSDB; ADP88441, ADP88440.
XX
PT Treating a primate to induce tolerance to at least one antigen comprises
PT administering at least one anti-CD4 antibody or its fragment in an
PT initial dose of at least 40 mg/kg and at least one compound that inhibits
PT CD8+ T cells.
XX
PS Disclosure; SEQ ID NO 19; 113pp; English.
XX
CC The present invention relates to a process of treating a primate to
CC induce tolerance to at least one antigen, which comprises administering
CC to the primate at least one anti-CD4 antibody or its fragment in an
CC initial dose of at least 40 mg/kg and at least one compound that inhibits
CC CD8+ T cells, where the anti-CD4 antibody or its fragment is present in
CC the primate when the antigen is present in the primate. The method is
CC useful in treating a primate to induce tolerance to at least one foreign
CC antigen to prevent transplant rejection. The present sequence is an
CC antibody fragment used in the exemplification of the invention.
XX
SQ Sequence 238 AA;
Query Match 83.3%; Score 572.5; DB 8; Length 238;
Best Local Similarity 88.9%; Pred. No. 1.7e-33;
Matches 112; Conservative 4; Mismatches 7; Indels 3; Gaps 1;
QY 6 IILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSDVDYDGSYMNWYQOKPGQ 65
DB 10 VLLWVPGSTG---DIVMTQSPDSLAVSLGERATINCKASQSDVDYDGSYMNWYQOKPGQ 66
QY 66 PPKLIYVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSDVDYDGSYMNWYQOKPGQ 125
DB 67 PPKLIYVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSDVDYDGSYMNWYQOKPGQ 126
QY 126 KVEIKR 131
DB 127 KVEIKR 132
RESULT 13
ADP88450
ID ADP88450 standard; protein; 238 AA.
XX
AC ADP88450;
XX
DT 09-SEP-2004 (first entry)
XX
DE Antibody TRX1 light chain with leader sequence SEQ ID NO: 27.
XX immunosuppressive; transplant rejection; antigen tolerance; antibody;
KW TRX1.
XX Unidentified.
OS
XX WO2004052398-A1.
PN
XX 24-JUN-2004.
PD
XX 09-DEC-2003; 2003WO-US039165.
PP
XX 09-DEC-2002; 2002US-0431839P.
PR
XX (TOLE-) TOLERRX INC.
PA Windsor-Hines D, Rao P, Ringler DJ;
PI WPI; 2004-468712/44.
XX
PT Treating a primate to induce tolerance to at least one antigen comprises
PT administering at least one anti-CD4 antibody or its fragment in an
PT initial dose of at least 40 mg/kg and at least one compound that inhibits
PT CD8+ T cells.
XX

```

PS Example 4; SEQ ID NO 27; 113pp; English.
XX
CC The present invention relates to a process of treating a primate to
CC induce tolerance to at least one antigen, which comprises administering
CC to the primate at least one anti-CD4 antibody or its fragment in an
CC initial dose of at least 40 mg/kg and at least one compound that inhibits
CC CD8+ T cells, where the anti-CD4 antibody or its fragment is present in
CC the primate when the antigen is present in the primate. The method is
CC useful in treating a primate to induce tolerance to at least one foreign
CC antigen to prevent transplant rejection. The present sequence is an
CC antibody fragment used in the exemplification of the invention.
XX
SQ Sequence 238 AA;
Query Match      83.3%; Score 572.5; DB 8; Length 238;
Best Local Similarity 88.9%; Pred. No. 1.7e-33;
Matches 112; Conservative 4; Mismatches 7; Indels 3; Gaps 1;

QY 6 IILFLVATATGVHSDIVMTQSPDLSAVSLGERATINCKASQSDVDGDSYNNWYQOKPQG 65
DB 10 VLLWVPGSTG---DIVMTQSPDLSAVSLGERATINCKASQSDVDGDSYNNWYQOKPQG 66

QY 66 PPKLLIYAASNLSEGVPRFSGSGGTDTLTITISLQAEADVAVYYCQOSNEDPPRFGGGT 125
DB 67 PPKLLIYASNLSEGVPRFSGSGGTDTLTITISLQAEADVAVYYCQOSLQDPPPTFGGGT 126

QY 126 KVEIKR 131
DB 127 KVEIKR 132

RESULT 14
ADP88426
ID ADP88426 standard; protein; 238 AA.
XX
AC ADP88426;
XX
XX 09-SEP-2004 (first entry)
DE Antibody TRX1 light chain with leader sequence SEQ ID NO: 3.
KW immunosuppressive; transplant rejection; antigen tolerance; antibody;
KW TRX1.
XX
OS Unidentified.
XX
XX WO2004052398-A1.
XX
XX 24-JUN-2004.
XX
XX 09-DEC-2003; 2003WO-US039165.
XX
XX 09-DEC-2002; 2002US-0431839P.
XX
XX (TOLE-) TOLERRX INC.
XX
XX Windsor-Hines D, Rao P, Ringler DJ;
XX
XX WPI; 2004-468712/44.
XX
XX N-PSDB; ADP88424.
XX
XX Treating a primate to induce tolerance to at least one antigen comprises
XX administering at least one anti-CD4 antibody or its fragment in an
XX initial dose of at least 40 mg/kg and at least one compound that inhibits
XX CD8+ T cells.
XX
XX Disclosure; SEQ ID NO 3; 113pp; English.
XX
XX The present invention relates to a process of treating a primate to
XX induce tolerance to at least one antigen, which comprises administering
XX to the primate at least one anti-CD4 antibody or its fragment in an
XX initial dose of at least 40 mg/kg and at least one compound that inhibits
XX CD8+ T cells, where the anti-CD4 antibody or its fragment is present in
XX

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```

CC the primate when the antigen is present in the primate. The method is
CC useful in treating a primate to induce tolerance to at least one foreign
CC antigen to prevent transplant rejection. The present sequence is an
CC antibody fragment used in the exemplification of the invention.
XX
SQ Sequence 238 AA;
Query Match      83.3%; Score 572.5; DB 8; Length 238;
Best Local Similarity 88.9%; Pred. No. 1.7e-33;
Matches 112; Conservative 4; Mismatches 7; Indels 3; Gaps 1;

QY 6 IILFLVATATGVHSDIVMTQSPDLSAVSLGERATINCKASQSDVDGDSYNNWYQOKPQG 65
DB 10 VLLWVPGSTG---DIVMTQSPDLSAVSLGERATINCKASQSDVDGDSYNNWYQOKPQG 66

QY 66 PPKLLIYAASNLSEGVPRFSGSGGTDTLTITISLQAEADVAVYYCQOSNEDPPRFGGGT 125
DB 67 PPKLLIYASNLSEGVPRFSGSGGTDTLTITISLQAEADVAVYYCQOSLQDPPPTFGGGT 126

QY 126 KVEIKR 131
DB 127 KVEIKR 132

RESULT 15
ADQ87972
ID ADQ87972 standard; protein; 238 AA.
XX
AC ADQ87972;
XX
XX 04-NOV-2004 (first entry)
DE Light chain of a humanised TRX1 antibody #3.
KW Primate; tolerance; antigen; mixed lymphocyte reaction; MLR; CD4+; CD25+;
KW IL-2; IL-4; IL-12; immune response; graft rejection; immunosuppressive;
KW antineumatic; antiarthritic; antidiabetic; neuroprotective;
KW antiinflammatory; antiallergic; antiasthmatic; cytostatic; antimicrobial;
KW transplant; graft-versus-host disease; autoimmune disease; inflammation;
KW allergy; asthma; cancer; infection; humanised; TRX1; light.
XX
OS Unidentified.
XX
XX Key Location/Qualifiers
XX Peptide 1..20
XX /label= Leader peptide
XX Region 21..43
XX /label= Framework region 1
XX Region 44..58
XX /label= Complementarity determining region 1
XX Region 59..73
XX /label= Framework region 2
XX Region 74..80
XX /label= Complementarity determining region 2
XX Region 81..112
XX /label= Framework region 3
XX Region 113..121
XX /label= Complementarity determining region 3
XX Region 122..131
XX /label= Framework region 4
XX Region 132..238
XX /label= Constant region
XX
XX WO2004067554-A2.
XX
XX 12-AUG-2004.
XX
XX 28-JAN-2004; 2004WO-US002643.
XX
XX 29-JAN-2003; 2003US-00353708.
XX
XX (TOLE-) TOLERRX INC.
XX (ISIS-) ISIS INNOVATION LTD.

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Search completed: February 23, 2006, 09:18:04
Job time : 126.702 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 09:18:23 ; Search time 23.1176 Seconds
(without alignments)
545.228 Million cell updates/sec

Title: US-10-723-872-14
Perfect score: 687
Sequence: 1 MGWSCIILFLVATATGVHSD.....QQSNEDPPRFGGKVKIKR 131

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 502.5 | 73.1 | 131 | 2 PH1226 | Ig kappa chain pre |
| 2 | 499 | 72.6 | 112 | 2 S19971 | Ig kappa chain v r |
| 3 | 493 | 71.8 | 111 | 1 KWS43 | Ig kappa chain v r |
| 4 | 492 | 71.6 | 111 | 1 KWS83 | Ig kappa chain v r |
| 5 | 489 | 71.2 | 111 | 1 KWS08 | Ig kappa chain v r |
| 6 | 486 | 70.7 | 111 | 1 KWS69 | Ig kappa chain v r |
| 7 | 478 | 69.6 | 134 | 1 K4HU17 | Ig kappa chain pre |
| 8 | 476.5 | 69.4 | 133 | 1 K4HUJ1 | Ig kappa chain pre |
| 9 | 476 | 69.3 | 111 | 1 KWS01 | Ig kappa chain v r |
| 10 | 475 | 69.1 | 112 | 2 S19976 | Ig kappa chain v r |
| 11 | 468.5 | 68.2 | 110 | 1 KWS10 | Ig kappa chain v r |
| 12 | 465 | 67.7 | 113 | 2 S34003 | Ig kappa chain v r |
| 13 | 464 | 67.5 | 112 | 2 S19972 | Ig kappa chain v r |
| 14 | 463 | 67.4 | 134 | 2 S49531 | Ig kappa chain v r |
| 15 | 462 | 67.2 | 111 | 1 KWS37 | anti-5m antibody v |
| 16 | 462 | 67.2 | 124 | 2 S40364 | Ig kappa chain v r |
| 17 | 459 | 66.8 | 113 | 2 S30523 | Ig kappa chain - h |
| 18 | 457.5 | 66.6 | 131 | 1 KWSM6 | Ig kappa chain pre |
| 19 | 457 | 66.5 | 113 | 2 S30520 | Ig kappa chain v r |
| 20 | 457 | 66.5 | 114 | 1 K4HULN | Ig kappa chain v r |
| 21 | 455 | 66.2 | 115 | 2 S63596 | Ig kappa chain v r |
| 22 | 451 | 65.6 | 111 | 2 S09966 | Ig kappa chain v r |
| 23 | 450 | 65.5 | 114 | 2 S44116 | Ig kappa chain v r |
| 24 | 450 | 65.5 | 129 | 2 S40347 | Ig kappa chain - h |
| 25 | 449 | 65.4 | 113 | 2 S34002 | Ig kappa chain v r |
| 26 | 444 | 64.6 | 111 | 2 D45722 | anti-glycoprotein |
| 27 | 443 | 64.5 | 114 | 2 S44119 | Ig kappa chain v r |
| 28 | 442 | 64.3 | 120 | 2 S51147 | antibody light cha |
| 29 | 440.5 | 64.1 | 138 | 2 A53261 | Ig kappa chain pre |

ALIGNMENTS

RESULT 1

PH1226

Ig kappa chain precursor V region (M-T310) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000

C:Accession: PH1226

R:Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; Lenz

Gene 121, 271-278, 1992

A>Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and or

A:Reference number: PH1224; MUID:93077041; PMID:1446824

A:Accession: PH1226

A:Molecule type: mRNA

A:Residues: 1-131 <WEI>

A:Cross-references: UNIPARC:UPI00001153EE; GB:S50265; NID:9260765; PIDN:AB24320.1; PID

A>Note: This mouse sequence was hybridized and fused with a human constant region gene

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-131/Product: Ig light chain V region #status predicted <MAT>

F:36-114/Domain: immunoglobulin homology <IMM>

Query Match 73.1%; Score 502.5; DB 2; Length 131;

Best Local Similarity 76.0%; Pred. No. 5.7e-35;

Matches 95; Conservative 13; Mismatches 14; Indels 3; Gaps 1;

QY 6 IILFLVATATGVHSDIVMTQSPDPSLAIVSGERATINCKASQSDYDGDSYMMWYQOKPGQ 65

Db 10 VLLLVWPGSTG---DIVLTQSPASLPMSIGQRATISCKASQSLDYDGDSYMMWYQOKPGQ 66

QY 66 PKLLIYAASNLSEGVDPFRFGSGSGTDTLTLTISLQAEADVAVYCCQSNEDPPRFGGTT 125

Db 67 PKLLIYAASNLSEGVDPFRFGSGSGTDTLTLTINHPVEEDAATYYCCQSSDPPPTPGGTT 126

QY 126 KVEIK 130

Db 127 KLEIK 131

RESULT 2

S19971

Ig kappa chain V region (CD4 mAb clone M-T310 and others) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000

R:Weissenhorn, W.; Riettmueller, G.; Weiss, E.M.; Rieber, E.P.

submitted to the EMBL Data Library, March 1992

A:Description: Structural characterization of CD4 mAb.

A:Reference number: S19963

A:Accession: S19971

A:Molecule type: mRNA

A:Residues: 1-112 <WEI>

A:Cross-references: UNIPARC:UPI0000116030; EMBL:X65091; NID:952288; PIDN:CAA46219.1; PID

A;Experimental source: clone M-T310
A;Accession: S19973
A;Molecule type: mRNA
A;Residues: 1-112 <WEW>
A;Cross-references: UNIPARC:UPI0000116030; EMBL:X65092; NID:g52292; PIDN:CAA46220.1; PID
A;Experimental source: M-T404
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>
F;723-92/Disulfide bonds: #status predicted

Query Match 72.6%; Score 499; DB 2; Length 112;
Best Local Similarity 82.1%; Pred. No. 9.6e-35;
Matches 92; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

Qy 20 DIVMTQSPDLSAVSLGERATINCKASQSDVDGDSYNNWYQKQPPKLLIYAASNLES 79
Db 1 DIVLTQSPASLPMSLQGRATISCKASQSLVDGDSYNNWYQKQPPKLLIYAASNLES 60

Qy 80 GVPDRFSGSGGTDFTLTISSLOAEDVAVYYCQSNEDPPRFGGTKVEIKR 131
Db 61 GIPARFSGSGGTDFTLNIHPVEEDAATYYCQSNEDPPTFGGTKLEIKR 112

RESULT 3
KWMS43
Ig kappa chain V region (PC7043) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C;Accession: A01937; S42187; S42194; S42189; S42188; S42191; S42192
R;Weigert, M.; Gattaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
A;Accession: A01937
A;Molecule type: protein
A;Residues: 1-111 <WEI>
A;Cross-references: UNIPROT:P01665; UNIPARC:UPI000002A100
R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec
A;Reference number: S42176; MUID:94009207; PMID:7691608
A;Accession: S42187
A;Molecule type: DNA
A;Residues: 10-99 <MOJ>
A;Cross-references: UNIPARC:UPI000011655C; EMBL:Z25444; NID:g407832; PIDN:CAA80931.1; PI
A;Note: V-kappa-21B; anti-collagen
A;Accession: S42194
A;Molecule type: DNA
A;Residues: 12-99 <MON>
A;Cross-references: UNIPARC:UPI000011655E; EMBL:Z25458; NID:g407844; PIDN:CAA80945.1; PI
A;Note: V-kappa-21B; anti-collagen
A;Accession: S42190
A;Molecule type: DNA
A;Residues: 13-99 <MOF>
A;Cross-references: UNIPARC:UPI0000116562; EMBL:Z25450; NID:g407838; PIDN:CAA80937.1; PI
A;Note: V-kappa-21B; anti-collagen
A;Accession: S42189
A;Molecule type: DNA
A;Residues: 15-99 <MOA>
A;Cross-references: UNIPARC:UPI0000116560; EMBL:Z25448; NID:g407836; PIDN:CAA80935.1; PI
A;Note: V-kappa-21B; anti-collagen
A;Accession: S42188
A;Molecule type: DNA
A;Residues: 12-99 <MOZ>
A;Cross-references: UNIPARC:UPI000011655E; EMBL:Z25446; NID:g407834; PIDN:CAA80933.1; PI
A;Note: V-kappa-21B; anti-collagen
A;Accession: S42191
A;Molecule type: DNA
A;Residues: 10-99 <MOY>
A;Cross-references: UNIPARC:UPI000011655C; EMBL:Z25452; NID:g407840; PIDN:CAA80939.1; PI
A;Note: V-kappa-21E ; anti-collagen
A;Accession: S42192
A;Molecule type: DNA

A;Residues: 10-99 <MOO>
A;Cross-references: UNIPARC:UPI000011655C; EMBL:Z25454; NID:g407842; PIDN:CAA80941.1; PI
A;Note: V-kappa-21E; anti-collagen
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kaf
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>
F;723-92/Disulfide bonds: #status predicted

Query Match 71.8%; Score 493; DB 1; Length 111;
Best Local Similarity 83.8%; Pred. No. 3e-34;
Matches 93; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

Qy 20 DIVMTQSPDLSAVSLGERATINCKASQSDVDGDSYNNWYQKQPPKLLIYAASNLES 79
Db 1 DIVLTQSPASLAVSLQGRATISCKASQSDVDGDSYNNWYQKQPPKLLIYAASNLES 60

Qy 80 GVPDRFSGSGGTDFTLTISSLOAEDVAVYYCQSNEDPPRFGGTKVEIK 130
Db 61 GIPARFSGSGGTDFTLNIHPVEEDAATYYCQSNEDPPTFGGTKLEIK 111

RESULT 4
KWMS83
Ig kappa chain V region (PC7183) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: B01937; A01937
R;Weigert, M.; Gattaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
A;Accession: B01937
A;Molecule type: protein
A;Residues: 1-111 <WEI>
A;Cross-references: UNIPROT:P01666; UNIPARC:UPI000002A101
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kaf
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>
F;723-92/Disulfide bonds: #status predicted

Query Match 71.6%; Score 492; DB 1; Length 111;
Best Local Similarity 82.9%; Pred. No. 3.6e-34;
Matches 92; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Qy 20 DIVMTQSPDLSAVSLGERATINCKASQSDVDGDSYNNWYQKQPPKLLIYAASNLES 79
Db 1 DIVLTQSPASLAVSLQGRATISCKASQSDVDGDSYNNWYQKQPPKLLIYAASNLES 60

Qy 80 GVPDRFSGSGGTDFTLTISSLOAEDVAVYYCQSNEDPPRFGGTKVEIK 130
Db 61 GIPARFSGSGGTDFTLNIHPVEEDAATYYCQSNEDPPTFGAGTKLELK 111

RESULT 5
KWMS08
Ig kappa chain V region (PC6308) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: C01937; A01937
R;Weigert, M.; Gattaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
A;Accession: C01937
A;Molecule type: protein
A;Residues: 1-111 <WEI>
A;Cross-references: UNIPROT:P01667; UNIPARC:UPI000002A102
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kaf
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la

C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-94/Domain: immunoglobulin homology <IMM>
 F:23-92/Disulfide bonds: #status predicted

Query Match 71.2%; Score 489; DB 1; Length 111;
 Best Local Similarity 82.9%; Pred. No. 6.4e-34;
 Matches 92; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 20 DIVMTQSPDLSAVSLGERATINCKASQSDYDGDSTYNNWYQKPGPPKLLIYAASNLSS 79
 DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSTYNNWYQKPGPPKLLIYAASNLSS 60

QY 80 GVPDRFSGSGGTDFLTITSSLAQEDVAVVYCOQSNEDPPRFGGGPKVEIK 130
 DB 61 GIPARFSGSGGTDFLTINHPVEEDAATYVCOQSNEDPWTFTSGGPKLEIK 111

RESULT 6

KWS69

Ig kappa chain V region (PC7769) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004

C:Accession: E01937

R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.

Nucleic Acids Res. 1978

A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.

A:Reference number: A93204; MUID:79073152; PMID:103003

A:Accession: E01937

A:Molecule type: protein

A:Residues: 1-111 <WEI>

A:Cross-references: UNIPROT:P01669; UNIPARC:UPI000002A104

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-94/Domain: immunoglobulin homology <IMM>

F:23-92/Disulfide bonds: #status predicted

Query Match 70.7%; Score 486; DB 1; Length 111;
 Best Local Similarity 82.0%; Pred. No. 1.1e-33;
 Matches 91; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 20 DIVMTQSPDLSAVSLGERATINCKASQSDYDGDSTYNNWYQKPGPPKLLIYAASNLSS 79
 DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSTYNNWYQKPGPPKLLIYAASNLSS 60

QY 80 GVPDRFSGSGGTDFLTITSSLAQEDVAVVYCOQSNEDPPRFGGGPKVEIK 130
 DB 61 GIPARFSGSGGTDFLTINHPVEEDAATYVCOQSNEDPWTFTSGGPKLEIK 111

RESULT 7

KAHU17

Ig kappa chain precursor V-IV region (B17) - human

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 21-Jan-2000

C:Accession: A01905

R:Marsh, P.; Mills, F.; Gould, H.

Nucleic Acids Res. 1985

A:Title: Detection of a unique human V kappa IV germline gene by a cloned cDNA probe.

A:Reference number: A01905; MUID:86041854; PMID:2997713

A:Accession: A01905

A:Molecule type: mRNA

A:Residues: 1-134 <MAR>

A:Cross-references: UNIPARC:UPI000017370A

A:Note: The sequence was determined from the differentiated gene

A:Note: The authors translated the codon TGC for residue 76 as TTP

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-134/Product: Ig kappa chain V-IV region (B17) #status predicted <MAT>
 F:21-43/Region: framework 1
 F:36-116/Domain: immunoglobulin homology <IMM>
 F:44-60/Region: complementarity-determining 1
 F:61-75/Region: framework 2
 F:76-82/Region: complementarity-determining 2
 F:83-114/Region: framework 3
 F:115-122/Region: complementarity-determining 3
 F:123-133/Region: framework 4
 F:43-114/Disulfide bonds: #status predicted

Query Match 69.6%; Score 478; DB 1; Length 134;
 Best Local Similarity 75.0%; Pred. No. 6.3e-33;
 Matches 96; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY 6 ILFLVATATGVHSDIVMTQSPDLSAVSLGERATINCKASQSDYDGD--SYNNWYQKPK 63
 DB 7 VFISLLWISGAYGDIVMTQSPDLSAVSLGERATINCKSSQSLYSNDKNKYLAWYQKPK 66

QY 64 GQPPKLLIYAASNLSSGVPDRFSGSGGTDFLTITSSLAQEDVAVVYCOQSNEDPPRFGG 123
 DB 67 GQPPKLLIYCASTRESGVPDRFSGSGGTDFLTITSSLAQEDVAVVYCOQYNLPTFTFGQ 126

QY 124 GTKVBIKR 131

DB 127 GTKVBIKR 134

RESULT 8

KAHUJ1

Ig kappa chain precursor V-IV region (JI) - human

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004

C:Accession: A01904

R:Klobeck, H.G.; Bornkamm, G.W.; Combriato, G.; Mocikat, R.; Pohlenz, H.D.; Zachau, H.G.

Nucleic Acids Res. 1985

A:Title: Subgroup IV of human immunoglobulin K light chains is encoded by a single germ line

A:Reference number: A93589; MUID:86041853; PMID:2997712

A:Accession: A01904

A:Molecule type: DNA

A:Residues: 1-133 <KLO>

A:Cross-references: UNIPROT:P06313; UNIPARC:UPI000012E165; GB:200022; GB:X51570; NID:93

A:Note: the sequence was determined from the differentiated gene

C:Genetics:

A:Gene: GDB:IGKV

A:Cross-references: GDB:119341; OMIM:146980

A:Map position: 2p12-2p12

A:Introns: 17/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-133/Product: Ig kappa chain V-IV region (JI) #status predicted <MAT>
 F:21-43/Region: framework 1
 F:36-116/Domain: immunoglobulin homology <IMM>
 F:44-60/Region: complementarity-determining 1
 F:61-75/Region: framework 2
 F:76-82/Region: complementarity-determining 2
 F:83-114/Region: framework 3
 F:115-122/Region: complementarity-determining 3
 F:123-133/Region: framework 4
 F:43-114/Disulfide bonds: #status predicted

Query Match 69.4%; Score 476.5; DB 1; Length 133;
 Best Local Similarity 75.8%; Pred. No. 8.4e-33;
 Matches 97; Conservative 10; Mismatches 18; Indels 3; Gaps 2;

QY 6 ILFLVATATGVHSDIVMTQSPDLSAVSLGERATINCKASQSDYDGD--SYNNWYQKPK 63
 DB 7 VFISLLWISGAYGDIVMTQSPDLSAVSLGERATINCKSSQSLYSNDKNKYLAWYQKPK 66

QY 64 GQPPKLLIYAASNLSSGVPDRFSGSGGTDFLTITSSLAQEDVAVVYCOQSNEDPPRFGG 123

```
Db 67 GQPPKLLIYWASTRESGVDRFSGSGTDFLTITSSLAQEDVAVYCCQ-YDTIPTFGG 125
Qy 124 GTKVEIKR 131
Db 126 GTKVEIKR 133

RESULT 9
KVMSCL
Ig kappa chain V region (CBPC 101) - mouse (tentative sequence)
C:Species: Mus musculus (house mouse)
C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 09-Jul-2004
C:Accession: A01936
R:McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related mo
A:Reference number: A93822; MUID:79012520; PMID:99744
A:Accession: A01936
A:Molecule type: protein
A:Residues: 1-111 <MCK>
A:Cross-references: UNIPROT:P01664; UNIPARC:UPI000002A0FF
C:Comment: This chain was isolated from a myeloma protein.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 69.3%; Score 476; DB 1; Length 111;
Best Local Similarity 81.1%; Pred. No. 7.7e-33;
Matches 90; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

Qy 20 DIVMTQSPDSLAVSLGERATINCKASQSDVDGSDYDGSYMNWYQKQPGQPKLLIYAASNLES 79
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSLDYDGSYMNWYQKQPGQPKLLIYAASNLES 60

Qy 80 GVPDRFSGSGTDFTLTISSLAQEDVAVYCCQSNEDPPRFGGKVEIK 130
Db 61 GIPARFSGSGTDFTLNIHPVEEDATYYCQSNEDPYTFGGGKLEIK 111

RESULT 10
SI9976
Ig kappa chain V region (M-T413) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: SI9976
R:Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: SI9963
A:Accession: SI9976
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <WEI>
A:Cross-references: UNIPARC:UPI0000116031; EMBL:X65093; NID:g52298; PIDN:CAA46221.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 69.1%; Score 475; DB 2; Length 112;
Best Local Similarity 79.5%; Pred. No. 9.4e-33;
Matches 89; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Qy 20 DIVMTQSPDSLAVSLGERATINCKASQSDVDGSDYDGSYMNWYQKQPGQPKLLIYAASNLES 79
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSLDYDGSYMNWYQKQPGQPKLLIYAASNLES 60

Qy 80 GVPDRFSGSGTDFTLTISSLAQEDVAVYCCQSNEDPPRFGGKVEIKR 131
Db 61 GIPARFSGSGTDFTLNIHPVEEDATYYCQSIQDPYTFGGGKLEIKR 112
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RESULT 11
KVMS10
Ig kappa chain V region (PC7210) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: D01937; A01937
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152; PMID:1033003
A:Accession: D01937
A:Molecule type: protein
A:Residues: 1-110 <WEI>
A:Cross-references: UNIPROT:P01668; UNIPARC:UPI000002A103
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 68.2%; Score 468.5; DB 1; Length 110;
Best Local Similarity 81.1%; Pred. No. 3.2e-32;
Matches 90; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

Qy 20 DIVMTQSPDSLAVSLGERATINCKASQSDVDGSDYDGSYMNWYQKQPGQPKLLIYAASNLES 79
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSLDYDGSYMNWYQKQPGQPKLLIYAASNLES 60

Qy 80 GVPDRFSGSGTDFTLTISSLAQEDVAVYCCQSNEDPPRFGGKVEIK 130
Db 61 GIPARFSGSGTDFTLNIHPVEEDATYYCHQS-EDPWTFGSGTKLEIK 110

RESULT 12
S34003
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S34003
R:Marlette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
A:Reference number: S34001; MUID:93209281; PMID:7681398
A:Accession: S34003
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <MAR>
A:Cross-references: UNIPARC:UPI0000176CCA
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 67.7%; Score 465; DB 2; Length 113;
Best Local Similarity 83.2%; Pred. No. 6.4e-32;
Matches 94; Conservative 4; Mismatches 13; Indels 2; Gaps 1;

Qy 20 DIVMTQSPDSLAVSLGERATINCKASQSDVDGSD--SYMNWYQKQPGQPKLLIYAASNL 77
Db 1 DIVMTQSPDSLAVSLGERATINCKSSQSLVLYSSNNKYLAWYQKQAGQPKLLITWASTR 60

Qy 78 ESGVDRFSGSGTDFTLTISSLAQEDVAVYCCQSNEDPPRFGGKVEIK 130
Db 61 ESGVDRFSGSGTDFTLTISSLAQEDVAVYCCQYLTPPTFGGKVEIK 113

RESULT 13
SI9972
Ig kappa chain V region (M-T321) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
```


C:Accession: S19972
R:Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: S19963
A:Accession: S19972
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <WEI>
A:Cross-references: UNIPARC:UPI0000116032; EMBL:X65094; NID:G52290; PIDN:CAA46222.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 67.5%; Score 464; DB 2; Length 112;
Best Local Similarity 78.6%; Pred. No. 7.7e-32;
Matches 88; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 20 DIVMTQSPDLSAVSLGERATINCKASQSYVDYDGSYMNWYQKPGQPPKLLIYAASNL 79
Db 1 DIVLTQSPASLAVSLGQRATIFCRASQSYDYNATSYMHWYQKPGQPPKLLIYAASNL 60

QY 80 GVPDRFSGSGGTDFLTITSSLAQEDVAVYVYCOQSNEDPPRFGGKTKVEIKR 131
Db 61 GIPARFSGSGGTDFLTIDHPVEEDATYVYCOQSNEDPYTFGGGKLEIKR 112

RESULT 14

S49531
anti-Sm antibody VL chain (V kappa 4/J kappa 3) - human
C:Species: Homo sapiens (man)
C>Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Jan-2000
C:Accession: S49531
R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S49531
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-134 <MAH>
A:Cross-references: UNIPARC:UPI000011666E; EMBL:Z46347; NID:G560841; PIDN:CAA86466.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:36-116/Domain: immunoglobulin homology <IMM>

Query Match 67.4%; Score 463; DB 2; Length 134;
Best Local Similarity 73.4%; Pred. No. 1.1e-31;
Matches 94; Conservative 10; Mismatches 22; Indels 2; Gaps 1;

QY 6 IILFLVATATGVHSDIVMTQSPDLSAVSLGERATINCKASQSYVDYDGD--SYMNWYQK 63
Db 7 VFISLLWLLSGAYGDIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNNKNVLAWYQK 66

QY 64 GQPPKLLIYAASNLGVPDRFSGSGGTDFLTITSSLAQEDVAVYVYCOQSNEDPPRFG 123
Db 67 GQPPKLLIYWASTRESGVPDRFSGSGGTDFLTITSSLAQEDVAVYVYCOQYSTAFTGP 126

QY 124 GTKVEIKR 131
Db 127 GTKVDIKR 134

RESULT 15

KWS37
Ig kappa chain V regions (PC3741, T111) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C:Accession: A93204; A93822; A01934
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152; PMID:103003
A:Contents: PC3741

A:Accession: A93204
A:Molecule type: protein
A:Residues: 1-111 <WEI>
A:Cross-references: UNIPROT:P01660; UNIPARC:UPI000002A0FB
R:McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related m
A:Reference number: A93822; MUID:79012520; PMID:99744
A:Contents: T111

A:Accession: A93822
A:Molecule type: protein
A:Residues: 1-111 <MCK>
A:Cross-references: UNIPARC:UPI000002A0FB
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kai
chain disulfide bonds. In some cases, such as IgA and IGM, the subunits associate into 1.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 67.2%; Score 462; DB 1; Length 111;
Best Local Similarity 78.4%; Pred. No. 1.1e-31;
Matches 87; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

QY 20 DIVMTQSPDLSAVSLGERATINCKASQSYVDYDGSYMNWYQKPGQPPKLLIYAASNL 79
Db 1 DIVLTQSPASLAVSLGQRATISCRASESDSYNSFMHWYQKPGQPPKLLIYRASNL 60

QY 80 GVPDRFSGSGGTDFLTITSSLAQEDVAVYVYCOQSNEDPPRFGGKTKVEIK 130
Db 61 GIPARFSGSGGTDFLTINPVEADVATYVYCOQSNEDPYTFGGGKLEIK 111

Search completed: February 23, 2006, 09:23:58
Job time : 24.1176 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 09:13:48 ; Search time 142.559 Seconds
(without alignments)
648.323 Million cell updates/sec

Title: US-10-723-872-14
Perfect score: 687
Sequence: 1 MGSWCIILFLVATATGVHSD.....QQSNEDPPRFGGKTVEIKR 131

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------|
| 1 | 493 | 71.8 | 111 | 1 | KV3M MOUSE |
| 2 | 492 | 71.6 | 111 | 1 | KV3N MOUSE |
| 3 | 489 | 71.2 | 111 | 1 | KV3Q MOUSE |
| 4 | 486 | 70.7 | 111 | 1 | KV3Q MOUSE |
| 5 | 476.5 | 69.4 | 133 | 1 | KV4B_HUMAN |
| 6 | 476 | 69.3 | 111 | 1 | KV3L MOUSE |
| 7 | 475 | 69.1 | 111 | 2 | Q811U6 MOUSE |
| 8 | 475 | 69.1 | 134 | 1 | KV4C_HUMAN |
| 9 | 468.5 | 68.2 | 110 | 1 | KV3P MOUSE |
| 10 | 462 | 67.2 | 111 | 1 | KV3H MOUSE |
| 11 | 462 | 67.2 | 114 | 1 | KV4A_HUMAN |
| 12 | 457.5 | 66.6 | 131 | 1 | KV3I MOUSE |
| 13 | 450 | 65.5 | 111 | 1 | KV3Q MOUSE |
| 14 | 442 | 64.3 | 111 | 1 | KV3K MOUSE |
| 15 | 437.5 | 63.7 | 132 | 1 | KV3F MOUSE |
| 16 | 436 | 63.5 | 111 | 1 | KV3T MOUSE |
| 17 | 434 | 63.2 | 111 | 1 | KV3R MOUSE |
| 18 | 433 | 63.0 | 111 | 2 | Q920E9 MOUSE |
| 19 | 430 | 62.6 | 121 | 1 | KV4O_HUMAN |
| 20 | 429 | 62.4 | 112 | 1 | KV3G MOUSE |
| 21 | 429 | 61.9 | 111 | 1 | KV3C MOUSE |
| 22 | 425 | 61.9 | 111 | 1 | KV3S MOUSE |
| 23 | 424 | 61.7 | 111 | 1 | KV3U MOUSE |
| 24 | 423.5 | 61.6 | 238 | 2 | Q66J57 MOUSE |
| 25 | 422.5 | 61.5 | 112 | 1 | KV3B MOUSE |
| 26 | 422 | 61.4 | 111 | 1 | KV3A MOUSE |
| 27 | 413 | 60.1 | 111 | 1 | KV3D MOUSE |
| 28 | 413 | 60.1 | 236 | 2 | Q6PIH7_HUMAN |
| 29 | 410 | 59.7 | 108 | 1 | KV1M_HUMAN |
| 30 | 408 | 59.4 | 240 | 2 | Q52164 MOUSE |
| 31 | 407.5 | 59.3 | 107 | 2 | Q96SA9_HUMAN |

| | | | | | |
|----|-------|------|-----|---|--------------|
| 32 | 406 | 59.1 | 111 | 2 | Q5F217 MOUSE |
| 33 | 403 | 58.7 | 108 | 2 | Q9UL77_HUMAN |
| 34 | 401.5 | 58.4 | 111 | 2 | Q65ZN3_MOUSE |
| 35 | 399.5 | 58.2 | 109 | 2 | Q9UL78_HUMAN |
| 36 | 399 | 58.1 | 236 | 2 | Q6GMX0_HUMAN |
| 37 | 396 | 57.6 | 103 | 2 | Q9JL80_MOUSE |
| 38 | 396 | 57.6 | 129 | 1 | KV3L_HUMAN |
| 39 | 395 | 57.5 | 108 | 1 | KV1H_HUMAN |
| 40 | 395 | 57.5 | 109 | 1 | KV4D_HUMAN |
| 41 | 394 | 57.4 | 108 | 2 | Q9UL70_HUMAN |
| 42 | 394 | 57.4 | 236 | 2 | Q6GMX8_HUMAN |
| 43 | 394 | 57.4 | 255 | 2 | Q6KB05_MOUSE |
| 44 | 393 | 57.2 | 108 | 2 | Q9UL79_HUMAN |
| 45 | 392 | 57.1 | 108 | 1 | KV1Y_HUMAN |

ALIGNMENTS

RESULT 1

| ID | KV3M MOUSE | STANDARD; | PRT; | 111 AA. |
|----|--|-----------|------|---------|
| AC | P01665; | | | |
| DT | 21-JUL-1986 (Rel. 01, Created) | | | |
| DT | 21-JUL-1986 (Rel. 01, Last sequence update) | | | |
| DT | 13-SEP-2005 (Rel. 48, Last annotation update) | | | |
| DE | Ig kappa chain V-III region PC 7043. | | | |
| OS | Mus musculus (Mouse) | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; | | | |
| OC | Muridae; Murinae; Mus. | | | |
| OX | NCBI_TaxID=10090; | | | |
| RN | [1]_TaxID=10090; | | | |
| RP | PROTEIN SEQUENCE. | | | |
| RX | MEDLINE=79073152; PubMed=103003; | | | |
| RA | Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; | | | |
| RT | "Rearrangement of genetic information may produce immunoglobulin | | | |
| RT | diversity."; | | | |
| RL | Nature 276:785-790(1978). | | | |
| RN | [2] | | | |
| RP | NUCLEOTIDE SEQUENCE OF 10-99. | | | |
| RX | MEDLINE=94009207; PubMed=7691608; | | | |
| RA | Mo J.A., Bona C.A., Holmdahl R.; | | | |
| RT | "Variable region gene selection of immunoglobulin G-expressing B cells | | | |
| RT | with specificity for a defined epitope on type II collagen."; | | | |
| RL | Eur. J. Immunol. 23:2503-2510(1993). | | | |
| RP | [3] | | | |
| RP | STRUCTURE BY NMR OF 1-111. | | | |
| RX | MEDLINE=20264305; PubMed=10801487; DOI=10.1016/S0969-2126(00)00119-2; | | | |
| RA | Tugarinov V., Zvi A., Levy R., Hayek Y., Mataushita S., Anglister J.; | | | |
| RT | "NMR structure of an anti-gp120 antibody complex with a V3 peptide | | | |
| RT | reveals a surface important for co-receptor binding."; | | | |
| RL | Structure 8:385-395(2000). | | | |
| CC | ----- | | | |
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| CC | use as long as its content is in no way modified and this statement is not | | | |
| CC | removed. | | | |
| CC | ----- | | | |
| DR | EMBL; Z25444; CAA80931.1; -; mRNA. | | | |
| DR | EMBL; Z25446; CAA80931.1; -; mRNA. | | | |
| DR | EMBL; Z25448; CAA80935.1; -; mRNA. | | | |
| DR | EMBL; Z25450; CAA80937.1; -; mRNA. | | | |
| DR | EMBL; Z25452; CAA80939.1; -; mRNA. | | | |
| DR | EMBL; Z25454; CAA80941.1; -; mRNA. | | | |
| DR | EMBL; Z25458; CAA80945.1; -; mRNA. | | | |
| DR | PIR; A01937; KVM543. | | | |
| DR | PDB; 1ONZ; NMR, E=1-111. | | | |
| DR | Ensembl; ENSMUSG00000053225; Mus musculus. | | | |
| DR | InterPro; IPR007110; Ig-like. | | | |
| DR | InterPro; IPR003596; Ig_v. | | | |
| DR | SMART; SM00406; IGV; 1. | | | |

| | |
|--------|-------------|
| Q5F217 | mus musculu |
| Q9UL77 | homo sapien |
| Q65ZN3 | mus musculu |
| Q9UL78 | homo sapien |
| Q6GMX0 | homo sapien |
| Q9JL80 | mus musculu |
| P18135 | homo sapien |
| P01600 | homo sapien |
| P83593 | homo sapien |
| P83593 | homo sapien |
| Q9UL70 | homo sapien |
| Q6GMX8 | homo sapien |
| Q6KB05 | mus musculu |
| Q9UL79 | homo sapien |
| P80362 | homo sapien |

```
DR PROSITE, PS50835; IG_LIKE; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 38
FT REGION 29 53
FT REGION 39 58
FT REGION 54 60
FT REGION 61 92
FT REGION 93 101
FT REGION 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12002 MW; 7ASFCB586C306D29 CRC64;

Query Match 71.8%; Score 493; DB 1; Length 111;
Best Local Similarity 83.8%; Pred. No. 4.8e-41;
Matches 93; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 20 DIVVTQSPDSLAVSLGERATINCKASQSDVDGDSYNNWYQOKPGPKLLIYAASNL 79
DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQOKPGPKLLIYAASNL 60
QY 80 GVPDRFSGSGGTDTFTLTISLQAEADVAVYYCQSNEDPPRFGGKVKV 130
DB 61 GIPARFSGSGGTDTFTLTINHPVEEDATYYCQSNEDPFTFGSTKLEIK 111

RESULT 2
KV3N_MOUSE
ID_KV3N_MOUSE STANDARD; PRT; 111 AA.
AC P01666;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE IG kappa chain V-III region PC 7183.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790 (1978).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC removed.
CC -----
CC PIR; B01937; KVM883.
CC HSP; P01665; 1QNZ.
CC SMR; P01666; 1-111.
CC Ensembl; ENSMUSG00000053225; Mus musculus.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003596; IG_v.
CC SMART; SM00406; IGV; 1_v.
CC PROSITE; PS50835; IG_LIKE; 1.
CC Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 38
FT REGION 29 53
FT REGION 39 58
FT REGION 54 60
FT REGION 61 92
FT REGION 93 101
FT REGION 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 71.2%; Score 489; DB 1; Length 111;
Best Local Similarity 82.9%; Pred. No. 1.2e-40;
Matches 92; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 20 DIVVTQSPDSLAVSLGERATINCKASQSDVDGDSYNNWYQOKPGPKLLIYAASNL 79
DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQOKPGPKLLIYAASNL 60
QY 80 GVPDRFSGSGGTDTFTLTISLQAEADVAVYYCQSNEDPPRFGGKVKV 130
DB 61 GIPARFSGSGGTDTFTLTINHPVEEDATYYCQSNEDPFTFGSTKLEIK 111

RESULT 3
KV3O_MOUSE
ID_KV3O_MOUSE STANDARD; PRT; 111 AA.
AC P01667;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE IG kappa chain V-III region PC 6308.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790 (1978).
CC -----
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CC -----
CC PIR; C01937; KVM508.
CC HSP; P01665; 1QNZ.
CC SMR; P01667; 1-111.
CC Ensembl; ENSMUSG00000053225; Mus musculus.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003596; IG_v.
CC SMART; SM00406; IGV; 1_v.
CC PROSITE; PS50835; IG_LIKE; 1.
CC Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 38
FT REGION 29 53
FT REGION 39 58
FT REGION 54 60
FT REGION 61 92
FT REGION 93 101
FT REGION 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 71.2%; Score 489; DB 1; Length 111;
Best Local Similarity 82.9%; Pred. No. 1.2e-40;
Matches 92; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 20 DIVVTQSPDSLAVSLGERATINCKASQSDVDGDSYNNWYQOKPGPKLLIYAASNL 79
DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQOKPGPKLLIYAASNL 60
QY 80 GVPDRFSGSGGTDTFTLTISLQAEADVAVYYCQSNEDPPRFGGKVKV 130
DB 61 GIPARFSGSGGTDTFTLTINHPVEEDATYYCQSNEDPFTFGSTKLEIK 111
```

Db 61 GIPARFSGSGTDFTLNIHPVEEDAAATYCCQSNEDPWTFGSGTKLEIK 111

RESULT 4

KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region PC 7769.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity."
RL Nature 276:785-790 (1978).

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CC PIR; E01937; KVM569.
DR HSSP; P01665; IQNZ.
DR SMR; P01669; 1-111.
DR Ensembl; ENSMUSG0000053225; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 38
FT REGION 39 53
FT REGION 54 60
FT REGION 61 92
FT REGION 93 101
FT REGION 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;

Query Match 70.7%; Score 486; DB 1; Length 111;
Best Local Similarity 82.0%; Pred. No. 2.4e-40;
Matches 91; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 20 DIVMTQSPDLSAVSLGERATINCKASQSDYDGDSTNNYQKPGPKLLIYAASNLES 79

Db 1 DIVLTQSPASVSLGORATISCKASQSDYDGDSTNNYQKPGPKLLIYAASNLES 60

QY 80 GVPDRFSGSGTDFTLTISSLOAEVAVVYCCQSNEDPRTFGSGTKLEIK 130

Db 61 GIPARFSGSGTDFTLNIHPVEEDAAATYCCQSNEDPWTFGSGTKLEIK 111

RESULT 5

KV4B_HUMAN STANDARD; PRT; 133 AA.
AC P06313;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-IV region JI precursor.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobbeck H.G., Bornkamm G.W., Combratio G., Mocikat R., Pohlenz H.D.,
RA Zschau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
single germline gene."
RL Nucleic Acids Res. 13:6515-6529 (1985).

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CC EMBL; Z00022; CAA77317.1; -; Genomic_DNA.
DR PIR; A01904; K4HUJI.
DR HSSP; P01625; ILVE.
DR SMR; P06313; 21-133.
DR GO; GO:0005576; Cretacellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133
FT REGION 21 43
FT REGION 44 60
FT REGION 61 75
FT REGION 76 82
FT REGION 83 114
FT REGION 115 122
FT REGION 123 132
FT DISULFID 43 114
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14633 MW; 5PB3953068744AF4 CRC64;

Query Match 69.4%; Score 476.5; DB 1; Length 133;
Best Local Similarity 75.8%; Pred. No. 2.6e-39;
Matches 97; Conservative 10; Mismatches 18; Indels 3; Gaps 2;

QY 6 IILFLVATATGVHSDIVMTQSPDLSAVSLGERATINCKASQSDYDGD--SYNNYQKPK 63

Db 7 VFISLLMTSGAYGDIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNNKNYLAQYQKPK 66

QY 64 GPPKLLIYAASNLESVPDRFSGSGTDFTLTISSLOAEVAVVYCCQSNEDPRTFG 123

Db 67 GPPKLLIYASTRESGVPDRFSGSGTDFTLTISSLOAEVAVVYCCQ-YDTPTFG 125

QY 124 GTKVEIKR 131

Db 126 GTKVEIKR 133

RESULT 6

KV3L_MOUSE STANDARD; PRT; 111 AA.
AC P01664;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region CBPC 101.
OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein.
CC -----
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CC removed.
CC -----
CC PIR; A01936; KVMSC1.
DR HSP; P01665; 1QNZ.
DR SMR; P01664; 1-111.
DR Ensembl; ENSMUSG00000053225; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 38
FT REGION 39 53
FT REGION 54 60
FT REGION 61 92
FT REGION 93 101
FT REGION 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11964 MW; E2B1AD98AD65962 CRC64;

Query Match 69.3%; Score 476; DB 1; Length 111;
Best Local Similarity 81.1%; Pred. No. 2.3e-39;
Matches 90; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 20 DIVMTQSPDLSAVSLGERATINCKASQSVYDGDSDYMMWYQKPGQPKLLIYAASNLSS 79
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSVYDGTGDSFMWYQKPGQPKLLIYTTSNLESG 60
QY 80 GVPDRFSGSGCTDFTLTITSLQAEDVAVYVYCCQSNEDPPRFGGGKVEIK 130
Db 61 GIPARFSGSGCTDFTLTNIHPVEEDATYYCQSNEDPYTFGGGKLEIK 111

RESULT 7
Q811U6 MOUSE PRELIMINARY; PRT; 111 AA.
AC Q811U6
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-human Fc gamma receptor III 3G8 kappa light chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RX PubMed=15059139; DOI=10.1111/j.1365-2141.2004.04893.x;
RA Bruenke J., Fischer B., Barbin K., Schreiter K., Wachter Y., Mahr K.,
RA Titgemeyer F., Niederweis M., Peipp M., Zunino S.J., Repp R.,
RA Valerius T., Fey G.H.;
RT "A recombinant bispecific single-chain Fv antibody against HLA class
RT II and FcgammaRIII (CD16) triggers effective lysis of lymphoma
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cells.";
RL Br. J. Haematol. 125:167-179(2004).
DR EMBL; AY173024; AAO18226.1; -; mRNA.
DR HSP; P01665; 1QNZ.
DR SMR; Q811U6; 1-111.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Receptor.
FT NON_TER 1 111
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12101 MW; CEDECEEL157F2C94A CRC64;

Query Match 69.1%; Score 475; DB 2; Length 111;
Best Local Similarity 79.3%; Pred. No. 2.9e-39;
Matches 88; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 21 IVMTQSPDLSAVSLGERATINCKASQSVYDGDSDYMMWYQKPGQPKLLIYAASNLSSG 80
Db 1 IVLTQSPASLAVSLGQRATISCKASQSVDFDGDSDYMMWYQKPGQPKLLIYTTSNLESG 60
QY 81 VPDREFSGSGCTDFTLTITSLQAEDVAVYVYCCQSNEDPPRFGGGKVEIKR 131
Db 61 IPARFSGSGCTDFTLTNIHPVEEDATYYCQSNEDPYTFGGGKLEIKR 111

RESULT 8
KV4C_HUMAN STANDARD; PRT; 134 AA.
ID KV4C_HUMAN
AC P06314;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-IV region B17 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86041854; PubMed=2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned cDNA
RT probe.";
RL Nucleic Acids Res. 13:6531-6544(1985).
RN [2]
RP SEQUENCE REVISION TO 76.
RA Marsh P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; X02990; CAA26733.1; -; mRNA.
DR HSP; P01625; 1LVE.
DR SMR; P06314; 21-134.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 134
FT REGION 21 43
FT REGION 21 43
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FT REGION 44 60 Complementarity-determining-1.
FT REGION 61 75 Framework-2.
FT REGION 76 82 Complementarity-determining-2.
FT REGION 83 114 Framework-3.
FT REGION 115 121 Complementarity-determining-3.
FT REGION 122 133 Framework-4.
FT DISULFID 43 114 By similarity.
FT NON_TER 134 134
SQ SEQUENCE 134 AA; 14966 MW; 6413A22FDD0738832 CRC64;

Query Match 69.1%; Score 475; DB 1; Length 134;
Best Local Similarity 75.0%; Pred. No. 3.7e-39;
Matches 96; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY 6 IILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSDYDGD--SYNNWYQKP 63
Db 7 VFISLLLTWISGAYGVMTQSPDSLAVSLGERATINCKSSQSLYSNDKNYLAWYQKP 66

QY 64 GPPKLLIYAASNLSEGVDPFRSGSGGTDFTLTISLQAEADVAVVYCCQSNEDPPRFGG 123
Db 67 GPPKLLIYWASTRESGVDPFRSGSGGTDFTLTISLQAEADVAVVYCCQYNLPWTFQG 126

QY 124 GTKVEIKR 131
Db 127 GTKVEIKR 134

RESULT 9
KV3P_MOUSE STANDARD; PRT; 110 AA.
AC P01668;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region PC 7210.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC PIR; D01937; KVM510.
DR HSSP; P01665; IONZ.
DR SMR; P01668; 1-110.
DR Ensembl; ENSMUSG0000053225; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 38 Complementarity-determining-1.
FT REGION 39 53 Framework-2.
FT REGION 54 60 Complementarity-determining-2.
FT REGION 61 92 Framework-3.
FT REGION 93 100 Framework-4.
FT DISULFID 101 110 By similarity.
FT NON_TER 110 110
```

```
SQ SEQUENCE 110 AA; 11950 MW; 69F1A5CE886B1249 CRC64;

Query Match 68.2%; Score 468.5; DB 1; Length 110;
Best Local Similarity 81.1%; Pred. No. 1.3e-38;
Matches 90; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

QY 20 DIVMTQSPDSLAVSLGERATINCKASQSDYDGDSDYNNWYQKPGPPKLLIYAASNLSE 79
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSLDYDGDSDYNNWYQKPGPPKLLIYAASNLSE 60

QY 80 GVPDRFSGSGGTDTLTITSSLQAEADVAVVYCCQSNEDPPRGGTKVEIK 130
Db 61 GIPARFSGSGGTDTLTITSSLQAEADVAVVYCCQSNEDPPRGGTKVEIK 110

RESULT 10
KV3H_MOUSE STANDARD; PRT; 111 AA.
AC P01660;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region PC 3741/TEPC 111.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE (PC 3741).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
RN [2]
RP PROTEIN SEQUENCE (TEPC 111).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -!- MISCELLANEOUS: The PC 3741 and TEPC 111 sequences are identical.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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removed.
CC PIR; A93204; KVM537.
DR HSSP; P01665; IONZ.
DR Ensembl; ENSMUSG0000060064; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 38 Complementarity-determining-1.
FT REGION 39 53 Framework-2.
FT REGION 54 60 Complementarity-determining-2.
FT REGION 61 92 Framework-3.
FT REGION 93 101 Framework-4.
FT DISULFID 102 111 By similarity.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;

Query Match 67.2%; Score 462; DB 1; Length 111;
Best Local Similarity 78.4%; Pred. No. 5.8e-38;
Matches 87; Conservative 14; Mismatches 10; Indels 0; Gaps 0;
```

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QY      20 DIVMTQSPDLSAVSLGERATINCKASQSVYDGDGSMYNNWYQKPGQPPKLLIYAASNL 79
      1 DIVLTQSPASLAVSLGQRATISCRASESVDSYSGNSFMHWYQKPGQPPKLLIYRASNL 60
QY      80 GVPDRFSGSGGTFTLTLSISLQAEADVAVYYCQSNEDPPRFGGGTKVEIK 130
      61 GIPARFSGSGRTDFTLTINPVEADVAVYYCQSNEDPYTFGGGTKLEIK 111
Db
```

RESULT 11

```
KV4A_HUMAN
ID KV4A_HUMAN STANDARD; PRT; 114 AA.
AC P01625;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-IV region Len.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=76004342; PubMed=50995;
RA Schneider M., Hilschmann N.;
RT "The primary structure of a monoclonic immunoglobulin-L-chain of
RT subgroup IV of the kappa type (Bence-Jones protein Len).";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
RN [2]
RP SEQUENCE REVISION TO 9.
RA Salomon A.;
RL Submitted (AUG-1996) to Swiss-Prot.
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
```

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DR PDB; 1EEU; X-ray; A/B=1-114.
DR PDB; 1EEU; X-ray; A/B=1-114.
DR PDB; 1EFQ; X-ray; A=1-114.
DR PDB; 1EK3; X-ray; A/B=1-114.
DR PDB; 1LVE; X-ray; @=1-114.
DR PDB; 2LVE; X-ray; @=1-114.
DR PDB; 3LVE; X-ray; @=1-114.
DR PDB; 4LVE; X-ray; A/B=1-114.
DR PDB; 5LVE; X-ray; A=1-114.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin domain; Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 40 Complementarity-determining-1.
FT REGION 41 55 Framework-2.
FT REGION 56 62 Complementarity-determining-2.
FT REGION 63 94 Complementarity-determining-3.
FT REGION 95 101 Complementarity-determining-3.
FT REGION 102 113 Framework-4.
FT DISULFID 23 94 By similarity.
FT NON_TER 114 114
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16
```

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FT STRAND 19 25
FT STRAND 30 31
FT TURN 32 35
FT STRAND 36 37
FT STRAND 39 44
FT TURN 46 47
FT STRAND 51 55
FT TURN 56 58
FT STRAND 59 60
FT TURN 62 63
FT TURN 66 67
FT STRAND 68 73
FT TURN 74 75
FT STRAND 76 81
FT HELIX 86 88
FT STRAND 90 96
FT STRAND 103 104
FT STRAND 108 112
SQ SEQUENCE 114 AA; 12640 MW; 0647F1D17F236485 CRC64;
Query Match 67.2%; Score 462; DB 1; Length 114;
Best Local Similarity 82.5%; Pred. No. 6e-38;
Matches 94; Conservative 4; Mismatches 14; Indels 2; Gaps 1;
QY      20 DIVMTQSPDLSAVSLGERATINCKASQSVYDGDGSMYNNWYQKPGQPPKLLIYAASNL 77
      1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSKNYLAWYQKPGQPPKLLIYWASTR 60
QY      78 ESVGDPDRFSGSGGTFTLTLSISLQAEADVAVYYCQSNEDPPRFGGGTKVEIKR 131
      61 ESVGDPDRFSGSGGTFTLTLSISLQAEADVAVYYCQYSTPYSGGKLEIKR 114
Db
RESULT 12
KV3I_MOUSE
ID KV3I_MOUSE STANDARD; PRT; 131 AA.
AC P01661;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region MOPC 63 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE OF 1-35.
RX MEDLINE=78235887; PubMed=98179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to the
RT variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled expression
RT of immunoglobulin genes.";
RL Biochemistry 17:2392-2400(1978).
RN [2]
RP PROTEIN SEQUENCE OF 21-131.
RX MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RT kappa chains with limited sequence differences.";
RL Biochemistry 12:760-771(1973).
RN [3]
RP SEQUENCE REVISION.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -----
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CC the European Bioinformatics Institute. There are no restrictions on its
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```
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 38 Framework-1.
FT REGION 39 53 Complementarity-determining-1.
FT REGION 54 60 Framework-2.
FT REGION 61 92 Complementarity-determining-2.
FT REGION 93 101 Framework-3.
FT REGION 102 111 Complementarity-determining-3.
FT DISULFID 23 92 By similarity.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12005 MW; 39D87619313453CB CRC64;

Query Match 64.3%; Score 442; DB 1; Length 111;
Best Local Similarity 74.8%; Pred. No. 5.6e-36;
Matches 83; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

QY 20 DIVMTQSPDSLAVSLGERATINCKASQSDVDGDSYMNWYQKQPPKLLIYAASNLLES 79
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 NIVLTQSPASLAVSLGQRATISCRASESDVSGNSFMHWYQKQPPKLLIYLASNLLES 60

QY 80 GVPDRFSGSGGTDTFTLTISLSLAQEDVAVYYCQSNEDPPRFGGKVEIK 130
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GVPARFSGSGKRTDTFTLIDPVEADDAATYYCQNNEDPLTFGAGTKLELK 111

RESULT 15
KV3F_MOUSE STANDARD; PRT; 132 AA.
AC P01658;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region MOPC 321 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE OF 1-37.
RX MEDLINE=78235887; PubMed=98179;
RA Birstein V., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to the
RT variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled expression
RT of immunoglobulin genes."
RL Biochemistry 17:2392-2400(1978).
RN [2]
RP PROTEIN SEQUENCE OF 21-132.
RX MEDLINE=73140224; PubMed=4120629;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Partial amino acid sequence of a kappa
RT chain."
RL Biochemistry 12:749-759(1973).
CC -!- MISCELLANEOUS: The partial sequence of the C region of this Bence-
CC Jones protein was also determined. It differs from that reported
CC for mouse MOPC 21 only in the transposition of two nearby
CC residues.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A90412; KVM832.
CC DR HSSP; P01665; 1QNZ.
CC DR SMR; P01658; 21-132.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003596; Ig_v.
CC DR SMART; SM00406; Igv; 1.
CC DR PROSITE; PS0835; IG_LIKE; 1.
CC Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
```

```
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 132 Ig kappa chain V-III region MOPC 321.
FT REGION 21 43 Framework-1.
FT REGION 44 58 Complementarity-determining-1.
FT REGION 59 73 Framework-2.
FT REGION 74 80 Complementarity-determining-2.
FT REGION 81 112 Framework-3.
FT REGION 113 121 Complementarity-determining-3.
FT REGION 122 131 Framework-4.
FT DISULFID 43 112 By similarity.
FT NON_TER 132 132
SQ SEQUENCE 132 AA; 14525 MW; 9F3B809BB773FBE9 CRC64;

Query Match 63.7%; Score 437.5; DB 1; Length 132;
Best Local Similarity 62.7%; Pred. No. 1.9e-35;
Matches 79; Conservative 27; Mismatches 17; Indels 3; Gaps 1;

QY 6 IILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKASQSDVDGDSYMNWYQKQPGQ 65
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 10 VLLLVTPGSTG--DIVLTQSPASLAVSLGQRATISCRASKSVNTYGNFWMZZKPGZ 66

QY 66 PPKLLIYAASNLSEGVDPDRFSGSGGTDTFTLTISLSLAQEDVAVYYCQSNEDPPRFGGKT 125
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 67 PPKLLIYASNLZSGIPARFSGSGSRTEFTLTIBPVZABDVATYFCZZSBZEPWTFSGGT 126

QY 126 KVEIKR 131
   :||||
Db 127 KLEIKR 132
```

Search completed: February 23, 2006, 09:23:06
Job time : 143.559 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 09:29:34 ; Search time 129.231 Seconds
(without alignments)
50.999 Million cell updates/sec

Title: US-10-723-872-16

Perfect score: 79

Sequence: 1 KASQSVYDGDSYMN 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 43937871 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

A_Geneseq_21.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001s.*

5: Geneseq2002s.*

6: Geneseq2003as.*

7: Geneseq2003bs.*

8: Geneseq2004s.*

9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|-------|---------------------|
| 1 | 79 | 100.0 | 15 | 2 | AAR70195 MAb 3B9 1 |
| 2 | 79 | 100.0 | 15 | 2 | AAW83027 Anti-Fas |
| 3 | 79 | 100.0 | 15 | 2 | AAW23772 CDR of th |
| 4 | 79 | 100.0 | 15 | 2 | AAV18114 |
| 5 | 79 | 100.0 | 15 | 3 | AAE14744 Mouse ant |
| 6 | 79 | 100.0 | 15 | 3 | AAV51136 Murine CD |
| 7 | 79 | 100.0 | 15 | 3 | AAW90894 Murine an |
| 8 | 79 | 100.0 | 15 | 3 | AAV59259 Antibody |
| 9 | 79 | 100.0 | 15 | 5 | ABB74909 Humanised |
| 10 | 79 | 100.0 | 15 | 5 | ABB74863 Humanised |
| 11 | 79 | 100.0 | 19 | 2 | AAE66143 CD-4 anti |
| 12 | 79 | 100.0 | 103 | 3 | AAV51140 Murine de |
| 13 | 79 | 100.0 | 103 | 3 | AAV59263 Antibody |
| 14 | 79 | 100.0 | 105 | 6 | AAE37732 MT413 mod |
| 15 | 79 | 100.0 | 106 | 2 | AAV33309 MAbE15 lig |
| 16 | 79 | 100.0 | 106 | 3 | AAV85197 Light cha |
| 17 | 79 | 100.0 | 111 | 1 | AAV90541 Immunoglo |
| 18 | 79 | 100.0 | 111 | 2 | AAV33305 MAbE11 lig |
| 19 | 79 | 100.0 | 111 | 2 | AAV55123 Mouse ant |
| 20 | 79 | 100.0 | 111 | 2 | AAV55127 Mouse-hum |
| 21 | 79 | 100.0 | 111 | 2 | AAV60302 Anti HIV |
| 22 | 79 | 100.0 | 111 | 2 | AAV60306 Chimeric |
| 23 | 79 | 100.0 | 111 | 2 | AAV23781 Light cha |
| 24 | 79 | 100.0 | 111 | 2 | AAV95650 MAb muscu |

| | | | | | |
|----|----|-------|-----|---|---------------------|
| 25 | 79 | 100.0 | 111 | 2 | AAV18123 |
| 26 | 79 | 100.0 | 111 | 3 | AAV85193 |
| 27 | 79 | 100.0 | 111 | 3 | AAV51146 |
| 28 | 79 | 100.0 | 111 | 3 | AAV51144 Murine de |
| 29 | 79 | 100.0 | 111 | 3 | AAV59267 Antibody |
| 30 | 79 | 100.0 | 111 | 4 | AAV76939 |
| 31 | 79 | 100.0 | 111 | 8 | ADN07026 Murine an |
| 32 | 79 | 100.0 | 111 | 9 | ADW0648 Murine Ma |
| 33 | 79 | 100.0 | 111 | 9 | ADY85020 Human HMG |
| 34 | 79 | 100.0 | 112 | 2 | AAR24575 Human x m |
| 35 | 79 | 100.0 | 112 | 9 | AE21888 Human DC- |
| 36 | 79 | 100.0 | 113 | 4 | AAE71895 Monoclonal |
| 37 | 79 | 100.0 | 113 | 8 | ADI26494 Human ECL |
| 38 | 79 | 100.0 | 113 | 8 | ADO06847 Virucidal |
| 39 | 79 | 100.0 | 113 | 8 | ADO06796 Virucidal |
| 40 | 79 | 100.0 | 113 | 8 | ADO06849 Virucidal |
| 41 | 79 | 100.0 | 113 | 8 | ADO06851 Virucidal |
| 42 | 79 | 100.0 | 115 | 2 | AAR04134 |
| 43 | 79 | 100.0 | 120 | 2 | AAE48618 |
| 44 | 79 | 100.0 | 131 | 1 | AAV90543 |
| 45 | 79 | 100.0 | 131 | 2 | AAV04132 Anti-Leu |
| 46 | 79 | 100.0 | 131 | 2 | AAV70202 Humanized |
| 47 | 79 | 100.0 | 131 | 2 | AAV75355 Humanized |
| 48 | 79 | 100.0 | 131 | 2 | AAV23771 Light cha |
| 49 | 79 | 100.0 | 131 | 2 | AAV23779 Light cha |
| 50 | 79 | 100.0 | 131 | 2 | AAV18118 Light cha |
| 51 | 79 | 100.0 | 131 | 2 | AAV18126 Light cha |
| 52 | 79 | 100.0 | 132 | 2 | AAV70189 Mouse Mab |
| 53 | 79 | 100.0 | 132 | 2 | AAV23767 Light cha |
| 54 | 79 | 100.0 | 132 | 2 | AAV18120 Light cha |
| 55 | 79 | 100.0 | 218 | 2 | AAW13563 Humanised |
| 56 | 79 | 100.0 | 218 | 8 | ADP88435 Antibody |
| 57 | 79 | 100.0 | 218 | 8 | ADP88427 Antibody |
| 58 | 79 | 100.0 | 218 | 8 | ADP88451 Antibody |
| 59 | 79 | 100.0 | 218 | 8 | ADP88443 Antibody |
| 60 | 79 | 100.0 | 220 | 8 | ADO06858 Virucidal |
| 61 | 79 | 100.0 | 222 | 8 | ADO06856 Virucidal |
| 62 | 79 | 100.0 | 232 | 2 | AAW01751 MH1 monocl |
| 63 | 79 | 100.0 | 232 | 2 | AAW83035 Anti-Fas |
| 64 | 79 | 100.0 | 238 | 2 | AAW83042 Anti-Fas |
| 65 | 79 | 100.0 | 238 | 2 | AAW83034 Anti-Fas |
| 66 | 79 | 100.0 | 238 | 2 | AAW83033 Anti-Fas |
| 67 | 79 | 100.0 | 238 | 2 | AAW83032 Anti-Fas |
| 68 | 79 | 100.0 | 238 | 2 | AAW83031 Anti-Fas |
| 69 | 79 | 100.0 | 238 | 3 | AAE14748 Mouse ant |
| 70 | 79 | 100.0 | 238 | 3 | AAE14774 Humanised |
| 71 | 79 | 100.0 | 238 | 3 | AAE14773 Humanised |
| 72 | 79 | 100.0 | 238 | 3 | AAE14777 Humanised |
| 73 | 79 | 100.0 | 238 | 3 | AAE14778 Humanised |
| 74 | 79 | 100.0 | 238 | 3 | AAV90931 Humanised |
| 75 | 79 | 100.0 | 238 | 3 | AAV90932 Humanised |
| 76 | 79 | 100.0 | 238 | 3 | AAV90927 Humanised |
| 77 | 79 | 100.0 | 238 | 3 | AAV90932 Humanised |
| 78 | 79 | 100.0 | 238 | 3 | AAV90924 Humanised |
| 79 | 79 | 100.0 | 238 | 3 | AAV90928 Humanised |
| 80 | 79 | 100.0 | 238 | 3 | AAV90928 Murine an |
| 81 | 79 | 100.0 | 238 | 3 | AAV90923 Humanised |
| 82 | 79 | 100.0 | 238 | 3 | AAV90922 Humanised |
| 83 | 79 | 100.0 | 238 | 3 | AAV90930 Humanised |
| 84 | 79 | 100.0 | 238 | 5 | AAE18371 Human pen |
| 85 | 79 | 100.0 | 238 | 5 | AAE74937 Humanised |
| 86 | 79 | 100.0 | 238 | 5 | ABB74938 Humanised |
| 87 | 79 | 100.0 | 238 | 5 | ABB74939 Humanised |
| 88 | 79 | 100.0 | 238 | 5 | ABB74942 Humanised |
| 89 | 79 | 100.0 | 238 | 5 | ABB74943 Humanised |
| 90 | 79 | 100.0 | 238 | 5 | ABB74913 Humanised |
| 91 | 79 | 100.0 | 238 | 5 | ABB74897 Humanised |
| 92 | 79 | 100.0 | 238 | 5 | ABB74899 Humanised |
| 93 | 79 | 100.0 | 238 | 5 | ABB74867 Humanised |
| 94 | 79 | 100.0 | 238 | 5 | ABB74900 Humanised |
| 95 | 79 | 100.0 | 238 | 5 | ABB74892 Humanised |
| 96 | 79 | 100.0 | 238 | 5 | ABB74893 Humanised |
| 97 | 79 | 100.0 | 238 | 5 | ABB74891 Humanised |

| | | | | | | | | | | | | | | | |
|-----|----|-------|-----|---|----------|----------|------------|-----|----|------|-----|---|----------|----------|-----------|
| 98 | 79 | 100.0 | 238 | 5 | ABB74896 | Abb74896 | Humanised | 171 | 76 | 96.2 | 497 | 9 | ADV21507 | Adv21507 | Mature fo |
| 99 | 79 | 100.0 | 238 | 5 | ABB74901 | Abb74901 | Humanised | 172 | 76 | 96.2 | 498 | 9 | ADV21503 | Adv21503 | Mature fo |
| 100 | 79 | 100.0 | 238 | 5 | ABG76346 | Abg76346 | Mouse DAV | 173 | 76 | 96.2 | 498 | 9 | ADV21513 | Adv21513 | Mature fo |
| 101 | 79 | 100.0 | 238 | 6 | ADA47339 | Ada47339 | TRX1 high | 174 | 76 | 96.2 | 498 | 9 | ADZ83558 | Adz83558 | Vector pE |
| 102 | 79 | 100.0 | 238 | 6 | ADA47330 | Ada47330 | TRX1 high | 175 | 76 | 96.2 | 498 | 9 | ADZ83761 | Adz83761 | CD3 speci |
| 103 | 79 | 100.0 | 238 | 6 | ADA47338 | Ada47338 | TRX1 high | 176 | 76 | 96.2 | 498 | 9 | ADZ83574 | Adz83574 | Vector pE |
| 104 | 79 | 100.0 | 238 | 6 | ADA47332 | Ada47332 | TRX1 high | 177 | 76 | 96.2 | 498 | 9 | ADZ83713 | Adz83713 | CD3 speci |
| 105 | 79 | 100.0 | 238 | 8 | ADP88434 | Adp88434 | Antibody | 178 | 76 | 96.2 | 498 | 9 | ADZ83725 | Adz83725 | CD3 speci |
| 106 | 79 | 100.0 | 238 | 8 | ADP88442 | Adp88442 | Antibody | 179 | 76 | 96.2 | 498 | 9 | ADZ83556 | Adz83556 | Vector pE |
| 107 | 79 | 100.0 | 238 | 8 | ADP88450 | Adp88450 | Antibody | 180 | 76 | 96.2 | 498 | 9 | ADZ83572 | Adz83572 | Vector pE |
| 108 | 79 | 100.0 | 238 | 8 | ADP88426 | Adp88426 | Antibody | 181 | 76 | 96.2 | 498 | 9 | ADZ83564 | Adz83564 | Vector pE |
| 109 | 79 | 100.0 | 238 | 8 | ADQ87972 | Adq87972 | Light cha | 182 | 76 | 96.2 | 498 | 9 | ADZ83741 | Adz83741 | CD3 speci |
| 110 | 79 | 100.0 | 238 | 8 | ADQ87976 | Adq87976 | Light cha | 183 | 76 | 96.2 | 498 | 9 | ADZ83733 | Adz83733 | CD3 speci |
| 111 | 79 | 100.0 | 238 | 8 | ADQ87964 | Adq87964 | Light cha | 184 | 76 | 96.2 | 498 | 9 | ADZ83755 | Adz83755 | CD3 speci |
| 112 | 79 | 100.0 | 238 | 8 | ADQ87968 | Adq87968 | Light cha | 185 | 76 | 96.2 | 498 | 9 | ADZ83566 | Adz83566 | Vector pE |
| 113 | 79 | 100.0 | 238 | 9 | AE896755 | Aeb96755 | DAV-1 ant | 186 | 76 | 96.2 | 498 | 9 | ADZ83568 | Adz83568 | Vector pE |
| 114 | 79 | 100.0 | 305 | 3 | AAV51142 | Aay51142 | Murine de | 187 | 76 | 96.2 | 498 | 9 | ADZ83570 | Adz83570 | Vector pE |
| 115 | 79 | 100.0 | 305 | 3 | AAV51141 | Aay51141 | Murine de | 188 | 76 | 96.2 | 498 | 9 | ADZ83709 | Adz83709 | CD3 speci |
| 116 | 79 | 100.0 | 305 | 3 | AAV59264 | Aay59264 | Antibody | 189 | 76 | 96.2 | 498 | 9 | ADZ83721 | Adz83721 | CD3 speci |
| 117 | 79 | 100.0 | 305 | 3 | AAV59265 | Aay59265 | Antibody | 190 | 76 | 96.2 | 498 | 9 | ADZ83578 | Adz83578 | Vector pE |
| 118 | 79 | 100.0 | 331 | 6 | AAE37727 | Aae37727 | Chemokine | 191 | 76 | 96.2 | 498 | 9 | ADZ83749 | Adz83749 | CD3 speci |
| 119 | 79 | 100.0 | 331 | 6 | AAE37733 | Aae37733 | Chemokine | 192 | 76 | 96.2 | 498 | 9 | ADZ83562 | Adz83562 | Vector pE |
| 120 | 79 | 100.0 | 339 | 6 | AAE37728 | Aae37728 | Chemokine | 193 | 76 | 96.2 | 498 | 9 | ADZ83705 | Adz83705 | CD3 speci |
| 121 | 76 | 96.2 | 15 | 8 | ADR15160 | Adr15160 | Mouse ant | 194 | 76 | 96.2 | 498 | 9 | ADZ83717 | Adz83717 | CD3 speci |
| 122 | 76 | 96.2 | 15 | 9 | ADV14587 | Adv14587 | CDRI pept | 195 | 76 | 96.2 | 498 | 9 | ADZ83729 | Adz83729 | CD3 speci |
| 123 | 76 | 96.2 | 15 | 9 | ADX58327 | Adx58327 | Amino aci | 196 | 76 | 96.2 | 498 | 9 | ADZ83773 | Adz83773 | CD3 speci |
| 124 | 76 | 96.2 | 111 | 2 | AAW95651 | Aaw95651 | Mus muscu | 197 | 76 | 96.2 | 498 | 9 | ADZ83785 | Adz83785 | Vector pE |
| 125 | 76 | 96.2 | 111 | 4 | AAW76940 | Aab76940 | Variable | 198 | 76 | 96.2 | 498 | 9 | ADZ83560 | Adz83560 | Vector pE |
| 126 | 76 | 96.2 | 111 | 8 | ADN07027 | Adn07027 | Murine ant | 199 | 76 | 96.2 | 498 | 9 | ADZ83576 | Adz83576 | Vector pE |
| 127 | 76 | 96.2 | 111 | 8 | ADN15140 | Adn15140 | Mouse ant | 200 | 76 | 96.2 | 498 | 9 | ADZ83582 | Adz83582 | Non-deimm |
| 128 | 76 | 96.2 | 111 | 9 | ADV21423 | Adv21423 | Human ant | 201 | 76 | 96.2 | 498 | 9 | ADZ83767 | Adz83767 | CD3 speci |
| 129 | 76 | 96.2 | 111 | 9 | ADW14593 | Adw14593 | VL(CD19) | 202 | 76 | 96.2 | 498 | 9 | ADZ83779 | Adz83779 | CD3 speci |
| 130 | 76 | 96.2 | 111 | 9 | ADW00649 | Adw00649 | Human F(a | 203 | 76 | 96.2 | 498 | 9 | ADZ83737 | Adz83737 | CD3 speci |
| 131 | 76 | 96.2 | 111 | 9 | ADZ83494 | Adz83494 | CD19 VL | 204 | 76 | 96.2 | 498 | 9 | ADZ83745 | Adz83745 | CD3 speci |
| 132 | 76 | 96.2 | 112 | 9 | ADX58342 | Adx58342 | Variable | 205 | 76 | 96.2 | 499 | 9 | ADZ83715 | Adz83715 | CD3 speci |
| 133 | 76 | 96.2 | 112 | 9 | ADX58346 | Adx58346 | Variable | 206 | 76 | 96.2 | 499 | 9 | ADZ83723 | Adz83723 | CD3 speci |
| 134 | 76 | 96.2 | 114 | 2 | AAW95655 | Aaw95655 | Mus muscu | 207 | 76 | 96.2 | 499 | 9 | ADZ83743 | Adz83743 | CD3 speci |
| 135 | 76 | 96.2 | 114 | 4 | AAW76944 | Aab76944 | Variable | 208 | 76 | 96.2 | 499 | 9 | ADZ83763 | Adz83763 | CD3 speci |
| 136 | 76 | 96.2 | 114 | 8 | ADN07031 | Adn07031 | Anti-IGR | 209 | 76 | 96.2 | 499 | 9 | ADZ83787 | Adz83787 | CD3 speci |
| 137 | 76 | 96.2 | 114 | 9 | ADW00653 | Adw00653 | Human ant | 210 | 76 | 96.2 | 499 | 9 | ADZ83707 | Adz83707 | CD3 speci |
| 138 | 76 | 96.2 | 114 | 9 | ADW79888 | Adw79888 | Anti-IGR | 211 | 76 | 96.2 | 499 | 9 | ADZ83769 | Adz83769 | CD3 speci |
| 139 | 76 | 96.2 | 131 | 2 | AAW32123 | Aar32123 | Anti-CD4 | 212 | 76 | 96.2 | 499 | 9 | ADZ83747 | Adz83747 | CD3 speci |
| 140 | 76 | 96.2 | 147 | 9 | ADY22013 | Ady22013 | Antibody | 213 | 76 | 96.2 | 499 | 9 | ADZ83765 | Adz83765 | CD3 speci |
| 141 | 76 | 96.2 | 218 | 2 | AAW33312 | Aar33312 | Humanised | 214 | 76 | 96.2 | 499 | 9 | ADZ83731 | Adz83731 | CD3 speci |
| 142 | 76 | 96.2 | 218 | 2 | AAW95658 | Aaw95658 | Mus muscu | 215 | 76 | 96.2 | 499 | 9 | ADZ83771 | Adz83771 | CD3 speci |
| 143 | 76 | 96.2 | 216 | 3 | AAW85200 | Aay85200 | Light cha | 216 | 76 | 96.2 | 499 | 9 | ADZ83739 | Adz83739 | CD3 speci |
| 144 | 76 | 96.2 | 218 | 4 | AAW76947 | Aab76947 | Full vari | 217 | 76 | 96.2 | 499 | 9 | ADZ83753 | Adz83753 | CD3 speci |
| 145 | 76 | 96.2 | 218 | 8 | ADN07034 | Adn07034 | Anti-IGR | 218 | 76 | 96.2 | 499 | 9 | ADZ83759 | Adz83759 | CD3 speci |
| 146 | 76 | 96.2 | 218 | 8 | ADT55438 | Adt55438 | Anti IGR | 219 | 76 | 96.2 | 499 | 9 | ADZ83775 | Adz83775 | CD3 speci |
| 147 | 76 | 96.2 | 218 | 9 | ADW00656 | Adw00656 | Human ant | 220 | 76 | 96.2 | 499 | 9 | ADZ83783 | Adz83783 | CD3 speci |
| 148 | 76 | 96.2 | 218 | 9 | ADW79891 | Adw79891 | Anti-IGR | 221 | 76 | 96.2 | 499 | 9 | ADZ83757 | Adz83757 | CD3 speci |
| 149 | 76 | 96.2 | 218 | 9 | AE856304 | Aeb56304 | Anti-IGR | 222 | 76 | 96.2 | 499 | 9 | ADZ83711 | Adz83711 | CD3 speci |
| 150 | 76 | 96.2 | 241 | 8 | ADQ90719 | Adq90719 | Anti-IGR | 223 | 76 | 96.2 | 499 | 9 | ADZ83727 | Adz83727 | CD3 speci |
| 151 | 76 | 96.2 | 241 | 8 | ADQ90717 | Adq90717 | Anti-IGR | 224 | 76 | 96.2 | 499 | 9 | ADZ83719 | Adz83719 | CD3 speci |
| 152 | 76 | 96.2 | 246 | 2 | AAW09434 | Aaw09434 | Anti-CD19 | 225 | 76 | 96.2 | 499 | 9 | ADZ83777 | Adz83777 | CD3 speci |
| 153 | 76 | 96.2 | 247 | 2 | AAW09443 | Aaw09443 | Modified | 226 | 76 | 96.2 | 499 | 9 | ADZ83735 | Adz83735 | CD3 speci |
| 154 | 76 | 96.2 | 250 | 9 | ADV14571 | Adv14571 | VH(CD19) - | 227 | 76 | 96.2 | 499 | 9 | ADZ83751 | Adz83751 | CD3 speci |
| 155 | 76 | 96.2 | 250 | 9 | ADV14575 | Adv14575 | VL(CD19) - | 228 | 76 | 96.2 | 499 | 9 | ADZ83781 | Adz83781 | CD3 speci |
| 156 | 76 | 96.2 | 264 | 7 | ADZ29202 | Adz29202 | Multivale | 229 | 76 | 96.2 | 502 | 9 | ADV14530 | Adv14530 | Bispecifi |
| 157 | 76 | 96.2 | 271 | 5 | ABG31022 | Abg31022 | Mouse sin | 230 | 76 | 96.2 | 503 | 9 | ADV21509 | Adv21509 | Mature fo |
| 158 | 76 | 96.2 | 271 | 7 | ADD25451 | Adz25451 | Binding d | 231 | 76 | 96.2 | 503 | 9 | ADV21499 | Adv21499 | Mature fo |
| 159 | 76 | 96.2 | 271 | 7 | ADM42726 | Adm42726 | Synthetic | 232 | 76 | 96.2 | 503 | 9 | ADV14538 | Adv14538 | Bispecifi |
| 160 | 76 | 96.2 | 271 | 9 | AE895394 | Aeb95394 | Mouse HD3 | 233 | 76 | 96.2 | 503 | 9 | ADV14532 | Adv14532 | Bispecifi |
| 161 | 76 | 96.2 | 271 | 9 | AE894428 | Aeb94428 | Mouse ant | 234 | 76 | 96.2 | 503 | 9 | ADV14540 | Adv14540 | Bispecifi |
| 162 | 76 | 96.2 | 273 | 9 | ADY22017 | Ady22017 | Single ch | 235 | 76 | 96.2 | 503 | 9 | AEA52452 | Aea52452 | Human CD3 |
| 163 | 76 | 96.2 | 273 | 9 | ADY22021 | Ady22021 | Antibody | 236 | 76 | 96.2 | 503 | 9 | AEA52450 | Aea52450 | Human CD3 |
| 164 | 76 | 96.2 | 281 | 2 | AAW82314 | Aaw82314 | Human ScF | 237 | 76 | 96.2 | 504 | 9 | ADV14534 | Adv14534 | Bispecifi |
| 165 | 76 | 96.2 | 288 | 2 | AAW82317 | Aaw82317 | Mouse bis | 238 | 76 | 96.2 | 504 | 9 | ADV14556 | Adv14556 | Bispecifi |
| 166 | 76 | 96.2 | 288 | 2 | AAW82316 | Aaw82316 | Mouse OKT | 239 | 76 | 96.2 | 504 | 9 | ADV14536 | Adv14536 | Bispecifi |
| 167 | 76 | 96.2 | 483 | 2 | AAW82315 | Aaw82315 | Chimeric | 240 | 76 | 96.2 | 504 | 9 | AEA52451 | Aea52451 | Human CD3 |
| 168 | 76 | 96.2 | 496 | 9 | ADV21501 | Adv21501 | Mature fo | 241 | 76 | 96.2 | 504 | 9 | AEA52447 | Aea52447 | Human CD3 |
| 169 | 76 | 96.2 | 496 | 9 | ADV21511 | Adv21511 | Mature fo | 242 | 76 | 96.2 | 504 | 9 | AEA52449 | Aea52449 | Human CD3 |
| 170 | 76 | 96.2 | 497 | 9 | ADV21497 | Adv21497 | Mature fo | 243 | 76 | 96.2 | 505 | 9 | ADV14528 | Adv14528 | Bispecifi |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|-----------|--------------------|-----|----|------|-----|---|----------|--------------------|
| 244 | 76 | 96.2 | 505 | 9 | ADY22027 | Ady22027 Antibody | 317 | 50 | 63.3 | 114 | 8 | ADN07029 | Adn07029 Anti-IgE |
| 245 | 76 | 96.2 | 505 | 9 | ADY22025 | Ady22025 Antibody | 318 | 50 | 63.3 | 114 | 9 | ADW00651 | Adw00651 Human ant |
| 246 | 76 | 96.2 | 505 | 9 | AEA52448 | Aea52448 Human CD3 | 319 | 50 | 63.3 | 218 | 2 | AAW95664 | Aaw95664 Mus muscu |
| 247 | 76 | 96.2 | 506 | 9 | ADV21505 | Adv21505 Mature fo | 320 | 50 | 63.3 | 218 | 2 | AAW95669 | Aaw95669 Mus muscu |
| 248 | 76 | 96.2 | 506 | 9 | ADV21515 | Adv21515 Mature fo | 321 | 50 | 63.3 | 218 | 4 | AAW47087 | Aaw47087 Anti-IgE |
| 249 | 76 | 96.2 | 521 | 9 | ADY22023 | Ady22023 Antibody | 322 | 50 | 63.3 | 218 | 4 | AAW76949 | Aaw76949 Full leng |
| 250 | 76 | 96.2 | 531 | 3 | AAy43749 | Aay43749 Amino aci | 323 | 50 | 63.3 | 218 | 4 | AAW76951 | Aaw76951 Full leng |
| 251 | 76 | 96.2 | 539 | 3 | AAy50823 | Aay50823 Fv-antibo | 324 | 50 | 63.3 | 218 | 4 | AAW76953 | Aaw76953 Variable |
| 252 | 76 | 96.2 | 554 | 3 | AAy50822 | Aay50822 Fv-antibo | 325 | 50 | 63.3 | 218 | 4 | AAW76958 | Aaw76958 Variable |
| 253 | 76 | 96.2 | 562 | 6 | ABR57059 | AbR57059 Plasmid p | 326 | 50 | 63.3 | 218 | 8 | ADN07045 | Adn07045 Anti-IgE |
| 254 | 76 | 96.2 | 562 | 6 | ABR57058 | AbR57058 Plasmid p | 327 | 50 | 63.3 | 218 | 8 | ADN07036 | Adn07036 Anti-IgE |
| 255 | 75 | 94.9 | 15 | 4 | AAW62873 | Aaw62873 Anti-SAF- | 328 | 50 | 63.3 | 218 | 8 | ADN07038 | Adn07038 Anti-IgE |
| 256 | 75 | 94.9 | 15 | 5 | AAU99853 | Aau99853 Mouse AC1 | 329 | 50 | 63.3 | 218 | 8 | ADN07040 | Adn07040 Anti-IgE |
| 257 | 75 | 94.9 | 15 | 7 | AAO29927 | Aao29927 Mouse ant | 330 | 50 | 63.3 | 218 | 8 | ADT55439 | Adt55439 Anti IgE |
| 258 | 75 | 94.9 | 15 | 8 | ADJ87914 | Adj87914 Mouse AC1 | 331 | 50 | 63.3 | 218 | 8 | ADW00660 | Adw00660 Human ant |
| 259 | 75 | 94.9 | 15 | 8 | ADQ37233 | Adq37233 Mouse mon | 332 | 50 | 63.3 | 218 | 9 | ADW00667 | Adw00667 Human ant |
| 260 | 75 | 94.9 | 111 | 5 | AAU99852 | Aau99852 Mouse AC1 | 333 | 50 | 63.3 | 218 | 9 | ADW00662 | Adw00662 Human ant |
| 261 | 75 | 94.9 | 111 | 7 | AAO29926 | Aao29926 Mouse ant | 334 | 50 | 63.3 | 218 | 9 | ADW00658 | Adw00658 Human ant |
| 262 | 75 | 94.9 | 111 | 8 | ADJ87912 | Adj87912 Mouse AC1 | 335 | 50 | 63.3 | 218 | 9 | ADW79897 | Adw79897 Anti-IgE |
| 263 | 75 | 94.9 | 111 | 8 | ADQ37211 | Adq37211 Mouse mon | 336 | 50 | 63.3 | 218 | 9 | ADW79902 | Adw79902 Anti-IgE |
| 264 | 75 | 94.9 | 111 | 8 | ADQ37216 | Adq37216 Mouse mon | 337 | 50 | 63.3 | 218 | 9 | AEBS6305 | Aeb56305 Anti-IgE |
| 265 | 75 | 94.9 | 111 | 8 | ADQ37218 | Adq37218 Mouse mon | 338 | 50 | 63.3 | 248 | 2 | AAW95668 | Aaw95668 Mus muscu |
| 266 | 75 | 94.9 | 111 | 8 | ADQ37217 | Adq37217 Mouse mon | 339 | 50 | 63.3 | 248 | 2 | AAW95667 | Aaw95667 Mus muscu |
| 267 | 75 | 94.9 | 111 | 9 | AEBS13684 | Aeb13684 Human ant | 340 | 50 | 63.3 | 248 | 4 | AAW76957 | Aaw76957 Sfv fragm |
| 268 | 75 | 94.9 | 111 | 9 | AEBS13678 | Aeb13678 Human lig | 341 | 50 | 63.3 | 248 | 4 | AAW76956 | Aaw76956 Sfv fragm |
| 269 | 75 | 94.9 | 112 | 4 | AAW62872 | Aaw62872 Anti-SAF- | 342 | 50 | 63.3 | 248 | 8 | ADN07044 | Adn07044 Anti-IgE |
| 270 | 73 | 92.4 | 14 | 5 | AAO18538 | Aao18538 Murine Ma | 343 | 50 | 63.3 | 248 | 8 | ADN07043 | Adn07043 Anti-IgE |
| 271 | 73 | 92.4 | 41 | 3 | AAy91014 | Aay91014 1P7 antib | 344 | 50 | 63.3 | 248 | 9 | ADW00666 | Adw00666 Human ant |
| 272 | 73 | 92.4 | 110 | 5 | AAO18536 | Aao18536 Murine Ma | 345 | 50 | 63.3 | 248 | 9 | ADW00665 | Adw00665 Human ant |
| 273 | 73 | 92.4 | 239 | 2 | AAW79866 | Aaw79866 Anti-IgE | 346 | 50 | 63.3 | 248 | 9 | ADW79900 | Adw79900 Anti-IgE |
| 274 | 72 | 91.1 | 111 | 9 | AEBS13688 | Aeb13688 Human ant | 347 | 50 | 63.3 | 248 | 9 | ADW79901 | Adw79901 Anti-IgE |
| 275 | 72 | 91.1 | 111 | 9 | AEBS13682 | Aeb13682 Human ant | 348 | 49 | 62.0 | 112 | 9 | ADX58345 | Adx58345 Variable |
| 276 | 72 | 91.1 | 111 | 9 | AEBS13689 | Aeb13689 Human ant | 349 | 47 | 59.5 | 96 | 5 | ABP02905 | Abp02905 Human ORF |
| 277 | 72 | 91.1 | 111 | 9 | AEBS13683 | Aeb13683 Human ant | 350 | 46 | 58.2 | 91 | 4 | AAW83209 | Aaw83209 Human imm |
| 278 | 72 | 91.1 | 114 | 2 | AAW95654 | Aaw95654 Mus muscu | 351 | 46 | 58.2 | 131 | 2 | AAW05089 | Aaw05089 Light cha |
| 279 | 72 | 91.1 | 114 | 9 | ADW00650 | Adw00650 Human ant | 352 | 46 | 58.2 | 131 | 5 | ABB79725 | Abb79725 Anti-Strc |
| 280 | 72 | 91.1 | 114 | 9 | ADW79887 | Adw79887 Anti-IgE | 353 | 46 | 58.2 | 238 | 5 | ADY91367 | Ady91367 Anti-KiD3 |
| 281 | 72 | 91.1 | 218 | 9 | ADW00691 | Adw00691 Human ant | 354 | 46 | 58.2 | 329 | 4 | AAW70840 | Aaw70840 SNV-env 1 |
| 282 | 72 | 91.1 | 218 | 9 | AEBS13693 | Aeb13693 Human ant | 355 | 46 | 58.2 | 111 | 2 | AAW95652 | Aaw95652 Mus muscu |
| 283 | 71 | 89.9 | 112 | 8 | ADF71897 | Adf71897 Hu3G8VL-1 | 356 | 45 | 57.0 | 111 | 4 | AAW76941 | Aaw76941 Variable |
| 284 | 71 | 89.9 | 112 | 6 | ABO27167 | AbO27167 Humanised | 357 | 45 | 57.0 | 111 | 8 | ADN07028 | Adn07028 Humili va |
| 285 | 71 | 89.9 | 112 | 6 | ABO27166 | AbO27166 Mouse ant | 358 | 45 | 57.0 | 111 | 8 | ADW00650 | Adw00650 Human hum |
| 286 | 71 | 89.9 | 218 | 8 | ADF71899 | Adf71899 Hu3G8VL-1 | 359 | 45 | 57.0 | 243 | 2 | AAW09436 | Aaw09436 Anti-CD19 |
| 287 | 69 | 87.3 | 114 | 4 | AAW76943 | Aaw76943 Variable | 360 | 44 | 56.3 | 114 | 7 | ADP03992 | Adp03992 Murine-ex |
| 288 | 69 | 87.3 | 114 | 8 | ADN07030 | Adn07030 Anti-IgE | 361 | 44 | 55.7 | 15 | 2 | AAW27412 | Aaw27412 CDRI from |
| 289 | 69 | 87.3 | 114 | 9 | ADW00652 | Adw00652 Human ant | 362 | 44 | 55.7 | 15 | 9 | ADZ69241 | Adz69241 IL-5R alp |
| 290 | 69 | 87.3 | 219 | 8 | ADN07066 | Adn07066 F(ab)-pha | 363 | 44 | 55.7 | 15 | 9 | ABE21453 | Aeb21453 Mouse ant |
| 291 | 69 | 87.3 | 219 | 9 | ADW00688 | Adw00688 Expressio | 364 | 44 | 55.7 | 15 | 9 | ABE31211 | Aeb31211 Antibody |
| 292 | 68 | 86.1 | 111 | 8 | ADF71901 | Adf71901 Hu3G8VL-4 | 365 | 44 | 55.7 | 131 | 2 | AAW21842 | Aaw21842 Light cha |
| 293 | 68 | 86.1 | 111 | 8 | ADF71919 | Adf71919 Hu3G8VL-2 | 366 | 44 | 55.7 | 218 | 9 | ADW00692 | Adw00692 Human ant |
| 294 | 68 | 86.1 | 218 | 8 | ADF71903 | Adf71903 Hu3G8VL-4 | 367 | 43 | 54.4 | 15 | 9 | ABE21504 | Aeb21504 Mouse ant |
| 295 | 68 | 86.1 | 218 | 8 | ADF71920 | Adf71920 Hu3G8VL-2 | 368 | 43 | 54.4 | 186 | 4 | ABW64402 | Abw64402 Drosophil |
| 296 | 66 | 83.5 | 12 | 6 | ABE37724 | Aeb37724 Mouse ant | 369 | 42 | 53.2 | 15 | 5 | AAU81248 | Aau81248 Murine tr |
| 297 | 66 | 83.5 | 14 | 9 | ADY93298 | Ady93298 mAb CG10 | 370 | 42 | 53.2 | 15 | 8 | ADW78099 | Adw78099 Human SJB |
| 298 | 63 | 79.7 | 111 | 9 | AEBS13680 | Aeb13680 Human vLk | 371 | 42 | 53.2 | 15 | 9 | ADW95717 | Adw95717 Anti-hil- |
| 299 | 63 | 79.7 | 209 | 2 | AAW63117 | Aaw63117 Light cha | 372 | 42 | 53.2 | 15 | 9 | ADX15722 | Adx15722 Mouse ant |
| 300 | 57 | 72.2 | 218 | 2 | AAW66140 | Aaw66140 CD-4 anti | 373 | 42 | 53.2 | 107 | 5 | ABW67137 | Abw67137 Human IGE |
| 301 | 57 | 72.2 | 218 | 6 | ABP96773 | Abp96773 TSH recep | 374 | 42 | 53.2 | 111 | 2 | AAW25725 | Aaw25725 Humanised |
| 302 | 57 | 72.2 | 218 | 6 | ABP96774 | Abp96774 TSH recep | 375 | 42 | 53.2 | 111 | 2 | AAW25725 | Aaw25725 Humanised |
| 303 | 55 | 69.6 | 111 | 7 | ADC27439 | Adc27439 TMF2F#10 | 376 | 42 | 53.2 | 111 | 4 | AAW69670 | Aaw69670 Humanised |
| 304 | 53 | 67.1 | 114 | 2 | AAW95653 | Aaw95653 Mus muscu | 377 | 42 | 53.2 | 111 | 4 | AAW69684 | Aaw69684 Human Eu |
| 305 | 53 | 67.1 | 114 | 9 | ADW79886 | Adw79886 Anti-IgE | 378 | 42 | 53.2 | 111 | 8 | AAW69669 | Aaw69669 Murine M1 |
| 306 | 53 | 67.1 | 218 | 2 | AAW95660 | Aaw95660 Mus muscu | 379 | 42 | 53.2 | 111 | 8 | ADO47717 | Ado47717 Humanised |
| 307 | 53 | 67.1 | 218 | 2 | AAW95662 | Aaw95662 Mus muscu | 380 | 42 | 53.2 | 111 | 8 | ADO47775 | Ado47775 Humanised |
| 308 | 53 | 67.1 | 218 | 2 | AAW50030 | Aaw50030 Human E27 | 381 | 42 | 53.2 | 111 | 8 | ADO47716 | Ado47716 Mouse M19 |
| 309 | 53 | 67.1 | 218 | 3 | AAW07472 | Aaw07472 Amino aci | 382 | 42 | 53.2 | 112 | 2 | AAW48098 | Aaw48098 Interleuk |
| 310 | 53 | 67.1 | 218 | 4 | AAW74211 | Aaw74211 E27 anti- | 383 | 42 | 53.2 | 112 | 4 | AAU77284 | Aau77284 Amino aci |
| 311 | 53 | 67.1 | 218 | 6 | ABU62797 | Abu62797 E27 anti- | 384 | 42 | 53.2 | 112 | 5 | ADG24519 | Adg24519 Mouse mon |
| 312 | 53 | 67.1 | 218 | 7 | ADF69597 | Adf69597 Human ant | 385 | 42 | 53.2 | 112 | 9 | ADW95716 | Adw95716 Mouse ant |
| 313 | 53 | 67.1 | 218 | 7 | ADF29038 | Adf29038 Anti-IgE | 386 | 42 | 53.2 | 112 | 9 | ADW95716 | Adw95716 Mouse ant |
| 314 | 53 | 67.1 | 218 | 9 | ADW79895 | Adw79895 Anti-IgE | 387 | 42 | 53.2 | 113 | 2 | AAW79860 | Aaw79860 Anti-EGFR |
| 315 | 53 | 67.1 | 218 | 9 | ADW79893 | Adw79893 Anti-IgE | 388 | 42 | 53.2 | 113 | 2 | AAW79862 | Aaw79862 Anti-EGFR |
| 316 | 50 | 63.3 | 114 | 4 | AAW76942 | Aaw76942 Variable | 389 | 42 | 53.2 | 113 | 2 | AAW79893 | Aaw79893 Anti-EGFR |

| | | | | | | | | | | | | | | | |
|-----|------|------|-----|---|-----------|-----------|-----------|-----|------|------|-----|---|----------|----------|-----------|
| 390 | 42 | 53.2 | 113 | 8 | ADT75142 | Adt75142 | Light cha | 463 | 41 | 51.9 | 112 | 8 | ADG25827 | Adg25827 | Anti-CD30 |
| 391 | 42 | 53.2 | 113 | 9 | ABE23213 | Aeb23213 | Mouse ant | 464 | 41 | 51.9 | 112 | 8 | ADR38689 | Adr38689 | Mouse lig |
| 392 | 42 | 53.2 | 114 | 5 | AAU81279 | Aau81279 | Murine tr | 465 | 41 | 51.9 | 112 | 8 | ADR38680 | Adr38680 | Mouse lig |
| 393 | 42 | 53.2 | 117 | 8 | ADM78053 | Adm78053 | Human SKB | 466 | 41 | 51.9 | 112 | 8 | ADT75130 | Adt75130 | Light cha |
| 394 | 42 | 53.2 | 131 | 2 | AAW68549 | Aaw68549 | Anti-CD33 | 467 | 41 | 51.9 | 112 | 8 | ADT75138 | Adt75138 | Light cha |
| 395 | 42 | 53.2 | 131 | 4 | AAW69681 | Aaw69681 | Murine M1 | 468 | 41 | 51.9 | 112 | 8 | ADT75123 | Adt75123 | Light cha |
| 396 | 42 | 53.2 | 131 | 8 | ADO47771 | Ado47771 | Mouse M19 | 469 | 41 | 51.9 | 112 | 8 | ADT75139 | Adt75139 | Light cha |
| 397 | 42 | 53.2 | 193 | 5 | ABP65774 | Abp65774 | Bifidobac | 470 | 41 | 51.9 | 112 | 8 | ADT75137 | Adt75137 | Light cha |
| 398 | 42 | 53.2 | 218 | 8 | ADN97507 | Adn97507 | Artificia | 471 | 41 | 51.9 | 112 | 8 | ADT75136 | Adt75136 | Light cha |
| 399 | 42 | 53.2 | 269 | 4 | AAW61541 | Aaw61541 | 3DX sfv p | 472 | 41 | 51.9 | 112 | 8 | ADU67960 | Adu67960 | Mouse kab |
| 400 | 42 | 53.2 | 306 | 8 | ADY08129 | Ady08129 | Plant ful | 473 | 41 | 51.9 | 112 | 8 | ADU67961 | Adu67961 | Mouse ant |
| 401 | 42 | 53.2 | 306 | 8 | ADX71084 | Adx71084 | Plant ful | 474 | 41 | 51.9 | 112 | 9 | ADV77267 | Adv77267 | Murine an |
| 402 | 42 | 53.2 | 512 | 8 | ADN97497 | Adn97497 | Artificia | 475 | 41 | 51.9 | 112 | 9 | ADV77266 | Adv77266 | Veneered |
| 403 | 42 | 53.2 | 517 | 8 | ADN97495 | Adn97495 | Artificia | 476 | 41 | 51.9 | 112 | 9 | ADW95764 | Adw95764 | Mouse ant |
| 404 | 42 | 53.2 | 519 | 8 | ADN97493 | Adn97493 | Artificia | 477 | 41 | 51.9 | 112 | 9 | ADX15769 | Adx15769 | Mouse ant |
| 405 | 42 | 53.2 | 552 | 8 | ADN97513 | Adn97513 | Artificia | 478 | 41 | 51.9 | 113 | 8 | ADQ90833 | Adq90833 | Kabat sub |
| 406 | 42 | 53.2 | 712 | 8 | ADN97543 | Adn97543 | Artificia | 479 | 41 | 51.9 | 113 | 8 | ADQ90832 | Adq90832 | Kabat sub |
| 407 | 42 | 53.2 | 713 | 8 | ADN97491 | Adn97491 | Artificia | 480 | 41 | 51.9 | 113 | 8 | ADT75140 | Adt75140 | Light cha |
| 408 | 42 | 53.2 | 715 | 8 | ADN97489 | Adn97489 | Artificia | 481 | 41 | 51.9 | 113 | 8 | ADT75124 | Adt75124 | Light cha |
| 409 | 41.5 | 52.5 | 222 | 8 | ADG73248 | Adg73248 | Cat parti | 482 | 41 | 51.9 | 113 | 8 | ADT75131 | Adt75131 | Light cha |
| 410 | 41.5 | 52.5 | 242 | 6 | ABU09337 | Abu09337 | Feline Ig | 483 | 41 | 51.9 | 113 | 8 | ADT75129 | Adt75129 | Light cha |
| 411 | 41.5 | 52.5 | 242 | 8 | ADG73243 | Adg73243 | Cat immun | 484 | 41 | 51.9 | 113 | 8 | ADT75127 | Adt75127 | Light cha |
| 412 | 41 | 51.9 | 15 | 2 | AAW27344 | Aaw27344 | CDR1 from | 485 | 41 | 51.9 | 113 | 8 | ADT75056 | Adt75056 | Light cha |
| 413 | 41 | 51.9 | 15 | 4 | AAU07460 | Aau07460 | Synthetic | 486 | 41 | 51.9 | 113 | 8 | ADT75135 | Adt75135 | Light cha |
| 414 | 41 | 51.9 | 15 | 5 | AAU070352 | Aau070352 | Mouse Kap | 487 | 41 | 51.9 | 113 | 8 | ADT75141 | Adt75141 | Light cha |
| 415 | 41 | 51.9 | 15 | 8 | ADN08049 | Adn08049 | HuCOL-1 v | 488 | 41 | 51.9 | 121 | 2 | AAW48615 | Aaw48615 | Sequence |
| 416 | 41 | 51.9 | 15 | 9 | ADW95765 | Adw95765 | Anti-hiL- | 489 | 41 | 51.9 | 121 | 2 | AAW09259 | Aaw09259 | Monoclona |
| 417 | 41 | 51.9 | 15 | 9 | ADX15770 | Adx15770 | Mouse ant | 490 | 41 | 51.9 | 121 | 2 | AAW09274 | Aaw09274 | MAB NM-01 |
| 418 | 41 | 51.9 | 60 | 6 | ABU56875 | Abu56875 | BoNT/A Hc | 491 | 41 | 51.9 | 131 | 2 | AAW29008 | Aaw29008 | p64-k4 pr |
| 419 | 41 | 51.9 | 60 | 6 | ABU56876 | Abu56876 | BoNT/A Hc | 492 | 41 | 51.9 | 131 | 2 | AAW30278 | Aaw30278 | Light cha |
| 420 | 41 | 51.9 | 60 | 6 | ABU56840 | Abu56840 | BoNT/A Hc | 493 | 41 | 51.9 | 131 | 2 | AAW30274 | Aaw30274 | Light cha |
| 421 | 41 | 51.9 | 60 | 6 | ABU56887 | Abu56887 | BoNT/A Hc | 494 | 41 | 51.9 | 138 | 9 | ADY74777 | Ady74777 | Rat anti- |
| 422 | 41 | 51.9 | 60 | 6 | ABU56879 | Abu56879 | BoNT/A Hc | 495 | 41 | 51.9 | 172 | 2 | AAW29507 | Aaw29507 | Human lun |
| 423 | 41 | 51.9 | 94 | 8 | ADT75143 | Adt75143 | Light cha | 496 | 41 | 51.9 | 172 | 3 | AAW44448 | Aaw44448 | Human lun |
| 424 | 41 | 51.9 | 107 | 2 | AAW27353 | Aaw27353 | Light cha | 497 | 41 | 51.9 | 172 | 4 | AAE13789 | Aae13789 | Human lun |
| 425 | 41 | 51.9 | 108 | 8 | ADT74998 | Adt74998 | Light cha | 498 | 41 | 51.9 | 172 | 7 | ADD66419 | Ad666419 | Human lun |
| 426 | 41 | 51.9 | 108 | 8 | ADT75001 | Adt75001 | Light cha | 499 | 41 | 51.9 | 172 | 7 | ADW87673 | Adw87673 | Human lun |
| 427 | 41 | 51.9 | 109 | 8 | ADT74994 | Adt74994 | Light cha | 500 | 41 | 51.9 | 217 | 9 | ADY74780 | Ady74780 | Rat anti- |
| 428 | 41 | 51.9 | 109 | 8 | ADT75009 | Adt75009 | Light cha | 501 | 41 | 51.9 | 218 | 9 | ADY74808 | Ady74808 | Rat anti- |
| 429 | 41 | 51.9 | 109 | 8 | ADT74995 | Adt74995 | Light cha | 502 | 41 | 51.9 | 223 | 4 | AAU31086 | Aau31086 | Novel hum |
| 430 | 41 | 51.9 | 109 | 8 | ADT75003 | Adt75003 | Light cha | 503 | 41 | 51.9 | 230 | 2 | AAW73873 | Aaw73873 | Human ant |
| 431 | 41 | 51.9 | 110 | 8 | ADN08042 | Adn08042 | HuCOL-1 v | 504 | 41 | 51.9 | 247 | 2 | AAW73875 | Aaw73875 | Human ant |
| 432 | 41 | 51.9 | 110 | 9 | ADY74788 | Ady74788 | Rat anti- | 505 | 41 | 51.9 | 248 | 9 | ADW95688 | Adw95688 | Anti-IL-6 |
| 433 | 41 | 51.9 | 111 | 2 | AAW47494 | Aaw47494 | Murine an | 506 | 41 | 51.9 | 248 | 9 | ADX15693 | Adx15693 | Mouse ant |
| 434 | 41 | 51.9 | 111 | 2 | AAW47492 | Aaw47492 | Humanised | 507 | 41 | 51.9 | 252 | 4 | AAU07497 | Aau07497 | Synthetic |
| 435 | 41 | 51.9 | 111 | 2 | AAW48622 | Aaw48622 | Sequence | 508 | 41 | 51.9 | 319 | 6 | ABU40207 | Abu40207 | Protein e |
| 436 | 41 | 51.9 | 111 | 2 | AAW48623 | Aaw48623 | Sequence | 509 | 41 | 51.9 | 323 | 6 | ABU41982 | Abu41982 | Protein e |
| 437 | 41 | 51.9 | 111 | 2 | AAW65172 | Aaw65172 | Murine NM | 510 | 41 | 51.9 | 340 | 6 | ABR42679 | AbR42679 | Pseudomon |
| 438 | 41 | 51.9 | 111 | 2 | AAW65174 | Aaw65174 | Region pr | 511 | 41 | 51.9 | 397 | 7 | ABO73489 | AbO73489 | Pseudomon |
| 439 | 41 | 51.9 | 111 | 8 | ADT75059 | Adt75059 | Light cha | 512 | 41 | 51.9 | 411 | 7 | ADH87903 | AdH87903 | Enterococ |
| 440 | 41 | 51.9 | 111 | 9 | ADY74792 | Ady74792 | Rat anti- | 513 | 41 | 51.9 | 535 | 7 | AAO31227 | Aao31227 | Eucalyptu |
| 441 | 41 | 51.9 | 111 | 9 | ADY74793 | Ady74793 | Rat anti- | 514 | 41 | 51.9 | 543 | 7 | ADD12876 | AdD12876 | CD28/mela |
| 442 | 41 | 51.9 | 111 | 9 | ADY74800 | Ady74800 | Rat anti- | 515 | 41 | 51.9 | 692 | 6 | ABU44346 | AbU44346 | Protein e |
| 443 | 41 | 51.9 | 111 | 9 | ADY74799 | Ady74799 | Rat anti- | 516 | 41 | 51.9 | 692 | 9 | ABE91503 | Aeb91503 | Microbial |
| 444 | 41 | 51.9 | 111 | 9 | ADY74801 | Ady74801 | Rat anti- | 517 | 40.5 | 51.3 | 16 | 4 | AAW86292 | Aaw86292 | Murine de |
| 445 | 41 | 51.9 | 111 | 9 | ADY74790 | Ady74790 | Rat anti- | 518 | 40.5 | 51.3 | 16 | 4 | AAW73652 | Aaw73652 | Murine mo |
| 446 | 41 | 51.9 | 111 | 9 | ADY74791 | Ady74791 | Rat anti- | 519 | 40.5 | 51.3 | 16 | 6 | ABP58262 | AbP58262 | Mouse mon |
| 447 | 41 | 51.9 | 111 | 9 | ADY74789 | Ady74789 | Rat anti- | 520 | 40.5 | 51.3 | 16 | 7 | ABR61869 | AbR61869 | Mouse MAB |
| 448 | 41 | 51.9 | 111 | 9 | ADY74794 | Ady74794 | Rat anti- | 521 | 40.5 | 51.3 | 16 | 8 | ADQ31250 | AdQ31250 | CDR1 pept |
| 449 | 41 | 51.9 | 112 | 2 | AAW10539 | Aaw10539 | Chimeric | 522 | 40.5 | 51.3 | 20 | 3 | AAW70796 | Aay70796 | Murine an |
| 450 | 41 | 51.9 | 112 | 2 | AAW13089 | Aaw13089 | Murine 1B | 523 | 40.5 | 51.3 | 100 | 4 | AAE06959 | Aae06959 | Mouse ger |
| 451 | 41 | 51.9 | 112 | 2 | AAW79156 | Aaw79156 | Human i9E | 524 | 40.5 | 51.3 | 100 | 8 | ADQ89244 | AdQ89244 | Mouse imm |
| 452 | 41 | 51.9 | 112 | 2 | AAW79158 | Aaw79158 | Human i9E | 525 | 40.5 | 51.3 | 100 | 9 | ABE09517 | Abe09517 | Murine ge |
| 453 | 41 | 51.9 | 112 | 2 | AAW27527 | Aaw27527 | Light cha | 526 | 40.5 | 51.3 | 110 | 3 | AAW70788 | Aay70788 | Murine an |
| 454 | 41 | 51.9 | 112 | 2 | AAW27358 | Aaw27358 | Light cha | 527 | 40.5 | 51.3 | 112 | 2 | AAW48248 | Aaw48248 | A77 anti- |
| 455 | 41 | 51.9 | 112 | 4 | AAU07516 | Aau07516 | Antibody | 528 | 40.5 | 51.3 | 112 | 2 | AAW52765 | Aay52765 | Anti-ties |
| 456 | 41 | 51.9 | 112 | 4 | AAU07480 | Aau07480 | Synthetic | 529 | 40.5 | 51.3 | 112 | 2 | AAW52766 | Aay52766 | Anti-ties |
| 457 | 41 | 51.9 | 112 | 5 | ABW77332 | Abw77332 | Mouse 1B4 | 530 | 40.5 | 51.3 | 112 | 2 | AAW89177 | Aaw89177 | Anti-P53 |
| 458 | 41 | 51.9 | 112 | 5 | ABW77331 | Abw77331 | Veneered | 531 | 40.5 | 51.3 | 112 | 4 | AAE06991 | Aae06991 | Human kap |
| 459 | 41 | 51.9 | 112 | 6 | ABO10750 | AbO10750 | Variable | 532 | 40.5 | 51.3 | 112 | 4 | AAE06995 | Aae06995 | Human kap |
| 460 | 41 | 51.9 | 112 | 6 | ABO10751 | AbO10751 | Consensus | 533 | 40.5 | 51.3 | 112 | 4 | AAW74621 | Aaw74621 | A77 anti- |
| 461 | 41 | 51.9 | 112 | 6 | ABR44695 | AbR44695 | Murine J5 | 534 | 40.5 | 51.3 | 112 | 4 | AAE08554 | Aae08554 | Murine A7 |
| 462 | 41 | 51.9 | 112 | 6 | ABR44694 | AbR44694 | Murine Mu | 535 | 40.5 | 51.3 | 112 | 7 | ABR61865 | AbR61865 | Mouse MAB |

| | | | | | | | | | | | | | |
|-----|------|------|-----|---|----------|---------------------|-----|------|------|------|---|----------|---------------------|
| 536 | 40.5 | 51.3 | 112 | 7 | ABR62960 | Abc62960 Monoclonal | 609 | 40 | 50.6 | 112 | 9 | ABE21493 | Aeb21493 Anti-IL13 |
| 537 | 40.5 | 51.3 | 112 | 8 | ADQ31290 | Adq31290 Humanised | 610 | 40 | 50.6 | 112 | 9 | ABE21495 | Aeb21495 Anti-IL13 |
| 538 | 40.5 | 51.3 | 112 | 8 | ADQ31246 | Adq31246 Murine 1A | 611 | 40 | 50.6 | 112 | 9 | ABE31253 | Aeb31253 Antibody |
| 539 | 40.5 | 51.3 | 112 | 8 | ADQ31289 | Adq31289 Humanised | 612 | 40 | 50.6 | 112 | 9 | ABE31251 | Aeb31251 Antibody |
| 540 | 40.5 | 51.3 | 112 | 8 | ADQ76094 | Adq76094 Heterorec | 613 | 40 | 50.6 | 113 | 9 | ABE21354 | Aeb21354 Mouse ant |
| 541 | 40.5 | 51.3 | 112 | 8 | ADQ76074 | Adq76074 Heterorec | 614 | 40 | 50.6 | 113 | 9 | ABE31112 | Aeb31112 Antibody |
| 542 | 40.5 | 51.3 | 112 | 8 | ADQ89280 | Adq89280 Human imm | 615 | 40 | 50.6 | 133 | 4 | ABG12430 | Abg12430 Novel hum |
| 543 | 40.5 | 51.3 | 112 | 8 | ADQ89276 | Adq89276 Human imm | 616 | 40 | 50.6 | 149 | 2 | AAW02292 | AAw02292 FvKc-II V |
| 544 | 40.5 | 51.3 | 112 | 9 | AD251189 | Ad251189 Amino aci | 617 | 40 | 50.6 | 246 | 5 | ABG78344 | Abg78344 Soybean c |
| 545 | 40.5 | 51.3 | 112 | 9 | AD251209 | Ad251209 Amino aci | 618 | 40 | 50.6 | 248 | 9 | ABE21503 | Aeb21503 Anti-IL13 |
| 546 | 40.5 | 51.3 | 112 | 9 | AD242083 | Ad242083 Human ant | 619 | 40 | 50.6 | 248 | 9 | ABE31161 | Aeb31161 Monoclonal |
| 547 | 40.5 | 51.3 | 112 | 9 | AD242063 | Ad242063 Human ant | 620 | 40 | 50.6 | 252 | 2 | AAW02294 | AAw02294 Yeast-FvK |
| 548 | 40.5 | 51.3 | 112 | 9 | ABE08797 | Aeb08797 Antibody | 621 | 40 | 50.6 | 271 | 2 | AAW02293 | AAw02293 FvKc-II-K |
| 549 | 40.5 | 51.3 | 112 | 9 | ABE09549 | Aeb09549 Human lig | 622 | 40 | 50.6 | 283 | 2 | AAH33551 | AAh33551 B. napus |
| 550 | 40.5 | 51.3 | 112 | 9 | ABE09553 | Aeb09553 Human lig | 623 | 40 | 50.6 | 283 | 8 | ADH75623 | Adh75623 Rape C-re |
| 551 | 40.5 | 51.3 | 113 | 4 | AAE03751 | Aae03751 Murine p5 | 624 | 40 | 50.6 | 283 | 9 | ADZ25861 | Adz25861 Brassaica |
| 552 | 40.5 | 51.3 | 113 | 6 | ABP58270 | Abp58270 Humanised | 625 | 40 | 50.6 | 294 | 6 | ABU24348 | Abu24348 Protein e |
| 553 | 40.5 | 51.3 | 113 | 6 | ABP58268 | Abp58268 Humanised | 626 | 40 | 50.6 | 420 | 8 | ADN73011 | Adn73011 Thale cre |
| 554 | 40.5 | 51.3 | 113 | 8 | ADG25828 | Adg25828 Anti-CD30 | 627 | 40 | 50.6 | 420 | 8 | ADT55770 | Adt55770 Plant pol |
| 555 | 40.5 | 51.3 | 113 | 8 | ADQ76088 | Adq76088 Heterorec | 628 | 40 | 50.6 | 456 | 3 | AAH78188 | AAh78188 Human sec |
| 556 | 40.5 | 51.3 | 113 | 8 | ADQ76082 | Adq76082 Heterorec | 629 | 40 | 50.6 | 456 | 4 | AAE06127 | AAe06127 Human gen |
| 557 | 40.5 | 51.3 | 113 | 8 | ADQ76076 | Adq76076 Heterorec | 630 | 40 | 50.6 | 456 | 4 | AAE06165 | AAe06165 Human gen |
| 558 | 40.5 | 51.3 | 113 | 8 | ADQ76078 | Adq76078 Heterorec | 631 | 40 | 50.6 | 456 | 5 | ABG33988 | Abg33988 Human sec |
| 559 | 40.5 | 51.3 | 113 | 8 | ADQ76092 | Adq76092 Heterorec | 632 | 40 | 50.6 | 456 | 5 | ABG33950 | Abg33950 Human sec |
| 560 | 40.5 | 51.3 | 113 | 8 | ADQ76084 | Adq76084 Heterorec | 633 | 40 | 50.6 | 456 | 6 | ADA57357 | Ada57357 Human sec |
| 561 | 40.5 | 51.3 | 113 | 8 | ADQ76090 | Adq76090 Heterorec | 634 | 40 | 50.6 | 456 | 6 | ADA41231 | Ada41231 Human sec |
| 562 | 40.5 | 51.3 | 113 | 8 | ADQ76080 | Adq76080 Heterorec | 635 | 40 | 50.6 | 456 | 6 | ABR47992 | AbR47992 Human sec |
| 563 | 40.5 | 51.3 | 113 | 8 | ADQ76086 | Adq76086 Heterorec | 636 | 40 | 50.6 | 457 | 3 | AAH87150 | AAh87150 Human sec |
| 564 | 40.5 | 51.3 | 113 | 9 | AD251203 | Ad251203 Amino aci | 637 | 40 | 50.6 | 495 | 4 | AAH72414 | AAh72414 Double-he |
| 565 | 40.5 | 51.3 | 113 | 9 | AD251207 | Ad251207 Amino aci | 638 | 40 | 50.6 | 558 | 5 | ABG33989 | Abg33989 Human sec |
| 566 | 40.5 | 51.3 | 113 | 9 | AD251195 | Ad251195 Amino aci | 639 | 40 | 50.6 | 563 | 6 | ABP6590 | Abp6590 Sheep IGE |
| 567 | 40.5 | 51.3 | 113 | 9 | AD251191 | Ad251191 Amino aci | 640 | 40 | 50.6 | 564 | 5 | ABP68918 | Abp68918 Human pol |
| 568 | 40.5 | 51.3 | 113 | 9 | AD251201 | Ad251201 Amino aci | 641 | 40 | 50.6 | 565 | 7 | ADP16581 | Adp16581 Human alb |
| 569 | 40.5 | 51.3 | 113 | 9 | AD251197 | Ad251197 Amino aci | 642 | 40 | 50.6 | 565 | 7 | ADP16580 | Adp16580 Human alb |
| 570 | 40.5 | 51.3 | 113 | 9 | AD251205 | Ad251205 Amino aci | 643 | 40 | 50.6 | 581 | 8 | ABM85148 | ABm85148 Human dia |
| 571 | 40.5 | 51.3 | 113 | 9 | AD251193 | Ad251193 Amino aci | 644 | 40 | 50.6 | 612 | 4 | AAH87088 | AAh87088 Human sec |
| 572 | 40.5 | 51.3 | 113 | 9 | AD251199 | Ad251199 Amino aci | 645 | 40 | 50.6 | 612 | 4 | AAH92993 | AAh92993 Human pro |
| 573 | 40.5 | 51.3 | 113 | 9 | AD242075 | Ad242075 Human ant | 646 | 40 | 50.6 | 612 | 4 | AAE06065 | AAe06065 Human gen |
| 574 | 40.5 | 51.3 | 113 | 9 | AD242069 | Ad242069 Human ant | 647 | 40 | 50.6 | 612 | 4 | AAH81364 | AAh81364 Human APP |
| 575 | 40.5 | 51.3 | 113 | 9 | AD242079 | Ad242079 Human ant | 648 | 40 | 50.6 | 612 | 5 | AAE17139 | AAe17139 Human mem |
| 576 | 40.5 | 51.3 | 113 | 9 | AD242073 | Ad242073 Human ant | 649 | 40 | 50.6 | 612 | 5 | ABG33887 | Abg33887 Human sec |
| 577 | 40.5 | 51.3 | 113 | 9 | AD242077 | Ad242077 Human ant | 650 | 40 | 50.6 | 612 | 5 | ABG33949 | Abg33949 Human sec |
| 578 | 40.5 | 51.3 | 113 | 9 | AD242081 | Ad242081 Human ant | 651 | 40 | 50.6 | 612 | 6 | ADA57356 | Ada57356 Human sec |
| 579 | 40.5 | 51.3 | 113 | 9 | AD242065 | Ad242065 Human ant | 652 | 40 | 50.6 | 612 | 6 | ADA56822 | Ada56822 Human sec |
| 580 | 40.5 | 51.3 | 113 | 9 | AD242067 | Ad242067 Human ant | 653 | 40 | 50.6 | 612 | 6 | ADA40670 | Ada40670 Human sec |
| 581 | 40.5 | 51.3 | 113 | 9 | AD242071 | Ad242071 Human ant | 654 | 40 | 50.6 | 612 | 6 | ADA41230 | Ada41230 Human sec |
| 582 | 40.5 | 51.3 | 113 | 9 | ABE21881 | Aeb21881 Human DC- | 655 | 40 | 50.6 | 612 | 6 | ABR47687 | AbR47687 Human sec |
| 583 | 40.5 | 51.3 | 114 | 8 | ADG25839 | Adg25839 Anti-CD30 | 656 | 40 | 50.6 | 612 | 6 | ABR47991 | AbR47991 Human sec |
| 584 | 40.5 | 51.3 | 114 | 8 | AD126467 | Adi26467 Murine 1A | 657 | 40 | 50.6 | 612 | 8 | ADO58715 | Ado58715 Human reg |
| 585 | 40.5 | 51.3 | 114 | 8 | ADG16519 | Adg16519 Human ant | 658 | 40 | 50.6 | 612 | 9 | ADY54265 | Ady54265 Human 581 |
| 586 | 40.5 | 51.3 | 132 | 5 | ABG76923 | Abg76923 Mouse 3D6 | 659 | 40 | 50.6 | 679 | 2 | AAH88456 | AAh88456 Human kin |
| 587 | 40.5 | 51.3 | 132 | 5 | ABG76925 | Abg76925 Humanised | 660 | 40 | 50.6 | 679 | 7 | ADK11358 | Adk11358 Human kin |
| 588 | 40.5 | 51.3 | 132 | 5 | ABG76931 | Abg76931 Humanised | 661 | 40 | 50.6 | 679 | 7 | ADU70160 | AdU70160 Human hea |
| 589 | 40.5 | 51.3 | 132 | 5 | ABG76931 | Abg76931 Humanised | 662 | 40 | 50.6 | 679 | 8 | ADQ15130 | Adq15130 Human can |
| 590 | 40.5 | 51.3 | 132 | 8 | ADR88409 | Adr88409 Humanised | 663 | 40 | 50.6 | 679 | 8 | ADP54422 | Adp54422 Human PRO |
| 591 | 40.5 | 51.3 | 132 | 8 | ADR88406 | Adr88406 Murine 3D | 664 | 40 | 50.6 | 679 | 9 | ADX07972 | Adx07972 Cyclin-de |
| 592 | 40.5 | 51.3 | 163 | 4 | ADS16620 | Adsl6620 Human ant | 665 | 40 | 50.6 | 679 | 9 | ADY14988 | Ady14988 PRO poly |
| 593 | 40.5 | 51.3 | 218 | 4 | AAE03756 | Aae03756 Chimeric | 666 | 40 | 50.6 | 690 | 4 | AAH39257 | AAh39257 Human pol |
| 594 | 40.5 | 51.3 | 219 | 6 | ABP58272 | Abp58272 Humanised | 667 | 40 | 50.6 | 690 | 4 | AAH41043 | AAh41043 Human pol |
| 595 | 40.5 | 51.3 | 238 | 8 | ADW72033 | Adw72033 Chimeric | 668 | 40 | 50.6 | 694 | 4 | AAH41044 | AAh41044 Human pol |
| 596 | 40.5 | 51.3 | 239 | 6 | ABP58274 | Abp58274 Humanised | 669 | 40 | 50.6 | 728 | 4 | AAH39258 | AAh39258 Human pol |
| 597 | 40.5 | 51.3 | 243 | 2 | AAW60769 | Aaw60769 Single ch | 670 | 40 | 50.6 | 1150 | 7 | ADP16417 | Adp16417 Human alb |
| 598 | 40.5 | 51.3 | 353 | 2 | AAW06273 | Aaw06273 Anti Fc a | 671 | 40 | 50.6 | 1150 | 7 | ADP16418 | Adp16418 Human alb |
| 599 | 40.5 | 51.3 | 535 | 2 | AAW28491 | Aaw28491 Human p53 | 672 | 40 | 50.6 | 2439 | 4 | ABE68896 | ABe68896 Drosophil |
| 600 | 40.5 | 51.3 | 535 | 2 | AAW28492 | Aaw28492 Human p53 | 673 | 39.5 | 50.0 | 16 | 2 | AAW39839 | AAw39839 Light cha |
| 601 | 40.5 | 51.3 | 535 | 2 | ABE21450 | Aeb21450 Mouse ant | 674 | 39.5 | 50.0 | 91 | 6 | ABR55905 | ABr55905 Human mAb |
| 602 | 40.5 | 50.6 | 15 | 9 | ABE31208 | Aeb31208 Antibody | 675 | 39.5 | 50.0 | 91 | 6 | ABR55889 | ABr55889 Human mAb |
| 603 | 40.5 | 50.6 | 108 | 2 | AAH42633 | AAh42633 Light cha | 676 | 39.5 | 50.0 | 93 | 8 | ADU04216 | Adu04216 Human imm |
| 604 | 40.5 | 50.6 | 108 | 2 | AAH80942 | AAh80942 Antibody | 677 | 39.5 | 50.0 | 100 | 6 | AAE35907 | AAe35907 Human Al7 |
| 605 | 40.5 | 50.6 | 111 | 2 | AAH85236 | AAh85236 Murine 20 | 678 | 39.5 | 50.0 | 100 | 6 | ABO27142 | ABo27142 Human ger |
| 606 | 40.5 | 50.6 | 111 | 2 | AAH85242 | AAh85242 Humanised | 679 | 39.5 | 50.0 | 100 | 6 | ABO27143 | ABo27143 Human ger |
| 607 | 40.5 | 50.6 | 111 | 7 | AD120695 | Adi20695 Light cha | 680 | 39.5 | 50.0 | 100 | 7 | ADP10190 | Adp10190 Antibody |
| 608 | 40.5 | 50.6 | 112 | 8 | ADR38679 | Adr38679 Mouse lig | 681 | 39.5 | 50.0 | 100 | 7 | ADP10088 | Adp10088 VEGF anti |

| | | | | | | | | | | | | | |
|-----|------|------|-----|---|----------|-----------|-----|------|------|------|---|-----------|-----------|
| 682 | 39.5 | 50.0 | 100 | 7 | ADP09983 | Antibody | 755 | 39 | 49.4 | 112 | 9 | AEb31206 | Antibody |
| 683 | 38.5 | 50.0 | 100 | 7 | ADP10189 | Antibody | 756 | 39 | 49.4 | 112 | 9 | AEb31202 | Antibody |
| 684 | 39.5 | 50.0 | 100 | 7 | ADP10087 | Antibody | 757 | 39 | 49.4 | 113 | 2 | AAR79892 | Anti-EGFR |
| 685 | 39.5 | 50.0 | 100 | 7 | ADP09982 | Antibody | 758 | 39 | 49.4 | 113 | 2 | AAR79882 | Anti-EGFR |
| 686 | 39.5 | 50.0 | 100 | 7 | ADJ80263 | Vkappa ge | 759 | 39 | 49.4 | 113 | 2 | AAR79891 | Anti-EGFR |
| 687 | 39.5 | 50.0 | 100 | 7 | ADJ80262 | Vkappa ge | 760 | 39 | 49.4 | 119 | 9 | Aea44092 | Anti-TPO |
| 688 | 39.5 | 50.0 | 100 | 8 | ADJ80262 | Human ant | 761 | 39 | 49.4 | 120 | 6 | ADA89198 | Human ant |
| 689 | 38.5 | 50.0 | 100 | 8 | ADJ80262 | Human ant | 762 | 39 | 49.4 | 120 | 6 | ADA89198 | Human ant |
| 690 | 39.5 | 50.0 | 100 | 9 | ADJ80262 | Human ant | 763 | 39 | 49.4 | 131 | 2 | AAR30881 | Antibody |
| 691 | 39.5 | 50.0 | 100 | 9 | ADJ80262 | Human ant | 764 | 39 | 49.4 | 147 | 9 | ADY94497 | Human/mou |
| 692 | 39.5 | 50.0 | 100 | 9 | ADJ80262 | Human ant | 765 | 39 | 49.4 | 199 | 3 | AAG45895 | Arabidops |
| 693 | 39.5 | 50.0 | 100 | 9 | ADJ80262 | Human ant | 766 | 39 | 49.4 | 215 | 2 | AAR74781 | Light cha |
| 694 | 39.5 | 50.0 | 100 | 9 | ADJ80262 | Human ant | 767 | 39 | 49.4 | 223 | 3 | AAG45894 | Arabidops |
| 695 | 38.5 | 50.0 | 100 | 9 | ADJ80262 | Human ant | 768 | 39 | 49.4 | 243 | 9 | ADW95684 | Anti-IL-6 |
| 696 | 39.5 | 50.0 | 103 | 7 | ADJ80262 | Human ant | 769 | 39 | 49.4 | 249 | 4 | ADX15689 | Mouse ant |
| 697 | 39.5 | 50.0 | 112 | 2 | ADJ80262 | Human ant | 770 | 39 | 49.4 | 262 | 3 | AAAG20436 | Anti-FIX/ |
| 698 | 39.5 | 50.0 | 112 | 4 | ADJ80262 | Human ant | 771 | 39 | 49.4 | 288 | 8 | AAG45893 | Arabidops |
| 699 | 39.5 | 50.0 | 112 | 4 | ADJ80262 | Human ant | 772 | 39 | 49.4 | 327 | 3 | ADW99139 | Environme |
| 700 | 39.5 | 50.0 | 112 | 7 | ADJ80262 | Human ant | 773 | 39 | 49.4 | 348 | 3 | AAG44509 | Arabidops |
| 701 | 39.5 | 50.0 | 112 | 7 | ADJ80262 | Human ant | 774 | 39 | 49.4 | 364 | 7 | ADW99139 | Environme |
| 702 | 39.5 | 50.0 | 112 | 7 | ADJ80262 | Human ant | 775 | 39 | 49.4 | 374 | 3 | AAG44507 | Arabidops |
| 703 | 39.5 | 50.0 | 112 | 8 | ADJ80262 | Human ant | 776 | 39 | 49.4 | 379 | 8 | ADN61354 | Paenibaci |
| 704 | 39.5 | 50.0 | 112 | 8 | ADJ80262 | Human ant | 777 | 39 | 49.4 | 474 | 7 | ABM86533 | Rice abio |
| 705 | 39.5 | 50.0 | 112 | 8 | ADJ80262 | Human ant | 778 | 39 | 49.4 | 599 | 2 | AAR90837 | 3B1 singl |
| 706 | 39.5 | 50.0 | 112 | 8 | ADJ80262 | Human ant | 779 | 39 | 49.4 | 784 | 2 | AAW53570 | Cucumber |
| 707 | 39.5 | 50.0 | 112 | 9 | ADJ80262 | Human ant | 780 | 39 | 49.4 | 784 | 2 | AAW53570 | Cucumber |
| 708 | 39.5 | 50.0 | 113 | 2 | ADJ80262 | Human ant | 781 | 39 | 49.4 | 869 | 8 | ADN20209 | Bacterial |
| 709 | 39.5 | 50.0 | 113 | 2 | ADJ80262 | Human ant | 782 | 39 | 49.4 | 952 | 3 | AAW68673 | Amino aci |
| 710 | 39.5 | 50.0 | 113 | 8 | ADJ80262 | Human ant | 783 | 39 | 49.4 | 1475 | 5 | ABW48897 | Listeria |
| 711 | 39.5 | 50.0 | 113 | 8 | ADJ80262 | Human ant | 784 | 38.5 | 48.7 | 16 | 5 | AAU70328 | Human Kap |
| 712 | 39.5 | 50.0 | 113 | 9 | ADJ80262 | Human ant | 785 | 38.5 | 48.7 | 114 | 8 | ADP22114 | Human ant |
| 713 | 39.5 | 50.0 | 113 | 9 | ADJ80262 | Human ant | 786 | 38.5 | 48.7 | 129 | 9 | ABE14811 | Light cha |
| 714 | 39.5 | 50.0 | 114 | 2 | ADJ80262 | Human ant | 787 | 38 | 48.1 | 15 | 8 | ADP38811 | Mouse lig |
| 715 | 39.5 | 50.0 | 114 | 7 | ADJ80262 | Human ant | 788 | 38 | 48.1 | 15 | 8 | ADP38807 | Mouse lig |
| 716 | 39.5 | 50.0 | 114 | 8 | ADJ80262 | Human ant | 789 | 38 | 48.1 | 15 | 8 | ADP38819 | Mouse lig |
| 717 | 39.5 | 50.0 | 132 | 2 | ADJ80262 | Human ant | 790 | 38 | 48.1 | 15 | 8 | ADP38823 | Mouse lig |
| 718 | 39.5 | 50.0 | 132 | 7 | ADJ80262 | Human ant | 791 | 38 | 48.1 | 15 | 8 | ADP38815 | Mouse lig |
| 719 | 39.5 | 50.0 | 132 | 7 | ADJ80262 | Human ant | 792 | 38 | 48.1 | 15 | 9 | ADP29435 | Mouse lig |
| 720 | 39.5 | 50.0 | 132 | 7 | ADJ80262 | Human ant | 793 | 38 | 48.1 | 15 | 9 | ADP29435 | Mouse lig |
| 721 | 39.5 | 50.0 | 133 | 9 | ADJ80262 | Human ant | 794 | 38 | 48.1 | 60 | 6 | ABU56881 | BoNT/A Hc |
| 722 | 39.5 | 50.0 | 139 | 3 | ADJ80262 | Human ant | 795 | 38 | 48.1 | 60 | 6 | ABU56883 | BoNT/A Hc |
| 723 | 39.5 | 50.0 | 139 | 6 | ADJ80262 | Human ant | 796 | 38 | 48.1 | 83 | 5 | AAU78274 | Serine pr |
| 724 | 39.5 | 50.0 | 247 | 5 | ADJ80262 | Human ant | 797 | 38 | 48.1 | 87 | 2 | AAW80081 | Mouse der |
| 725 | 38.5 | 50.0 | 253 | 5 | ADJ80262 | Human ant | 798 | 38 | 48.1 | 110 | 3 | AAW37143 | Arabidops |
| 726 | 39.5 | 50.0 | 253 | 5 | ADJ80262 | Human ant | 799 | 38 | 48.1 | 110 | 8 | ADP77285 | Plant ful |
| 727 | 39.5 | 50.0 | 257 | 8 | ADJ80262 | Human ant | 800 | 38 | 48.1 | 111 | 2 | AAW60528 | Light cha |
| 728 | 39.5 | 50.0 | 257 | 8 | ADJ80262 | Human ant | 801 | 38 | 48.1 | 111 | 4 | AAW66456 | VEGF ScFv |
| 729 | 39.5 | 50.0 | 287 | 8 | ADJ80262 | Human ant | 802 | 38 | 48.1 | 111 | 8 | ADW93272 | VEGF mono |
| 730 | 39 | 49.4 | 11 | 9 | ADJ80262 | Human ant | 803 | 38 | 48.1 | 112 | 8 | ADP38682 | Mouse lig |
| 731 | 39 | 49.4 | 11 | 9 | ADJ80262 | Human ant | 804 | 38 | 48.1 | 112 | 8 | ADP38684 | Mouse lig |
| 732 | 39 | 49.4 | 15 | 9 | ADJ80262 | Human ant | 805 | 38 | 48.1 | 114 | 3 | AAW25245 | Arabidops |
| 733 | 39 | 49.4 | 15 | 9 | ADJ80262 | Human ant | 806 | 38 | 48.1 | 121 | 2 | AAW33346 | Sequence |
| 734 | 39 | 49.4 | 15 | 9 | ADJ80262 | Human ant | 807 | 38 | 48.1 | 130 | 4 | ABW66054 | Drosophi |
| 735 | 39 | 49.4 | 60 | 6 | ADJ80262 | Human ant | 808 | 38 | 48.1 | 140 | 2 | AAW55215 | Murine va |
| 736 | 39 | 49.4 | 60 | 6 | ADJ80262 | Human ant | 809 | 38 | 48.1 | 152 | 3 | AAW07152 | Arabidops |
| 737 | 39 | 49.4 | 60 | 6 | ADJ80262 | Human ant | 810 | 38 | 48.1 | 152 | 3 | AAW53555 | Arabidops |
| 738 | 39 | 49.4 | 103 | 2 | ADJ80262 | Human ant | 811 | 38 | 48.1 | 152 | 4 | AAW99934 | Human pol |
| 739 | 39 | 49.4 | 108 | 5 | ADJ80262 | Human ant | 812 | 38 | 48.1 | 168 | 3 | AAW24896 | Plant SDF |
| 740 | 39 | 49.4 | 108 | 6 | ADJ80262 | Human ant | 813 | 38 | 48.1 | 186 | 3 | AAW16954 | Arabidops |
| 741 | 39 | 49.4 | 108 | 9 | ADJ80262 | Human ant | 814 | 38 | 48.1 | 218 | 6 | ABP96770 | TSH recep |
| 742 | 39 | 49.4 | 108 | 9 | ADJ80262 | Human ant | 815 | 38 | 48.1 | 218 | 6 | ABP96769 | TSH recep |
| 743 | 39 | 49.4 | 111 | 2 | ADJ80262 | Human ant | 816 | 38 | 48.1 | 218 | 9 | ADZ99438 | Humanized |
| 744 | 39 | 49.4 | 111 | 2 | ADJ80262 | Human ant | 817 | 38 | 48.1 | 232 | 3 | AAW07151 | Arabidops |
| 745 | 39 | 49.4 | 111 | 3 | ADJ80262 | Human ant | 818 | 38 | 48.1 | 232 | 3 | AAW53554 | Arabidops |
| 746 | 39 | 49.4 | 111 | 3 | ADJ80262 | Human ant | 819 | 38 | 48.1 | 236 | 3 | AAW29858 | Arabidops |
| 747 | 39 | 49.4 | 112 | 8 | ADJ80262 | Human ant | 820 | 38 | 48.1 | 239 | 3 | AAW07150 | Arabidops |
| 748 | 39 | 49.4 | 112 | 8 | ADJ80262 | Human ant | 821 | 38 | 48.1 | 239 | 3 | AAW53553 | Arabidops |
| 749 | 39 | 49.4 | 112 | 8 | ADJ80262 | Human ant | 822 | 38 | 48.1 | 250 | 4 | AAW99921 | Human pol |
| 750 | 39 | 49.4 | 112 | 9 | ADJ80262 | Human ant | 823 | 38 | 48.1 | 291 | 7 | ABO74080 | Pseudomon |
| 751 | 39 | 49.4 | 112 | 9 | ADJ80262 | Human ant | 824 | 38 | 48.1 | 299 | 6 | ABU24936 | Protein e |
| 752 | 39 | 49.4 | 112 | 9 | ADJ80262 | Human ant | 825 | 38 | 48.1 | 307 | 8 | ADX91197 | Plant ful |
| 753 | 39 | 49.4 | 112 | 9 | ADJ80262 | Human ant | 826 | 38 | 48.1 | 315 | 2 | AAW37865 | Human pro |
| 754 | 39 | 49.4 | 112 | 9 | ADJ80262 | Human ant | 827 | 38 | 48.1 | 315 | 2 | AAW00917 | Human ret |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|----------|--------------------|-----|------|------|------|---|----------|---------------------|
| 828 | 38 | 48.1 | 315 | 2 | AAW67886 | Aaw67886 Human sec | 901 | 37.5 | 47.5 | 1301 | 5 | ABB77633 | Abb77633 AnEPV fif |
| 829 | 38 | 48.1 | 315 | 4 | AAW93808 | Aaw93808 Human pol | 902 | 37 | 46.8 | 15 | 2 | AAW01147 | Aaw01147 MAB 1.4 l |
| 830 | 38 | 48.1 | 315 | 4 | AAW94090 | Aaw94090 Human pro | 903 | 37 | 46.8 | 15 | 2 | AAW44170 | Aaw44170 Monoclonal |
| 831 | 38 | 48.1 | 315 | 5 | AAU84387 | Aau84387 Novel hum | 904 | 37 | 46.8 | 15 | 5 | AAU81246 | Aau81246 Murine tr |
| 832 | 38 | 48.1 | 315 | 7 | ADJ18600 | Adj18600 Human dis | 905 | 37 | 46.8 | 15 | 8 | ADN08048 | Adn08048 HuCOL-1 d |
| 833 | 38 | 48.1 | 315 | 7 | ADE55542 | Ade55542 Human pro | 906 | 37 | 46.8 | 15 | 8 | ADN08048 | Adn08048 Murine CO |
| 834 | 38 | 48.1 | 315 | 7 | ADK65773 | Adk65773 Angiogene | 907 | 37 | 46.8 | 15 | 9 | AE21454 | Aeb21454 Mouse ant |
| 835 | 38 | 48.1 | 315 | 7 | ADK65822 | Adk65822 Angiogene | 908 | 37 | 46.8 | 15 | 9 | AE21454 | Aeb21454 Mouse ant |
| 836 | 38 | 48.1 | 315 | 7 | ADK65822 | Adk65822 Angiogene | 909 | 37 | 46.8 | 16 | 2 | AAW74945 | Aar74945 L-CDR-1 o |
| 837 | 38 | 48.1 | 315 | 8 | ADL31818 | Adl31818 Human cal | 910 | 37 | 46.8 | 20 | 6 | ABR42159 | Abf42159 Peptide u |
| 838 | 38 | 48.1 | 315 | 8 | ADP23015 | Adp23015 PRO polyp | 911 | 37 | 46.8 | 20 | 8 | ADF29035 | Adf29035 Synthetic |
| 839 | 38 | 48.1 | 315 | 9 | ADM08841 | Adm08841 Human pro | 912 | 37 | 46.8 | 61 | 7 | ADP02185 | Adp02185 Human ORF |
| 840 | 38 | 48.1 | 315 | 9 | ADM08841 | Adm08841 Human pro | 913 | 37 | 46.8 | 65 | 5 | ADP02185 | Adp02185 Human ORF |
| 841 | 38 | 48.1 | 330 | 5 | AAU72991 | Aau72991 Neisseria | 914 | 37 | 46.8 | 72 | 4 | AAU28270 | Aau28270 Novel hum |
| 842 | 38 | 48.1 | 330 | 6 | ABU37998 | Abu37998 Protein e | 915 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 843 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 916 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 844 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 917 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 845 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 918 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 846 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 919 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 847 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 920 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 848 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 921 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 849 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 922 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 850 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 923 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 851 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 924 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 852 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 925 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 853 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 926 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 854 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 927 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 855 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 928 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 856 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 929 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 857 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 930 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 858 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 931 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 859 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 932 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 860 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 933 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 861 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 934 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 862 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 935 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 863 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 936 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 864 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 937 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 865 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 938 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 866 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 939 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 867 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 940 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 868 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 941 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 869 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 942 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 870 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 943 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 871 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 944 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 872 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 945 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 873 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 946 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 874 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 947 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 875 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 948 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 876 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 949 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 877 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 950 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 878 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 951 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 879 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 952 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 880 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 953 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 881 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 954 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 882 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 955 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 883 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 956 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 884 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 957 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 885 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 958 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 886 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 959 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 887 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 960 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 888 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 961 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 889 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 962 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 890 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 963 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 891 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 964 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 892 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 965 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 893 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 966 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 894 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 967 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 895 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 968 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 896 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 969 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 897 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 970 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 898 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 971 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 899 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 972 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |
| 900 | 38 | 48.1 | 342 | 6 | ABU78851 | Abu78851 N. gonorr | 973 | 37 | 46.8 | 81 | 9 | ADW26719 | Adw26719 Fructo-ol |

974 37 46.8 112 6 ABB98912 Variable
 975 37 46.8 112 8 AD089279 Human Imm
 976 37 46.8 112 9 ADW50593 Protein o
 977 37 46.8 112 9 ADY28825 Murine an
 978 37 46.8 112 9 ADY28849 Murine an
 979 37 46.8 112 9 ADZ81895 Mouse an
 980 37 46.8 112 9 AEB09552
 981 37 46.8 124 2 AAR15442 Light cha
 982 37 46.8 128 2 AAR95947 HNK-20 va
 983 37 46.8 128 5 ABB79731 Anti-Stre
 984 37 46.8 130 2 AAR74967
 985 37 46.8 131 2 AAR28668 p12-k2.3
 986 37 46.8 131 2 AAW01143 Mab 1.4.1
 987 37 46.8 131 2 AAW44168 Monoclonal
 988 37 46.8 131 5 AAU76130 Mouse mAb
 989 37 46.8 131 5 AAU76121 Mouse mon
 990 37 46.8 131 5 AAU76131 Mouse mAb
 991 37 46.8 132 2 AAW03723 Anti-huma
 992 37 46.8 135 2 AAR54052 Sequence
 993 37 46.8 135 2 AAW01525 Monoclonal
 994 37 46.8 135 2 AAW24989 Monoclonal
 995 37 46.8 146 2 AAR74966 Anti-idio
 996 37 46.8 146 2 AAW19578 Mouse ant
 997 37 46.8 147 9 AEB48772 Talaromyc
 998 37 46.8 175 5 AEG60106 Human DIT
 999 37 46.8 182 5 ABP40177 Staphyloc
 1000 37 46.8 182 8 ADS07227 Staphyloc

ALIGNMENTS

RESULT 1
 AAR70195
 ID AAR70195 standard; protein; 15 AA.
 AC AAR70195;
 XX
 XX 25-MAR-2003 (revised)
 DT 20-SEP-1995 (first entry)
 XX
 DE Mab 3B9 light chain CDR.
 XX
 XX Chimeric antibody; humanized antibody; antibody engineering;
 KW monoclonal antibody; MAB; interleukin-4; IL-4; allergy; CDR;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX WO9507301-A1.
 XX
 PD 16-MAR-1995.
 XX
 PF 07-SEP-1994; 94WO-US010308.
 XX
 XX 07-SEP-1993; 93US-00117366.
 PR 14-OCT-1993; 93US-00136783.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 XX Holmes S, Gross MS, Sylvester DR;
 XX WPI; 1995-123387/16.
 XX
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from
 PT high affinity mAbs - useful in treatment of IL-4-mediated and IgE-
 PT mediated allergic conditions.
 XX
 PS Disclosure; Page 54; 97pp; English.
 XX
 CC Spleen cells from mice immunized with human IL-4 were used to prepare
 CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only clone

CC 3B9 was positive. cDNA clones of the 3B9 light and heavy chains were
 CC cloned into pEMVif+ and transformed into E. coli DH5-alpha. A light chain
 CC cDNA clone was sequenced (AAQ83490) that encoded the protein given in
 CC AAR70189. 3 CDRs (AAR70195-97) were identified. (Updated on 25-MAR-2003
 CC to correct PN field.)
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 79; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSYNN 15
 |||||
 DB 1 KASQSVYDGDSYNN 15
 |||||

RESULT 2

AAW83027
 ID AAW83027 standard; peptide; 15 AA.

XX
 AC AAW83027;

XX
 DT 25-MAR-2003 (revised)

DT 15-MAR-1999 (first entry)

XX
 DE Anti-Fas Mab HFE7A light chain CDR-L1.

XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis;
 KW autoimmune disease; Hashimoto's disease; systemic lupus erythematosus;
 KW graft versus host disease; Sjogren syndrome; pernicious anaemia;
 KW Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease;
 KW sterility; rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy; atopy;
 KW arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis;
 KW hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy;
 KW complementarity determining region; CDR.

XX Mus musculus.

XX AU9859701-A.

XX 08-OCT-1998.

XX 30-MAR-1998; 98AU-00059701.

XX 01-APR-1997; 97JP-00082953.

XX 25-JUN-1997; 97JP-00169088.

XX 08-OCT-1997; 97JP-00276064.

XX (SANY) SANKYO CO LTD.

XX Nobufusa S, Kimihisa I, Jun O, Masahiko O, Hideyuki H, Tohru T;
 PI Hiroko Y, Akio S, Shin Y;

XX WPI; 1998-543440/01.

XX New antibodies and proteins bind conserved epitope of Fas antigen - used
 PT to evaluate drugs in animal models and to treat Fas-associated diseases
 PT e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis,
 PT hepatitis and AIDS.

XX Claim 9; Page 184; 292pp; English.

XX This is the amino acid of complementarity determining region 1 (CDR-L1)
 CC of the light chain (see AAW83042) of murine anti-human Fas monoclonal
 CC antibody HFE7A. The invention relates to antibodies, especially humanised
 CC antibodies (see AAW83031-37), recognising the Fas antigen. Such
 CC antibodies preferably comprise a heavy chain and a light chain including
 CC CDRs (see AAW83024-29) from the heavy and light chains of HFE7A.
 CC Humanised antibodies are produced by CDR grafting. The antibodies are
 CC capable of inducing apoptosis in abnormal cells expressing Fas, and of

CC inhibiting Fas-induced apoptosis in normal cells. They are used to
 CC evaluate, in animal models, treatments of diseases that involve Fas/Fas
 CC ligand interactions, and also to treat such diseases, including
 CC autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's
 CC disease, graft versus host disease, Sjogren syndrome, pernicious anaemia,
 CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease,
 CC rheumatoid arthritis, autoimmune haemolytic anaemia, sterility,
 CC myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia
 CC purpura and insulin-dependent diabetes), allergies, atopy,
 CC arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis,
 CC hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all
 CC claimed). (Updated on 25-MAR-2003 to correct DR field.)
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 79; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGD SYMN 15
 |||||
 DB 1 KASQSVYDGD SYMN 15

RESULT 3
 AAY23772
 ID AAY23772 standard; peptide; 15 AA.

AC AAY23772;
 XX
 DT 13-SEP-1999 (first entry)
 XX
 DE CDR of the light chain variable region of antibody 3B9.
 XX
 KW Light chain variable region; interleukin-4; IL-4; antibody 3B9;
 KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
 KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy;
 KW complementarity determining region.

OS Mus sp.
 XX
 XX US528904-A.
 XX
 XX 27-JUL-1999.
 XX
 XX 07-JUN-1995; 95US-00483632.
 XX
 XX 07-SEP-1993; 93US-00117366.
 XX
 XX 14-OCT-1993; 93US-00136783.
 XX
 XX 07-SEP-1994; 94WO-US010308.
 XX
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Holmes SD, Sylvester DR, Gross MS;
 XX
 XX WPI; 1999-429500/36.
 XX N-PSDB; AAX85889.

XX New DNA molecules encoding recombinant antibodies useful for treating IL4
 XX mediated conditions.

XX Example 3; Col 43-44; 50pp; English.

XX The present sequence represents a complementarity determining region
 CC (CDR) of the light chain variable region of murine interleukin-4 (IL-4)
 CC antibody 3B9. The specification describes chimeric and humanised IL-4
 CC monoclonal antibodies. The antibodies of the invention are used in
 CC therapeutic and pharmaceutical compositions for treating IL-4 mediated
 CC and immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis,
 CC conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock,

CC rheumatoid arthritis, host-versus-graft disease and renal disease. They
 CC are also useful in the diagnosis of an allergy or condition associated
 CC with excess IL-4 production through the measurement e.g. by ELISA of
 CC circulating endogenous IL-4 levels in humans
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 79; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGD SYMN 15
 |||||
 DB 1 KASQSVYDGD SYMN 15

RESULT 4
 AAY18114
 ID AAY18114 standard; peptide; 15 AA.

XX AAY18114;
 XX
 DT 11-AUG-1999 (first entry)
 XX
 DE Light chain CDR for hIL-4 specific antibody.
 XX
 KW Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;
 KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
 KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
 KW autoimmune disease; graft versus host disease;
 KW complementarity determining region; CDR.
 XX
 OS Synthetic.

XX US5914110-A.

XX 22-JUN-1999.

XX 07-JUN-1995; 95US-00483636.

XX 07-SEP-1993; 93US-00117366.

XX 14-OCT-1993; 93US-00136783.

XX 07-SEP-1994; 94WO-US010308.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Sylvester DR, Holmes SD, Gross MS;

XX WPI; 1999-370482/31.

XX N-PSDB; AAX79513.

XX Recombinant IL4 antibodies useful for treatment of allergic rhinitis,
 XX atopic asthma and anaphylactic shock.

XX Claim 7; Col 43; 50pp; English.

XX This sequence represents a light chain complementarity determining region
 CC (CDR) from an antibody of the invention. The antibody is a chimeric or
 CC humanised interleukin-4 (IL4) monoclonal antibody for the treatment of
 CC immunoglobulin E (IgE) mediated diseases. The antibodies are useful for
 CC the treatment of allergic disorders such as allergic rhinitis,
 CC conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.
 CC The antibodies are also useful for regulating B and T cell proliferation
 CC and as such are useful in the treatment of autoimmune diseases and graft
 CC versus host disease

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 KASQSDVDGDSYMN 15
Db      1 KASQSDVDGDSYMN 15

RESULT 5
AAB14744
ID AAB14744 standard; peptide; 15 AA.
XX
XX AC AAB14744;
XX
XX DT 24-NOV-2000 (first entry)
XX
XX DE Mouse anti-Fas antibody HFE7A light chain CDR1.
XX
XX KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine;
KW complementarity determining region; CDR; human Fas; Fas ligand;
KW apoptosis modulator; programmed cell death; autoimmune disease; allergy;
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis;
KW aplastic anaemia; pancytopenia; hepatitis; AIDS; graft rejection;
XX light chain.
XX
XX OS Mus musculus.
XX
XX PN JP2000169393-A.
XX
XX PD 20-JUN-2000.
XX
XX PF 30-SEP-1999; 99JP-00278301.
XX
XX PR 30-SEP-1998; 98JP-00276883.
XX
XX PA (SANY ) SANKYO CO LTD.
XX
XX DR WPI; 2000-485645/43.
XX
XX PT Preventive or treating agent for the diseases caused by an abnormality in
PT the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas
PT antibody.
XX
XX PS Claim 10; Page 65; 139pp; Japanese.
XX
XX CC The invention relates to compositions for the prevention or treatment or
CC diseases caused by an abnormality in the Fas/Fas ligand system containing
CC an anti-Fas antibody as the active component. The anti-Fas antibody is
CC either the murine anti-human Fas monoclonal antibody HFE7A, or a
CC humanised version of HFE7A containing identical CDRs (complementarity
CC determining regions) to antibody HFE7A. Via its interaction with Fas, the
CC antibody of the invention acts as a modulator of apoptosis. The
CC compositions of the invention may therefore be used in the treatment or
CC prevention of conditions such as autoimmune diseases, allergy, atopy,
CC arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis,
CC aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft
CC rejection. Sequences AAB14744-B14746 represent CDRs 1-3 of the light
CC chain of the murine anti-human Fas monoclonal antibody HFE7A, which is
CC produced by hybridoma HFE7A (FERM-BP-5828)
XX
XX SQ Sequence 15 AA;

Query Match      100.0%; Score 79; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KASQSDVDGDSYMN 15
Db      1 KASQSDVDGDSYMN 15

RESULT 6
AAY51136
ID AAY51136 standard; protein; 15 AA.
XX
XX AC AAY51136;

Query Match      100.0%; Score 79; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KASQSDVDGDSYMN 15
Db      1 KASQSDVDGDSYMN 15

RESULT 7
AAW90894
ID AAW90894 standard; peptide; 15 AA.
XX
XX AC AAW90894;
XX
XX DT 08-AUG-2000 (first entry)
XX
XX DE Murine anti-Fas antibody peptide fragment #4.
XX
XX KW Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic;
XX anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
XX dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
XX nephrotropic; infertility; neuroprotective; antiatherosclerotic;
XX hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
XX Hashimoto disease; rheumatoid arthritis; graft versus host disease;
XX Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
XX Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;

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XX DT 31-MAR-2000 (first entry)
XX
XX DE Murine CD4/CD34 recognizing antibody light chain CDR-1 region #1.
XX
XX KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
KW HIV infection; autoimmune disease; complementarity determining region;
KW CDR-1; light chain; murine.
XX
XX OS Mus sp.
XX
XX PN WO9961629-A1.
XX
XX PD 02-DEC-1999.
XX
XX PF 24-MAY-1999; 99WO-JP002711.
XX
XX PR 25-MAY-1998; 98JP-00159957.
XX
XX PR 26-MAY-1998; 98JP-00163023.
XX
XX PA (ASAH ) ASAH KASEI KOGYO KK.
XX
XX PA (ASAH ) ASAH MEDICAL CO LTD.
XX
XX PI Ono M, Soka T, Morimoto I, Miyamura K;
XX
XX DR WPI; 2000-086720/07.
XX
XX PT Devices containing antibodies recognising CD4 or CD34 and their use for
PT the separation of CD4 or CD34 positive cells.
XX
XX PS Claim 3; Page 76; 111pp; Japanese.
XX
XX CC This invention describes a novel device (I) for separating cluster
XX differentiation (CD)-positive cells using a recombinant (chimeric or
XX single-chain) antibody recognising CD4 or CD34. The devices are useful
XX for the separation of CD4 or CD34 positive cells, which is useful for the
XX collection of hematopoietic undifferentiated cells, elimination of
XX lymphocytes from cells to be used in bone marrow transplantation, the
XX detection of leukemic cells and the production of medicinal compositions
XX for the treatment of HIV infection and autoimmune diseases. This sequence
XX represents a murine derived complementarity determining region CDR-1
XX protein fragment which is used to illustrate the method of the invention
XX
XX SQ Sequence 15 AA;

Query Match      100.0%; Score 79; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KASQSDVDGDSYMN 15
Db      1 KASQSDVDGDSYMN 15

RESULT 7
AAW90894
ID AAW90894 standard; peptide; 15 AA.
XX
XX AC AAW90894;
XX
XX DT 08-AUG-2000 (first entry)
XX
XX DE Murine anti-Fas antibody peptide fragment #4.
XX
XX KW Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic;
XX anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
XX dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
XX nephrotropic; infertility; neuroprotective; antiatherosclerotic;
XX hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
XX Hashimoto disease; rheumatoid arthritis; graft versus host disease;
XX Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
XX Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;

```

KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 OS Mus musculus.
 XX EP990663-A2.
 XX 05-APR-2000.
 XX 29-SEP-1999; 99EP-00307711.
 XX 30-SEP-1998; 98JP-00276881.
 XX 30-SEP-1998; 98JP-00276882.
 XX (SANY) SANKYO CO LTD.
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX WPI; 2000-258930/23.
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems.
 XX Disclosure; Page 98; 263pp; English.
 XX This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatotropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a murine anti-Fas antibody peptide fragment described in the method of
 CC the invention
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 79; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KASQSVVDYDGD SYMN 15
 DB 1 KASQSVVDYDGD SYMN 15
 RESULT 8
 AAY59259
 ID AAY59259 standard; peptide; 15 AA.
 XX
 AC AAY59259;
 XX
 DT 17-APR-2000 (first entry)

XX Antobody 4H5 L chain variable region CDR1 fragment.
 DE CD4 antigen; anti-human; antibody; 4H5; drug; CDR;
 XX complementarity determining region.
 KW Mus sp.
 XX JP11332563-A.
 XX 07-DEC-1999.
 XX 26-MAY-1998; 98JP-00163034.
 XX 26-MAY-1998; 98JP-00163034.
 XX (ASAH) ASahi KASEI KOGYO KK.
 XX WPI; 2000-091351/08.
 XX An antibody and the nucleic acid coding the antibody.
 PT Claim 2; Page 14; 25pp; Japanese.
 PS The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. Sequences
 CC AAY59259-61 represent the complementarity determining region (CDR)-1, CDR
 CC -2 and CDR-3 fragments in the L chain variable region of the antibody 4H5
 CC respectively
 XX Sequence 15 AA;
 SQ
 Query Match 100.0%; Score 79; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KASQSVVDYDGD SYMN 15
 DB 1 KASQSVVDYDGD SYMN 15
 RESULT 9
 ABB74909
 ID ABB74909 standard; peptide; 15 AA.
 XX
 AC ABB74909;
 XX
 DT 30-APR-2002 (first entry)
 DE Humanised anti-Fas antibody related peptide SEQ ID NO 26.
 XX Human; mouse; Fas/Fas ligand system; Fas; antibody; light chain;
 KW heavy chain; apoptosis; antiallergic; immunosuppressive; apoptotic;
 KW autoimmune disease; allergy; atopy.
 XX Homo sapiens.
 XX JP2001342149-A.
 XX 11-DEC-2001.
 XX 28-MAR-2001; 2001JP-00093243.
 XX 29-MAR-2000; 2000JP-00091144.
 XX (SANY) SANKYO CO LTD.
 XX WPI; 2002-145114/19.
 XX Drug for preventing or treating e.g. autoimmune disease or allergy,
 PT comprises humanized anti-Fas antibody.
 XX

PS Example 6 (preparatory); Page 26; 154pp; Japanese.
 XX The invention relates to a preventive or treating agent for diseases
 CC caused by abnormality in the Fas/Fas ligand system containing, as the
 CC active component, an antibody having a light chain subunit and a heavy
 CC chain subunit and an activity of combining specifically with mammalian
 CC Fas and an activity of inducing apoptosis in a cell expressing Fas. The
 CC agent has antiallergic, immunosuppressive and apoptotic activity and is
 CC used for preventing and treating autoimmune diseases, allergy, atopy and
 CC others. The present sequence is that of a peptide useful to the invention
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 79; DB 5; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSDVDGDSYNN 15
 |||||
 Db 1 KASQSDVDGDSYNN 15

RESULT 10
 ABB74863
 ID ABB74863 standard; peptide; 15 AA.
 XX
 AC ABB74863;
 XX

DT 26-APR-2002 (first entry)
 XX Humanised anti-Fas antibody related peptide SEQ ID NO 29.
 DE
 XX Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;
 KW light chain subunit; apoptosis; immunosuppressive; antiallergic;
 KW autoimmune disease; allergy; atopic.
 XX

OS Homo sapiens.
 XX JP2001342148-A.
 PN

PD 11-DEC-2001.
 XX 28-MAR-2001; 2001JP-00093106.
 PF
 XX 29-MAR-2000; 2000JP-00090918.
 PR

PA (SANY) SANKYO CO LTD.
 XX WPI; 2002-145113/19.
 DR
 XX Drug containing humanized anti-Fas antibody, used for preventing and
 PT treating autoimmune diseases, allergy, and atopy.
 PT

PS Example 6 (Preparatory); Page 26; 194pp; Japanese.
 XX The invention relates to a preventive or treating agent for diseases
 CC caused by abnormality in Fas/Fas ligand system containing as the active
 CC component an antibody having as the light chain subunit a polypeptide
 CC containing residues 1-218 of one of 3, 239 residue amino acid sequences,
 CC or residues 1-451 of one of 3, 470 residue amino acid sequences, all
 CC fully defined in the specification and having an activity of combining
 CC specifically with mammalian Fas and an activity of inducing apoptosis in
 CC a cell expressing Fas. The agent has immunosuppressive and antiallergic
 CC activity and is used for preventing and treating autoimmune diseases,
 CC allergy, atopy and others. The present sequence is that of a peptide,
 CC useful to the invention
 XX

SQ Sequence 15 AA;
 Query Match 100.0%; Score 79; DB 5; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSDVDGDSYNN 15
 |||||
 Db 1 KASQSDVDGDSYNN 15

RESULT 11
 AAR66143
 ID AAR66143 standard; peptide; 19 AA.
 XX
 AC AAR66143;
 XX

DT 12-JUL-1995 (first entry)
 XX CD-4 antibody variable region complementary peptide.
 DE
 XX CD-4 antibody variable region; complementary peptide;
 KW extra-corporeal blood circulation; cell filter material.
 KW

OS Synthetic.
 XX JP06269663-A.
 PN
 XX 27-SEP-1994.
 PD
 XX 17-MAR-1993; 93JP-00057206.
 PF
 XX 17-MAR-1993; 93JP-00057206.
 PR
 XX (TOYM) TOYOCO KK.
 PA
 XX WPI; 1994-346316/43.
 DR

XX Material for collecting cells positive for CD-4 antibody - comprises
 PT nonwoven fabric having keto-alkyl halide functional gp.
 PT
 PS Example 1; Page 6; 9pp; Japanese.
 XX

CC AAR66140-R66146 are peptides complementary to the variable region of the
 CC CD-4 antibody, these peptides are fixed onto a claimed nonwoven fabric
 CC (average fibre dia. of 1-30 microns) coated with keto-alkyl halide
 CC functional groups. This material can be used as a filter for CD-4
 CC positive cells in a medical treatment involving the extra-corporeal
 CC circulation of blood
 CC

SQ Sequence 19 AA;

Query Match 100.0%; Score 79; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 5.5e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSDVDGDSYNN 15
 |||||
 Db 5 KASQSDVDGDSYNN 19

RESULT 12
 AAY51140
 ID AAY51140 standard; protein; 103 AA.
 XX
 AC AAY51140;
 XX

DT 31-MAR-2000 (first entry)
 XX Murine derived protein fragment #2.
 DE
 XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
 KW HIV infection; autoimmune disease; murine.
 XX

OS Mus sp.
 XX WO9961629-A1.
 PN
 XX

PD 02-DEC-1999.
 XX 24-MAY-1999; 99WO-JP002711.
 XX 25-MAY-1998; 98JP-00159957.
 PR 26-MAY-1998; 98JP-00163023.
 XX (ASAH) ASahi KASEI KOGYO KK.
 PA (ASAH) ASahi MEDICAL CO LTD.
 XX Ono M, Soka T, Morimoto I, Miyamura K;
 XX WPI; 2000-086720/07.
 DR N-PSDB; AAZ44204.
 XX
 PT Devices containing antibodies recognising CD4 or CD34 and their use for
 PT the separation of CD4 or CD34 positive cells.
 XX
 PS Claim 22; Page 79; 11pp; Japanese.
 XX
 CC This invention describes a novel device (I) for separating cluster
 CC differentiation (CD)-positive cells using a recombinant (chimeric or
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful
 CC for the separation of CD4 or CD34 positive cells, which is useful for the
 CC collection of hematopoietic undifferentiated cells, elimination of
 CC lymphocytes from cells to be used in bone marrow transplantation, the
 CC detection of leukemic cells and the production of medicinal compositions
 CC for the treatment of HIV infection and autoimmune diseases. This sequence
 CC represents a murine derived protein fragment which is used to illustrate
 CC the method of the invention
 XX
 SQ Sequence 103 AA;
 Query Match 100.0%; Score 79; DB 3; Length 103;
 Best Local Similarity 100.0%; Pred. No. 3.6e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 KASQSVVDYDGD SYMN 15
 DB 16 KASQSVVDYDGD SYMN 30
 |||||
 RESULT 13
 AAY59263
 ID AAY59263 standard; protein; 103 AA.
 XX
 AC AAY59263;
 XX
 DT 17-APR-2000 (first entry)
 XX
 DE Antibody 4H5 L chain variable region.
 XX
 KW CD4 antigen; anti-human; antibody; 4H5; drug.
 XX
 OS Mus sp.
 XX
 PN JP11332563-A.
 XX
 PD 07-DEC-1999.
 XX
 PF 26-MAY-1998; 98JP-00163034.
 XX
 PR 26-MAY-1998; 98JP-00163034.
 XX
 PA (ASAH) ASahi KASEI KOGYO KK.
 XX
 DR WPI; 2000-091351/08.
 DR N-PSDB; AAZ58662.
 XX
 PT An antibody and the nucleic acid coding the antibody.
 XX
 PS Claim 5; Page 15-16; 25pp; Japanese.
 XX

CC The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. The present
 CC sequence represents the L chain variable region of the antibody 4H5
 XX
 SQ Sequence 103 AA;
 Query Match 100.0%; Score 79; DB 3; Length 103;
 Best Local Similarity 100.0%; Pred. No. 3.6e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 KASQSVVDYDGD SYMN 15
 DB 16 KASQSVVDYDGD SYMN 30
 |||||
 RESULT 14
 AAE37732
 ID AAE37732 standard; protein; 105 AA.
 XX
 AC AAE37732;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE MT413 modified VL protein.
 XX
 KW Chemokine; scFv; CD4 antibody; human immunodeficiency virus; HIV; RANTES;
 KW pharmaceutical; infection; acquired immune deficiency syndrome; AIDS;
 KW inflammatory; autoimmune disease; gene therapy; immunosuppressive;
 KW vaccine.
 XX
 OS Unidentified.
 XX
 PN WO2003054017-A2.
 XX
 PD 03-JUL-2003.
 XX
 PF 20-DEC-2002; 2002WO-EP014683.
 XX
 PR 21-DEC-2001; 2001EP-00130746.
 XX
 PA (MICR-) MICROMET AG.
 XX
 PI Mack M, Schloendorff D;
 XX
 DR WPI; 2003-559125/52.
 DR N-PSDB; AAD56804.
 XX
 PT New chemokine construct comprising scFv anti-CD4 and a RANTES chemokine,
 PT useful for the preparing a composition for treating HIV-infection or
 PT inflammatory or autoimmune diseases.
 XX
 PS Disclosure; Page 19; 109pp; English.
 XX
 CC The present invention relates to a chemokine construct comprising scFv
 CC anti-CD4 and a RANTES chemokine or their fragments. Sequences of the
 CC invention are useful for preparing a pharmaceutical composition for
 CC treating human immunodeficiency virus (HIV)-infection or acquired immune
 CC deficiency syndrome (AIDS) or inflammatory and/or autoimmune diseases.
 CC They are used as vaccines and in gene therapy. The present sequence is
 CC MT413 modified VL protein
 XX
 SQ Sequence 105 AA;
 Query Match 100.0%; Score 79; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 3.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 KASQSVVDYDGD SYMN 15
 DB 18 KASQSVVDYDGD SYMN 32
 |||||

```

RESULT 15
AAR33309
ID AAR33309 standard; protein; 106 AA.
XX
XX AC AAR33309;
XX
XX DT 25-MAR-2003 (revised)
XX DT 05-JUL-1993 (first entry)
XX DE MAE15 light chain.
XX
XX KW Antibody; high affinity; FCEH; low affinity; FCEL; IgE receptor;
XX KW histamine; mast cell; basophil; Kabat; CDR; murine; MAE11; MAE13; MAE15;
XX KW MAE17.
XX
XX OS Synthetic.
XX
XX PN WO9304173-A1.
XX
XX PD 04-MAR-1993.
XX
XX PF 14-AUG-1992; 92WO-US006860.
XX
XX PR 14-AUG-1991; 91US-00744768.
XX PR 07-MAY-1992; 92US-00879495.
XX
XX PA (GETH ) GENENTECH INC.
XX
XX PI Jardieu PM, Presta LG;
XX
XX DR WPI; 1993-094004/11.
XX
XX PT Polypeptide(s) binding to specific Fc epsilon receptors - act as IgE
XX PT antagonists; useful for treating and preventing IgE-mediated disorders
XX PT e.g. allergies.
XX
XX PS Disclosure; Fig 2; 113pp; English.
XX
XX CC Antibodies capable of binding FCEL-bound IgE but which are substantially
XX CC incapable of binding FCBH-bound IgE or inducing histamine release from
XX CC mast cells or basophils, comprise a human Kabat CDR domain into which has
XX CC been substituted a positionally analogous residue from a Kabat CDR domain
XX CC of the murine anti-huIgE antibodies MAE11, MAE13, MAE15 or MAE17.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 106 AA;
    Query Match 100.0%; Score 79; DB 2; Length 106;
    Best Local Similarity 100.0%; Pred. No. 3.7e-05;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSDVDYDGSYMN 15
Db |||||
24 KASQSDVDYDGSYMN 38

RESULT 16
AAV85197
ID AAV85197 standard; protein; 106 AA.
XX
XX AC AAV85197;
XX
XX DT 29-JUN-2000 (first entry)
XX
XX DE Light chain amino acid sequence of mouse antibody MAE15.
XX
XX KW Immunoglobulin E; IgE; anti-human IgE; bispecific antibody; FCEL; FCEH;
XX KW low affinity binding receptor; high affinity binding receptor; allergy;
XX KW diagnosis; treatment; histamine release; prevent; light chain.
XX
XX OS Mus sp.
XX
XX PN US6037453-A.

```

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XX PD 14-MAR-2000.
XX
XX PF 06-JUN-1995; 95US-00466151.
XX
XX PR 14-AUG-1992; 92WO-US006860.
XX PR 26-JAN-1994; 94US-00185899.
XX PR 15-MAR-1995; 95US-00405617.
XX
XX PA (GETH ) GENENTECH INC.
XX
XX PI Presta LG, Jardieu PM;
XX
XX DR WPI; 2000-269913/23.
XX
XX PT New bispecific antibodies, useful for treating immunoglobulin E-mediated
XX PT disease, binds to IgE, but only when on the low affinity receptor, and to
XX PT an antigen other than IgE.
XX
XX PS Claim 1; Fig 2; 48pp; English.
XX
XX CC This sequence represents the light chain amino acid sequence of a mouse
XX CC anti-human immunoglobulin E (IgE) antibody. The invention relates to a
XX CC bispecific antibody that binds specifically to IgE when IgE is bound to
XX CC its low affinity receptor (FCEL), but does not bind to IgE, when IgE is
XX CC bound to its high affinity receptor (FCBH). The bispecific antibody
XX CC comprises an IgE-binding arm with human framework residues of a recipient
XX CC human antibody and donor murine CDR (complementarity determining region)
XX CC murine residue. The antibody also comprises an Fv that is specific for a
XX CC predetermined antigen other than IgE. The antibodies work by displacing
XX CC bound IgE from its receptor, or via competitive inhibition of its
XX CC binding. The bispecific antibodies are used for diagnosis, treatment and
XX CC prevention of allergy and other IgE-mediated diseases, also, when
XX CC immobilised, for the isolation of FCEL from cells (for research or
XX CC therapy). The bispecific antibodies of the invention do not cause
XX CC granulation or release of histamine from mast cells
XX
XX SQ Sequence 106 AA;
    Query Match 100.0%; Score 79; DB 3; Length 106;
    Best Local Similarity 100.0%; Pred. No. 3.7e-05;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSDVDYDGSYMN 15
Db |||||
24 KASQSDVDYDGSYMN 38

RESULT 17
AAP90541
ID AAP90541 standard; protein; 111 AA.
XX
XX AC AAP90541;
XX
XX DT 24-OCT-2003 (revised)
XX DT 27-AUG-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 20-OCT-1989 (first entry)
XX
XX DE Immunoglobulin L chain variable region.
XX
XX KW Immunoglobulin; L chain variable region; HIV.
XX
XX OS Mus musculus.
XX
XX PN EP327000-A.
XX
XX PD 09-AUG-1989.
XX
XX PF 30-JAN-1989; 89EP-00101583.
XX
XX PR 30-JAN-1988; 88JP-00020255.

```


PR 08-JUL-1988; 88JP-00171385.
 XX (KAGA) CHEMO SERO THERAPEUTIC RES INS.
 PA
 PI Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Matsushita S, Hattori T;
 PI Takatsuki K;
 XX
 XX WPI; 1989-229050/32.
 DR N-PSDB; AAN90491, AAN90492, AAN90493.
 XX
 PT Chimeric anti-human immune virus antibodies - contg. mouse variable
 PT regions and human constant regions for diagnosis, treatment and
 PT prevention of AIDS.
 XX
 PS Claim 5; Page 15; 33pp; English.
 XX
 CC The sequence is an L chain variable region from an immunoglobulin with
 CC anti-HIV neutralising activity. See AAN90491-3, and AAN90495. (Updated on
 CC 25-MAR-2003 to correct PA field.) (Updated on 27-AUG-2003 to correct OS
 CC field.) (Updated on 24-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 111 AA;
 Query Match 100.0%; Score 79; DB 1; Length 111;
 Best Local Similarity 100.0%; Pred. No. 3.9e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KASQSVVDYDGSYMN 15
 DB 24 KASQSVVDYDGSYMN 38
 |||||
 RESULT 18
 AAR33305
 ID AAR33305 standard; protein; 111 AA.
 XX
 AC AAR33305;
 DT
 XX 25-MAR-2003 (revised)
 DT 05-JUL-1993 (first entry)
 XX
 DE MaE11 light chain.
 XX
 KW Antibody; high affinity; FCEH; low affinity; FCEL; IgE receptor;
 KW histamine; mast cell; basophil; Kabat; CDR; murine; MAE11; MAE13; MAE15;
 KW MAE17.
 XX
 OS Synthetic.
 XX
 PN WO9304173-A1.
 XX
 PD 04-MAR-1993.
 XX
 PP 14-AUG-1992; 92NO-US006860.
 XX
 PR 14-AUG-1991; 91US-00744768.
 PR 07-MAY-1992; 92US-00879495.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Jardieu PM, Presta LG;
 PI
 XX WPI; 1993-094004/11.
 DR
 XX Polypeptide(s) binding to specific Fc epsilon receptors - act as IgE
 PT antagonists; useful for treating and preventing IgE-mediated disorders
 PT e.g. allergies.
 PT
 XX Disclosure; Fig 2; 113pp; English.
 PS
 CC Antibodies capable of binding FCEL-bound IgE but which are substantially
 CC incapable of binding FCEH-bound IgE or inducing histamine release from
 CC mast cells or basophils, comprise a human Kabat CDR domain into which has

CC been substituted a positionally analogous residue from a Kabat CDR domain
 CC of the murine anti-huIGE antibodies MAE11, MAE13, MAE15 or MAE17.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 111 AA;
 Query Match 100.0%; Score 79; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 3.9e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KASQSVVDYDGSYMN 15
 DB 24 KASQSVVDYDGSYMN 38
 |||||
 RESULT 19
 AAR55123
 ID AAR55123 standard; protein; 111 AA.
 XX
 AC AAR55123;
 DT
 XX 27-JAN-1995 (first entry)
 DT
 XX Mouse anti-HIV mu5.5 light chain variable region.
 DE
 XX Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;
 KW human immunodeficiency virus; variable region; VH chain; murine.
 KW
 XX Mus musculus.
 OS
 XX
 FH Key
 FT Region
 FT /label= FR1
 FT Region
 FT /label= CDR1
 FT Region
 FT /label= FR2
 FT Region
 FT /label= CDR2
 FT Region
 FT /label= FR3
 FT Region
 FT /label= CDR3
 FT Region
 FT /label= FR4
 XX
 PN JP06125783-A.
 XX
 XX 10-MAY-1994.
 PD
 XX 28-DEC-1991; 91JP-00359808.
 PP
 XX 28-DEC-1991; 91JP-00359808.
 PR
 XX (KAGA-) ZH KAGAKU KESSEI-RYOHO KENKYUSHO.
 PA
 XX WPI; 1994-187942/23.
 XX N-PSDB; AAQ65554.
 DR
 XX Mouse-human chimeric anti-HIV antibody heavy and light chains - and
 PT recombinant antibody consisting of the H- and L-chains, useful in AIDS
 PT therapy.
 PT
 XX Example 3; Fig 4; 22pp; Japanese.
 PS
 CC Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV. The
 CC heavy and light chain variable regions from these antibodies were
 CC sequenced (AAR55120-R55123). The murine anti-HIV CDRs were introduced
 CC into human framework regions to construct chimeric antibodies (AAR55124-
 CC R55127)
 XX
 SQ Sequence 111 AA;

```
Query Match      100.0%; Score 79; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KASQSVDDYDGDYSYN 15
Db      24 KASQSVDDYDGDYSYN 38

RESULT 20
ID AAR55127 standard; protein; 111 AA.
XX AAR55127;
XX
DT 16-OCT-2003 (revised)
DT 30-JAN-1995 (first entry)
XX
DE Mouse-human chimeric anti-HIV mu5.5-derived light chain V region.
XX
KW Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;
KW human immunodeficiency virus; variable region; VL chain; murine;
KW chimeric; humanised.
XX
OS Mus musculus.
OS Homo sapiens.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT 1..23
FT /label= FR1
FT /note= "human"
FT Region
FT 24..38
FT /label= CDR1
FT /note= "murine"
FT Region
FT 39..53
FT /label= FR2
FT Region
FT 54..60
FT /label= CDR2
FT /note= "murine"
FT Region
FT 61..92
FT /label= FR3
FT /note= "human"
FT Region
FT 93..101
FT /label= CDR3
FT /note= "murine"
FT Region
FT 102..111
FT /label= FR4
FT /note= "human"
XX
PN JP06125783-A.
XX
XX 10-MAY-1994.
XX
XX 28-DEC-1991; 91JP-00359808.
XX
XX 28-DEC-1991; 91JP-00359808.
XX
XX (KAGA-) ZH KAGAKU KESSEI-RYOHO KENKYUSHO.
XX
XX WPI; 1994-187942/23.
XX N-PSDB; AAQ65558.
XX
XX Mouse-human chimeric anti-HIV antibody heavy and light chains - and
XX recombinant antibody consisting of the H- and L-chains, useful in AIDS
XX therapy.
XX
XX Claim 5; Fig 12; 22pp; Japanese.
XX
CC Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV. The
CC heavy and light chain variable regions from these antibodies were
CC sequenced (AAR55120-R55123). The murine anti-HIV CDRs were introduced
CC into human framework regions to construct chimeric antibodies (AAR55124-
```

```
CC R55127). (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 111 AA;

Query Match      100.0%; Score 79; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KASQSVDDYDGDYSYN 15
Db      24 KASQSVDDYDGDYSYN 38

RESULT 21
ID AAR60302 standard; protein; 111 AA.
XX AAR60302;
XX AAR60302;
XX
DT 25-MAR-2003 (revised)
DT 09-MAR-1995 (first entry)
XX
DE Anti HIV antibody light chain variable region.
XX
KW Antibody; heavy chain; light chain; human immunodeficiency virus; HIV;
KW acquired immune deficiency syndrome; AIDS: treatment; prophylaxis;
KW Mus musculus; Homo sapiens.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT 1..23
FT /label= Framework region 1.
FT Region
FT 24..38
FT /label= CDR1.
FT Region
FT 39..53
FT /label= Framework region 2.
FT Region
FT 54..60
FT /label= CDR2.
FT Region
FT 61..92
FT /label= Framework region 3.
FT Region
FT 93..101
FT /label= CDR3.
FT Region
FT 102..111
FT /label= Framework region 4.
XX
PN WO9415969-A1.
XX
XX 21-JUL-1994.
XX
XX 14-JAN-1993; 93WO-JP000039.
XX
XX 14-JAN-1993; 93WO-JP000039.
XX
XX (KAGA ) CHEMA SERO THERAPEUTIC RES INST.
XX
XX Maeda H, Kimachi K, Eda Y, Shiosaki K, Osatomi K, Tokiyoshi S;
XX WPI; 1994-249145/30.
XX N-PSDB; AAQ70372.
XX
XX Recombinant chimeric anti HIV antibody - useful for the treatment and
XX prevention of HIV.
XX
XX Claim 15; Fig 4; 51pp; Japanese.
XX
XX The recombinant antibody light chain has neutralising activity against
XX HIV. Chimeric antibodies comprising both mouse and human sequences are
XX useful in the treatment/prevention of AIDS caused by HIV. (Updated on 25-
XX MAR-2003 to correct PN field.)
XX
XX Sequence 111 AA;
```

Query Match 100.0%; Score 79; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 3.9e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDDYDGD SYMN 15
 DB 24 KASQSVDDYDGD SYMN 38

RESULT 22
 AAR60306
 ID AAR60306 standard; protein; 111 AA.
 XX
 AC AAR60306;
 XX
 DT 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 13-MAR-1995 (first entry)
 XX
 DE Chimeric anti HIV antibody light chain variable region.
 XX
 KW Antibody; heavy chain; light chain; human immunodeficiency virus; HIV;
 KW acquired immune deficiency syndrome; AIDS: treatment; prophylaxis;
 KW Mus musculus; Homo sapiens.
 XX
 OS Homo sapiens.
 OS Mus musculus.
 OS Chimeric.
 XX
 FH Key
 FT Region
 FT 1. .23
 FT /label= Framework region 1.
 FT Region
 FT 24. .38
 FT /label= CDR1.
 FT /note= "Mouse derived amino acid sequence."
 FT Region
 FT 39. .53
 FT /label= Framework region 2.
 FT Region
 FT 54. .60
 FT /label= CDR2.
 FT /note= "Mouse derived amino acid sequence."
 FT Region
 FT 61. .92
 FT /label= Framework region 3.
 FT Region
 FT 93. .101
 FT /label= CDR3.
 FT /note= "Mouse derived amino acid sequence."
 FT Region
 FT 102. .111
 FT /label= Framework region 4.
 XX
 PN W09415969-A1.
 XX
 XX 21-JUL-1994.
 XX
 XX 14-JAN-1993; 93WO-JP0000039.
 XX
 XX 14-JAN-1993; 93WO-JP0000039.
 XX
 XX (KAGA) CHERO SERO THERAPEUTIC RES INST.
 XX
 XX Maeda H, Kimachi K, Eda Y, Shiosaki K, Osatomi K, Tokiyoshi S;
 XX WPI; 1994-249145/30.
 XX N-PSDB; AAR60306.
 XX
 XX Recombinant chimeric anti HIV antibody - useful for the treatment and
 XX prevention of HIV.
 XX
 XX Claim 14; Fig 12; 51pp; Japanese.
 XX
 CC The recombinant antibody light chain has neutralising activity against
 CC HIV. Chimeric antibodies comprising both mouse and human sequences are
 CC useful in the treatment/prevention of AIDS caused by HIV. (Updated on 25-
 CC MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise OS
 CC field)

XX Sequence 111 AA;
 SQ Query Match 100.0%; Score 79; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 3.9e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDDYDGD SYMN 15
 DB 24 KASQSVDDYDGD SYMN 38

RESULT 23
 AAY23781
 ID AAY23781 standard; protein; 111 AA.
 XX
 AC AAY23781;
 XX
 DT 13-SEP-1999 (first entry)
 XX
 DE Light chain variable region of Ig REI.
 XX
 KW Light chain variable region; interleukin-4; IL-4; antibody 3B9;
 KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
 KW Immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy;
 KW Ig REI.
 XX
 OS Synthetic.
 XX
 PN US5928904-A.
 XX
 PD 27-JUL-1999.
 XX
 PF 07-JUN-1995; 95US-00483632.
 XX
 PR 07-SEP-1993; 93US-00117366.
 PR 14-OCT-1993; 93US-00136783.
 PR 07-SEP-1994; 94WO-US010308.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Holmes SD, Sylvestre DR, Gross MS;
 XX
 XX WPI; 1999-429500/36.
 XX N-PSDB; AAX85937.
 XX
 PT New DNA molecules encoding recombinant antibodies useful for treating IL4
 PT -mediated conditions.
 XX
 XX Disclosure; Col 69-70; 50pp; English.
 XX
 CC The specification describes chimeric and humanised IL-4 monoclonal
 CC antibodies. The antibodies of the invention are used in therapeutic and
 CC pharmaceutical compositions for treating IL-4 mediated and immunoglobulin
 CC E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis,
 CC atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid
 CC arthritis, host-versus-graft disease and renal disease. They are also
 CC useful in the diagnosis of an allergy or condition associated with excess
 CC IL-4 production through the measurement e.g. by ELISA of circulating
 CC endogenous IL-4 levels in humans. The present sequence represents the
 CC light chain variable region of Ig REI, and is used in the course of the
 CC invention
 XX
 SQ Sequence 111 AA;
 XX
 XX Query Match 100.0%; Score 79; DB 2; Length 111;
 XX Best Local Similarity 100.0%; Pred. No. 3.9e-05;
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDDYDGD SYMN 15

```

Db      24 KASQSDVDYDGDSDYMN 38
|||||
RESULT 24
AAW95650
ID AAW95650 standard; protein; 111 AA.
XX
AC AAW95650;
XX
DT 08-JUN-1999 (first entry)
XX
DE Mus musculus anti-IgE MaE11 variable light chain.
XX
KW Variable light chain; IgE; antibody; anti-IgE; reduction; prevention;
KW histamine; production; hypersensitivity; allergen; anaphylaxis;
KW atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;
KW eczema; anaphylactic shock; urticaria.
XX
OS Mus musculus.
XX
PN WO9901556-A2.
XX
PD 14-JAN-1999.
XX
PF 30-JUN-1998; 98WO-US013410.
XX
PR 02-JUL-1997; 97US-00887352.
XX
PA (GETH ) GENENTECH INC.
XX
PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX
DR WPI; 1999-106057/09.
XX
PT Improving affinity of polypeptides, particularly anti-IgE antibodies - by
PT identifying aspartyl residues which undergo isomerisation and
PT substituting alternative residues and screening for affinity against the
PT target.
XX
PS Disclosure; Page 87-88; 129pp; English.
XX
PX
CC The sequence is that of the variable light chain of MaE11. It was used as
CC part of a method to improve the affinity of anti-IgE antibodies such as
CC e26 and e27. The e26 and e27 antibodies can be used for reducing or
CC preventing IgE mediated production of histamine in a mammal. They can be
CC used for treating a disorder mediated by IgE such as hypersensitivity,
CC atopic allergy, asthma, allergic rhinitis, conjunctivitis, hay fever,
CC eczema, anaphylactic shock and urticaria. The antibodies can also be used
CC for affinity purification, detection and diagnosis
XX
SQ Sequence 111 AA;

Query Match      100.0%; Score 79; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.9e-05; Mismatches 0; Gaps 0;
Matches 15; Conservative 0; Indels 0;

QY      1 KASQSDVDYDGDSDYMN 15
Db      24 KASQSDVDYDGDSDYMN 38
|||||
RESULT 25
AAW18123
ID AAW18123 standard; protein; 111 AA.
XX
AC AAW18123;
XX
DT 11-AUG-1999 (first entry)
XX
DE Light chain sequence for humanised 3B9 antibody.
XX
KW Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;
allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
autoimmune disease; graft versus host disease.
Synthetic.
US5914110-A.
22-JUN-1999.
07-JUN-1995; 95US-00483636.
07-SEP-1993; 93US-00117366.
14-OCT-1993; 93US-00136783.
07-SEP-1994; 94WO-US010308.
(SMIK ) SMITHKLINE BEECHAM PLC.
(SMIK ) SMITHKLINE BEECHAM CORP.
Sylvester DR, Holmes SD, Gross MS;
WPI; 1999-370482/31.
N-PSDB; AAX79531.
Recombinant IL4 antibodies useful for treatment of allergic rhinitis,
atopic asthma and anaphylactic shock.
Example 3; Col 69-70; 50pp; English.
This sequence represents the light chain of the humanised 3B9 antibody of
the invention. The antibody is a chimeric or humanised interleukin-4
(IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE)
mediated diseases. The antibodies are useful for the treatment of
allergic disorders such as allergic rhinitis, conjunctivitis, atopic
dermatitis, atopic asthma and anaphylactic shock. The antibodies are also
useful for regulating B and T cell proliferation and as such are useful
in the treatment of autoimmune diseases and graft versus host disease
Sequence 111 AA;

Query Match      100.0%; Score 79; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.9e-05; Mismatches 0; Gaps 0;
Matches 15; Conservative 0; Indels 0;

QY      1 KASQSDVDYDGDSDYMN 15
Db      24 KASQSDVDYDGDSDYMN 38
|||||
RESULT 26
AAW85193
ID AAW85193 standard; protein; 111 AA.
XX
AC AAW85193;
XX
DT 29-JUN-2000 (first entry)
XX
DE Light chain amino acid sequence of mouse antibody MaE11.
XX
KW Immunoglobulin E; IgE; anti-human IgE; bispecific antibody; FcEL; FCEH;
KW low affinity binding receptor; high affinity binding receptor; allergy;
KW diagnosis; treatment; histamine release; prevent; light chain.
XX
OS Mus sp.
XX
PN US6037453-A.
XX
PD 14-MAR-2000.
XX
PF 06-JUN-1995; 95US-00466151.
XX
PR 14-AUG-1992; 92WO-US006860.
PR 26-JAN-1994; 94US-00185899.

```


CC for the treatment of HIV infection and autoimmune diseases. This sequence
CC represents a murine derived protein fragment which is used to illustrate
CC the method of the invention

XX SQ Sequence 111 AA;

Query Match 100.0%; Score 79; DB 3; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDDYDGD SYMN 15
|||||
Db 24 KASQSVDDYDGD SYMN 38

RESULT 29
AAV59267
ID AAV59267 standard; protein; 111 AA.

XX AC AAV59267;

XX DT 17-APR-2000 (first entry)

XX DE Antibody 4H5 L chain fragment.

XX KW CD4 antigen; anti-human; antibody; 4H5; drug.

XX OS Mus sp.

XX PN JP11332563-A.

XX PD 07-DEC-1999.

XX PF 26-MAY-1998; 98JP-00163034.

XX PR 26-MAY-1998; 98JP-00163034.

XX PA (ASAH) ASAMI KASEI KOGYO KK.

XX DR WPI; 2000-091351/08.

XX DR N-PSDB; AAZ58690.

XX PT An antibody and the nucleic acid coding the antibody.

XX PS Disclosure; Page 22-23; 25pp; Japanese.

XX CC The invention provides an antibody having affinity to CD4 antigen. The
CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
CC application for drugs. It is highly safe in human dose. The present
CC sequence represents a L chain fragment of the antibody 4H5

XX SQ Sequence 111 AA;

Query Match 100.0%; Score 79; DB 3; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDDYDGD SYMN 15
|||||
Db 24 KASQSVDDYDGD SYMN 38

RESULT 30
AAB76939
ID AAB76939 standard; protein; 111 AA.

XX AC AAB76939;

XX DT 17-APR-2001 (first entry)

XX DE Variable light chain sequence of MaE11 SEQ ID 5.

XX KW Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;

KW antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
KW conjunctivitis; eczema; urticaria; food allergy.

XX OS Synthetic.

XX PN US6172213-B1.

XX PD 09-JAN-2001.

XX PF 30-JUN-1998; 98US-00109207.

XX PR 02-JUL-1997; 97US-0051554P.

XX PA (GETH) GENENTECH INC.

XX PI Lowman HB, Presta LG, Jardieu PM, Lowe J;

XX DR WPI; 2001-122353/13.

XX CC New nucleic acid encoding anti-immunoglobulin E antibody with improved
PT properties, produced by substituting aspartyl residues in unimproved
PT immunoglobulin E prone to isomerization by other residues by affinity
PT maturation with phage display.

XX PS Example 2; Fig 1; 87pp; English.

XX CC This invention relates to a nucleotide sequence encoding an antibody with
CC improved anti-IgE antibody activity. The antibody has improved action due
CC to a process comprising, a) identifying aspartyl residues prone to
CC isomerisation in unimproved anti-IgE (immunoglobulin E) antibody; b)
CC substituting alternative residues to create candidate molecules; and c)
CC selecting those candidate molecules which display affinity against the
CC target molecule. Use of the antibody results in antiasthmatic;
CC antiallergic; ophthalmological; dermatological and antiinflammatory
CC activity. The antibodies are useful for treating IgE-mediated disorders
CC such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and
CC nucleic acids may also be used as affinity purification agents and in
CC diagnostic assays for detecting the expression of an antigen of interest
CC in specific cell, tissues or serum. Amino acid sequences AAB76936-
CC AAB76960 represent fragments of anti-IgE antibodies of the invention.
CC Polynucleotide sequence AAF69253 represents an expression plasmid used in
CC the course of the invention, and oligonucleotides AAF69254 - AAF69271 are
XX used in the generation of affinity improved anti-IgE antibodies

XX SQ Sequence 111 AA;

Query Match 100.0%; Score 79; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDDYDGD SYMN 15
|||||
Db 24 KASQSVDDYDGD SYMN 38

RESULT 31
ADN07026
ID ADN07026 standard; protein; 111 AA.

XX AC ADN07026;

XX DT 01-JUL-2004 (first entry)

XX DE Murine anti-human IgE mAb MaE11 variable light chain domain (VL) .

XX KW Anti-IgE antibody; immunosuppressive agent; IgE-mediated disorder;
KW therapy; atopic allergy; anaphylactic hypersensitivity; asthma;
KW allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy;
KW murine; MaE11; variable light chain domain; VL.

XX OS Mus musculus.

PN US6723833-B1.
 XX
 PD 20-APR-2004.
 XX
 PF 17-NOV-2000; 2000US-00716028.
 XX
 PR 02-JUL-1997; 97US-0051554P.
 PR 30-JUN-1998; 98US-00109207.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
 XX
 DR WPI; 2004-326922/30.
 XX
 PT New composition of an improved anti-IgE antibody or IgE binding fragment,
 PT useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma,
 PT conjunctivitis, eczema, urticaria or food allergies.
 XX
 PS Example 2; SEQ ID NO 5; 89pp; English.
 XX
 CC The invention relates to therapeutic compositions comprising anti-IgE
 CC antibody or IgE binding fragment in combination with an adjunct
 CC immunosuppressive agent. The composition is useful for treating IgE-
 CC mediated disorders. The disorders include atopic allergy associated with
 CC anaphylactic hypersensitivity and asthma, allergic rhinitis and
 CC conjunctivitis, eczema, urticaria and food allergies. The present
 CC sequence is murine anti-human IgE mAb MaE11 variable light chain domain
 CC (VL).
 XX
 SQ Sequence 111 AA;
 Query Match 100.0%; Score 79; DB 8; Length 111;
 Best Local Similarity 100.0%; Pred. No. 3.9e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KASQSVYDGD SYMN 15
 Db 24 KASQSVYDGD SYMN 38
 |||||
 RESULT 32
 ID ADW00648
 AC ADW00648 standard; protein; 111 AA.
 AC ADW00648;
 DT 10-MAR-2005 (first entry)
 XX
 DE Murine MaE11 light chain variable region protein.
 XX
 KW Chemotherapy; IgE-mediated disorder; asthma; allergic rhinitis; eczema;
 KW urticaria; food allergy; hypersensitivity; anaphylactic hypersensitivity;
 KW antiasthmatic; antiallergic; dermatological; antibacterial;
 KW immune disorder; inflammation; ear disease; nose disease; throat disease;
 KW respiratory disease; antiinflammatory; dermatological disease;
 KW immunosuppressive; antibody.
 XX
 OS Mus musculus.
 XX
 PN US2004259077-A1.
 PD 23-DEC-2004.
 XX
 PF 02-MAR-2004; 2004US-00791619.
 XX
 PR 02-JUL-1997; 97US-0051554P.
 PR 30-JUN-1998; 98US-00109207.
 PR 17-NOV-2000; 2000US-00716028.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
 WPI; 2005-038757/04.
 Treating an IgE-mediated disorder, e.g. asthma, allergic rhinitis,
 eczema, urticaria, food allergies, or hypersensitivity, by administering
 an anti-IgE antibody or its antigen-binding fragment.
 Example 2; SEQ ID NO 5; 92pp; English.
 The present invention relates to a method for treating an IgE-mediated
 disorder. The method involves administering a therapeutical amount of an
 anti-IgE antibody or its IgE binding fragment. The invention is useful
 for treating an IgE-mediated disorder e.g. asthma, allergic rhinitis,
 eczema, urticaria, food allergies and hypersensitivity e.g. anaphylactic
 hypersensitivity. The present sequence is the murine MaE11 light chain
 variable region protein.
 Sequence 111 AA;
 Query Match 100.0%; Score 79; DB 9; Length 111;
 Best Local Similarity 100.0%; Pred. No. 3.9e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KASQSVYDGD SYMN 15
 Db 24 KASQSVYDGD SYMN 38
 |||||
 RESULT 33
 ID ADY85020
 AC ADY85020 standard; protein; 111 AA.
 AC ADY85020;
 DT 16-JUN-2005 (first entry)
 XX
 DE Human HMGB1 A box.
 XX
 KW High mobility group box; HMGB1; monoclonal antibody; antibody therapy;
 KW sepsis; antibacterial immunosuppressive; graft rejection; arthritis;
 KW antiarthritic; asthma; antiasthmatic; lupus erythematosus;
 KW antiinflammatory; inflammation; dermatological;
 KW respiratory distress syndrome; respiratory-gen.; psoriasis;
 KW antipsoriatic; chronic obstructive pulmonary disease; pancreatitis;
 KW peritonitis; burns; vulnary; ischemia; vasotropic; Behcets disease;
 KW graft versus host disease; inflammatory bowel disease;
 KW gastrointestinal-gen.; multiple sclerosis neuroprotective; cachexia;
 KW anabolic; infection; musculoskeletal disease; immune disorder.
 XX
 OS Homo sapiens.
 OS Mus sp.
 OS Rattus sp.
 PN WO2005026209-A2.
 XX
 PD 24-MAR-2005.
 XX
 PF 10-SEP-2004; 2004WO-US029527.
 XX
 PR 11-SEP-2003; 2003US-0502568P.
 XX
 PA (CRIT-) CRITICAL THERAPEUTICS INC.
 XX
 PI Newman W, Qin S, Okeefe T, Obar R;
 XX
 DR WPI; 2005-233483/24.
 XX
 PT New antibody or its antigen-binding fragment specific to a vertebrate
 PT high mobility group box (HMGB) A box that inhibits release of a
 PT proinflammatory cytokine from a cell treated with HMGB protein, useful
 PT for treating, e.g. sepsis.
 XX
 PS Disclosure; SEQ ID NO 2; 123pp; English.

XX The invention provides antibodies, or their antigen-binding fragments,
 CC that bind to a vertebrate high mobility group box (HMGB) polypeptide, to
 CC methods of detecting and/or identifying an agent that binds to an HMGB
 CC polypeptide, methods of treating a condition in a subject characterized
 CC by activation of an inflammatory cytokine cascade, and methods of
 CC detecting an HMGB polypeptide in a sample. The antibody (or antigen-
 CC binding fragment) binds to a vertebrate HMGB A box but does not
 CC specifically bind to non-A box epitopes of HMGB, and inhibits release of
 CC a proinflammatory cytokine from a vertebrate cell treated with an HMGB
 CC protein. A method of treating a condition characterized by activation of
 CC an inflammatory cytokine cascade comprises administering an antibody of
 CC the invention, or its antigen-binding fragment. The condition is selected
 CC from sepsis, allograft rejection, arthritis, asthma, lupus, adult
 CC respiratory distress syndrome, chronic obstructive pulmonary disease,
 CC psoriasis, pancreatitis, peritonitis, burns, ischemia, Behcet's disease,
 CC graft versus host disease, inflammatory bowel disease, multiple sclerosis
 CC and cachexia, especially sepsis, arthritis, or lupus. The present
 CC sequence is that of the A box of human HMGB1 ADY85012. An identical
 CC sequence is also found in rat and mouse HMGB1.
 XX
 SQ Sequence 111 AA;

Query Match 100.0%; Score 79; DB 9; Length 111;
 Best Local Similarity 100.0%; Pred. No. 3.9e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 15; Conservative 0;

QY 1 KASQSVYDGDSDYNN 15
 |||||
 Db 24 KASQSVYDGDSDYNN 38

RESULT 34
 AAR24575
 ID AAR24575 standard; protein; 112 AA.

AC AAR24575;

XX 08-DEC-1992 (first entry)

DE Human x mouse modified anti-HIV antibody Light chain RL0.5beta.

KW Heavy; light; CDR; HIV; AIDS; REI; 0.5beta.

XX Synthetic.

| Key | Location/Qualifiers |
|-----------|---------------------|
| FT Region | 1..23 |
| FT | /label= FR1 |
| FT Region | 24..38 |
| FT | /label= CDR1 |
| FT Region | 39..53 |
| FT | /label= FR2 |
| FT Region | 54..60 |
| FT | /label= CDR2 |
| FT Region | 61..92 |
| FT | /label= FR3 |
| FT Region | 93..101 |
| FT | /label= CDR3 |
| FT Region | 102..112 |
| FT | /label= FR4 |

XX JP04141095-A.

PN 14-MAY-1992.

PD 02-OCT-1990; 90JP-00266091.

PF 02-OCT-1990; 90JP-00266091.

PR (KAGA) KAGAKU OYOBI KESSEI RYOHO.

XX WPI; 1992-212765/26.

XX New recombinant modified anti-HIV antibodies - comprise human x mouse
 PT modified antibody H and L chains.
 XX
 PS Disclosure; Fig 2; 15pp; Japanese.

CC The framework regions (FR) are derived from the human antibody REI. The
 CC CDRs are mouse monoclonal antibody 0.5beta derived sequences. The anti-
 CC HIV modified antibody can be used for the prophylaxis and treatment of
 CC AIDS. Specific examples of the H chain are given in AAR24556-58 and
 CC AAR24560-62. A specific example of the L chain is given in AAR24575
 XX
 SQ Sequence 112 AA;

Query Match 100.0%; Score 79; DB 2; Length 112;
 Best Local Similarity 100.0%; Pred. No. 4e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDYNN 15
 |||||
 Db 24 KASQSVYDGDSDYNN 38

RESULT 35
 AEB21888
 ID AEB21888 standard; protein; 112 AA.

AC AEB21888;

XX 08-SEP-2005 (first entry)

DE Human DC-SIGN antibody, light chain, SEQ ID NO:44.

KW antibody; DC-SIGN; dendritic cell-specific ICAM-3 grabbing non-integrin;
 KW cancer; neoplasm; cytostatic; inflammation; antiinflammatory;
 KW ectoparasite infection; antiparasitic; infection; viral infection;
 KW bacterial infection; antibacterial; virucide; autoimmune disease;
 KW immunosuppressive; immune disorder; allergy; antiallergic; immunotherapy;
 KW transplant rejection; humanized antibody; single chain antibody;
 KW light chain.

XX Homo sapiens.

XX WO2005058244-A2.

XX 30-JUN-2005.

XX 15-DEC-2004; 2004WO-US041788.

XX 15-DEC-2003; 2003US-0529517P.

XX (ALEX-) ALEXION PHARM INC.

XX Bowdish KS, Kretz-Rommel A;

XX WPI; 2005-506067/51.

XX Novel antibody capable of binding or recognizing human dendritic cell-
 PT specific intercellular adhesion molecule-3 grabbing non-integrin receptor
 on cell, useful for treating cancer, and viral and bacterial infections.

PS Example 5; SEQ ID NO 44; 44pp; English.

CC The invention relates to an antibody (I) capable of binding human
 CC Dendritic cell-specific intercellular adhesion molecule (ICAM)-3 grabbing
 CC non-integrin (DC-SIGN) or recognizing a DC-SIGN receptor on a cell,
 CC comprising an amino acid sequence having at least 80% homology to any one
 CC of 18 fully defined 4-10 amino acid sequences (AEB21889 to AEB21906). An
 CC antibody (I) capable of binding human DC-SIGN or recognizing a DC-SIGN
 CC receptor on a cell, is chosen from : an antibody (A1) capable of binding
 CC human DC-SIGN or recognizing a DC-SIGN receptor on a cell; and an
 CC antibody (A4) capable of recognizing a DC-SIGN receptor on a cell. A4
 CC effectively blocks binding of a virus to the cell, blocks infection of

the cell by a virus, and/or blocks transmission of a virus from the cell to another cell, where the virus is chosen from HIV, hepatitis C virus (HCV), Ebola, severe acute respiratory syndrome (SARS), cytomegalovirus (CMV), Sindbis and Dengue; or effectively blocks binding of a bacteria or parasite to the cell, blocks infection of the cell by a bacteria or parasite, and/or blocks transmission of a bacteria or parasite from the cell to another cell, where the bacteria is chosen from Helicobacter pylori, Klebsiella pneumoniae, Mycobacterium tuberculosis and M. bovis, and the parasite is chosen from Leishmania pifanoi and Schistosoma mansoni. Also described are: a vaccine comprising A1; a composition comprising A1 and a carrier; a diagnostic agent (I1) for a tumor characterized by increased DC-SIGN expression, comprising (I1); a diagnostic kit comprising (I1); a therapeutic agent for treating a cancer characterized by increased DC-SIGN expression, comprising A1; treating (M1) a cancer, involves administering to a subject, a cancer cell killing amount of a composition comprising A1; and treating (M2) an inflammatory disease, which involves administering to a subject, a dendritic cell killing amount of a composition comprising A1. A1 further comprises a peptide attached to it. The peptide comprises an antigen, where the antigen comprises a cancer antigen. A1 is humanized antibody or an scFv. The amino acid sequence appears in the heavy chain CDR3 of the antibody or the light chain CDR3 of the antibody. A4 capable of blocking and transmitting virus, also binds to L-SIGN. (I) is useful in interfering with the interaction of DC-SIGN expressing cells and ICAM-expressing cells, which involves administering immune-modulating amount of (I), to a subject. (I) is useful for generating an immune response, which involves administering immune-modulating amount of (I), to a subject. It is useful for delivering an antigen to DC-SIGN expressing cells, which involves attaching the antigen to (I). (I) is useful for diagnosing cancer, which involves obtaining a tissue sample from a subject suspected of having cancer, and determining the degree to which the tissue sample binds with (I), where an increase in the degree of binding compared to corresponding normal tissue indicates the presence of cancer. The determining step involves staining for the presence of DC-SIGN. (I) is useful for treating cancer or inflammatory diseases. (I) is useful for blocking binding of a virus, bacteria or parasite to the cell, blocking infection of the cell by a virus, bacteria or parasite, and/or blocking transmission of a virus, bacteria or parasite from the cell to another cell, where the virus is chosen from HIV, HCV, Ebola, SARS, CMV, Sindbis and Dengue, the bacteria is chosen from H.pylori, K.pneumoniae, M.tuberculosis and M.bovis, and the parasite is chosen from L.pifanoi and S.mansoni. (I) is useful in treating autoimmune diseases (e.g., rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis), preventing transplant rejection, preventing and treating allergies, and to prevent, inhibit or at least delay T cell activation for slowing the onset and/or the progress of a viral disease such as HIV. (I) is useful in inducing tolerance, immunotherapy, and in diagnostic and research for studying dendritic cells and/or their function and interaction, studying immune system and for detecting dendritic cells and/or C-type lectins in biological samples. The present sequence represents a human DC-SIGN antibody, light chain, SEQ ID NO:44.

Sequence 112 AA;
Query Match 100.0%; Score 79; DB 9; Length 112;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVVDYDGSYNN 15
DB 24 KASQSVVDYDGSYNN 38
|||||

RESULT 36

AAB71895

ID AAB71895 standard; protein; 113 AA.

XX AC AAB71895;

XX DT 09-MAY-2001 (first entry)

XX PF Monoclonal antibody ST40 light chain.

XX

KW Antibody; ST40; molecular mimetic; CD4; human immunodeficiency virus;
HIV; infection.

XX OS Unidentified.

XX PN WO200109191-A1.

XX PD 08-FEB-2001.

XX PF 02-AUG-2000; 2000WO-GB002972.

XX PR 02-AUG-1999; 99EP-00401968.

XX (SYNT-) SYNT:EM SA.

XX Casset F, Granier C, Kaczorek M, Lahana R, Rees A, Roux F;

XX WPI; 2001-168699/17.

Designing molecular mimetics to mimic a parent molecule activity, useful e.g. therapeutically and diagnostically, uses computational screening to identify active chemical groups by accessibility within the parent molecule.

XX Example 1; Fig 1; 85pp; English.

The present sequence was used in a method for designing a mimetic which exhibits an activity associated with a parent molecule. Such mimetics may be smaller than the parent molecule and correspondingly easier and cheaper to make, since the active region of the parent molecule is normally relatively small. The method is useful where the parent molecule is a binding domain or the hypervariable region of an antibody or other member of the immunoglobulin superfamily. It is useful when the parent molecule is an antibody and the mimetic a peptide, especially an antibody which binds CD4 and a peptide which binds CD4. The mimetics designed and produced are useful diagnostically to detect cells bearing CD4 on their surfaces or may be included in pharmaceuticals e.g. to treat conditions in which CD4 is implicated (e.g. HIV)

XX Sequence 113 AA;

Query Match 100.0%; Score 79; DB 4; Length 113;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVVDYDGSYNN 15
DB 24 KASQSVVDYDGSYNN 38
|||||

RESULT 37

ADI26494

ID ADI26494 standard; protein; 113 AA.

XX AC ADI26494;

XX DT 15-APR-2004 (first entry)

XX DE Human ECL2B-3-L SEQ ID NO:30.

antibody; enzyme; virucide; anti-HIV; cytostatic; antibacterial;
Helicobacter pylori urease inhibitor;
chemokine receptor CCR-5 antagonist; cancer; infectious disease;
Helicobacter pylori; HIV; human.

XX OS Homo sapiens.

XX PN WO2004009805-A1.

XX PD 29-JAN-2004.

XX PF 18-JUL-2003; 2003WO-JP009147.

XX

| | |
|-----------|--|
| PR | 19-JUL-2002; 2002JP-00211756. |
| PR | 19-JUL-2002; 2002JP-00211768. |
| PR | 27-FEB-2003; 2003JP-00051943. |
| PR | 17-JUL-2003; 2003JP-00198270. |
| PR | 17-JUL-2003; 2003JP-00198281. |
| PR | 17-JUL-2003; 2003JP-00198292. |
| PA | (NISC-) JAPAN SCI & TECHNOLOGY CORP. |
| XX | |
| XX | Uda T, Hifumi E; |
| DR | WPI; 2004-132963/13. |
| DR | N-PSDB; ADI26495. |
| XX | |
| PT | Screening potential antibody enzymes by identification of a catalytic |
| PT | tripeptide residue in the stereostructure for production of antibody enzymes |
| PT | as diagnostic and therapeutic agents for cancer and infectious diseases |
| PT | including HIV infection. |
| XX | |
| PS | Claim 40; SEQ ID NO 30; 232pp; Japanese. |
| XX | |
| CC | The invention relates to a novel method for producing antibody enzymes |
| CC | comprising a structural analysis step which confirms the existence in the |
| CC | predicted stereostructure of the antibody based on its amino acid |
| CC | sequence of a catalytic tripeptide residue structure in which a serine |
| CC | residue, an aspartic acid residue, and a histidine or glutamic acid |
| CC | residue are located sterically close to one another. An enzyme produced |
| CC | by the method of the invention has virucide, anti-HIV, cytostatic, and |
| CC | antibacterial activity. The enzyme acts as a helicobacter pylori urease |
| CC | inhibitor, or chemokine receptor CCR-5 (HIV target) antagonist. The |
| CC | method of the invention is useful for the treatment, prevention and |
| CC | diagnosis of cancer and infectious diseases, especially infection by |
| CC | Helicobacter pylori or HIV. The present sequence is used in the |
| CC | exemplification of the invention. |
| XX | |
| SQ | Sequence 113 AA; |
| | |
| | Query Match 100.0%; Score 79; DB 8; Length 113; |
| | Best Local Similarity 100.0%; Pred. No. 4e-05; |
| | Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0 |
| Qy | 1 KASQSVDDYDGSYMN 15 |
| | |
| Db | 24 KASQSVDDYDGSYMN 38 |
| | |
| RESULT 38 | |
| ADO06847 | |
| ID | ADO06847 standard; protein; 113 AA. |
| XX | |
| AC | ADO06847; |
| XX | |
| DT | 29-JUL-2004 (first entry) |
| XX | |
| DE | Virucidal antibody-related HY4 26a light chain protein sequence SeqID91. |
| XX | |
| KW | humanised antibody; epitope; envelope glycoprotein; |
| KW | Venezuelan equine encephalitis virus; complementary determining region; |
| KW | CDR; non-human antibody; framework region; virucide; vaccine; |
| KW | viral infection; HY4; light chain. |
| XX | |
| OS | Homo sapiens. |
| OS | Mus sp. |
| OS | Synthetic. |
| XX | |
| PN | WO2004039234-A2. |
| XX | |
| PD | 13-MAY-2004. |
| XX | |
| XX | 13-MAY-2003; 2003WO-US015083. |
| XX | |
| PR | 13-MAY-2002; 2002US-0379994P. |
| XX | |

CC This invention relates to a novel humanised antibody or antibody fragment
CC which binds to an epitope on an envelope glycoprotein of the Venezuelan
CC equine encephalitis virus, and comprises at least one complementary
CC determining region (CDR) from a non-human antibody and at least one
CC framework region from a human antibody. The invention may be useful for
CC the production of compounds with a virucide activity or vaccines. The
CC humanised antibody is useful for preventing or neutralising viral
CC infection. The present sequence is that of a human 3B4C4 HY4 light chain
CC protein which was used in the exemplification of the invention.

XX SQ Sequence 113 AA;

Query Match 100.0%; Score 79; DB 8; Length 113;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVVDYDGD SYMN 15
Db 26 KASQSVVDYDGD SYMN 40
|||||

RESULT 40

ADO06849
ID ADO06849 standard; protein; 113 AA.

XX ADO06849;

AC AC

DT 29-JUL-2004 (first entry)

XX Virucidal antibody-related HY4 26b light chain protein sequence SeqID93.

XX humanised antibody; epitope; envelope glycoprotein;

KW Venezuelan equine encephalitis virus; complementary determining region;

KW CDR; non-human antibody; framework region; virucide; vaccine;

KW viral infection; HY4; light chain.

XX Homo sapiens.

OS Mus sp.

OS Synthetic.

XX WO2004039234-A2.

XX 13-MAY-2004.

XX 13-MAY-2003; 2003WO-US015083.

XX 13-MAY-2002; 2002US-0379994P.

XX (ALEX-) ALEXION PHARM INC.

XX Frederickson S, Hinkel C;

XX WPI; 2004-376022/35.

XX N-PSDB; ADO06848.

XX New humanized antibody or antibody fragment comprising at least one

XX complementary determining region from a non-human antibody and at least

XX one framework region from a human antibody, useful for preventing viral

XX infection.

XX Example; SEQ ID NO 93; 70pp; English.

XX This invention relates to a novel humanised antibody or antibody fragment

XX which binds to an epitope on an envelope glycoprotein of the Venezuelan

XX equine encephalitis virus, and comprises at least one complementary

XX determining region (CDR) from a non-human antibody and at least one

XX framework region from a human antibody. The invention may be useful for

CC the production of compounds with a virucide activity or vaccines. The
CC humanised antibody is useful for preventing or neutralising viral
CC infection. The present sequence is that of a human 3B4C4 HY4 light chain
CC protein which was used in the exemplification of the invention.

XX SQ Sequence 113 AA;

Query Match 100.0%; Score 79; DB 8; Length 113;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVVDYDGD SYMN 15
Db 26 KASQSVVDYDGD SYMN 40
|||||

RESULT 40

ADO06849
ID ADO06849 standard; protein; 113 AA.

XX ADO06849;

AC AC

DT 29-JUL-2004 (first entry)

XX Virucidal antibody-related HY4 26b light chain protein sequence SeqID93.

XX humanised antibody; epitope; envelope glycoprotein;

KW Venezuelan equine encephalitis virus; complementary determining region;

KW CDR; non-human antibody; framework region; virucide; vaccine;

KW viral infection; HY4; light chain.

XX Homo sapiens.

OS Mus sp.

OS Synthetic.

XX WO2004039234-A2.

XX 13-MAY-2004.

XX 13-MAY-2003; 2003WO-US015083.

XX 13-MAY-2002; 2002US-0379994P.

XX (ALEX-) ALEXION PHARM INC.

XX Frederickson S, Hinkel C;

XX WPI; 2004-376022/35.

XX N-PSDB; ADO06848.

XX New humanized antibody or antibody fragment comprising at least one

XX complementary determining region from a non-human antibody and at least

XX one framework region from a human antibody, useful for preventing viral

XX infection.

XX Example; SEQ ID NO 93; 70pp; English.

XX This invention relates to a novel humanised antibody or antibody fragment

XX which binds to an epitope on an envelope glycoprotein of the Venezuelan

XX equine encephalitis virus, and comprises at least one complementary

XX determining region (CDR) from a non-human antibody and at least one

Query Match 100.0%; Score 79; DB 8; Length 113;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVVDYDGD SYMN 15
Db 26 KASQSVVDYDGD SYMN 40
|||||

RESULT 41

ADO06851
ID ADO06851 standard; protein; 113 AA.

XX ADO06851;

AC AC

DT 29-JUL-2004 (first entry)

XX Virucidal antibody-related HY4 26c light chain protein sequence SeqID95.

XX humanised antibody; epitope; envelope glycoprotein;

KW Venezuelan equine encephalitis virus; complementary determining region;

KW CDR; non-human antibody; framework region; virucide; vaccine;

KW viral infection; HY4; light chain.

XX Homo sapiens.

OS Mus sp.

OS Synthetic.

XX WO2004039234-A2.

XX 13-MAY-2004.

XX 13-MAY-2003; 2003WO-US015083.

XX 13-MAY-2002; 2002US-0379994P.

XX (ALEX-) ALEXION PHARM INC.

XX Frederickson S, Hinkel C;

XX WPI; 2004-376022/35.

XX N-PSDB; ADO06850.

XX New humanized antibody or antibody fragment comprising at least one

XX complementary determining region from a non-human antibody and at least

XX one framework region from a human antibody, useful for preventing viral

XX infection.

XX Example; SEQ ID NO 95; 70pp; English.

XX This invention relates to a novel humanised antibody or antibody fragment

XX which binds to an epitope on an envelope glycoprotein of the Venezuelan

XX equine encephalitis virus, and comprises at least one complementary

XX determining region (CDR) from a non-human antibody and at least one

XX framework region from a human antibody. The invention may be useful for

XX the production of compounds with a virucide activity or vaccines. The

XX humanised antibody is useful for preventing or neutralising viral

XX infection. The present sequence is that of a HY4 26 light chain protein

XX which was used in the exemplification of the invention.

Query Match 100.0%; Score 79; DB 8; Length 113;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVVDYDGD SYMN 15
Db 26 KASQSVVDYDGD SYMN 40
|||||

RESULT 42

ADO06851
ID ADO06851 standard; protein; 113 AA.

XX ADO06851;

AC AC

DT 29-JUL-2004 (first entry)

XX Virucidal antibody-related HY4 26c light chain protein sequence SeqID95.

XX humanised antibody; epitope; envelope glycoprotein;

KW Venezuelan equine encephalitis virus; complementary determining region;

KW CDR; non-human antibody; framework region; virucide; vaccine;

KW viral infection; HY4; light chain.

XX Homo sapiens.

OS Mus sp.

OS Synthetic.

XX WO2004039234-A2.

XX 13-MAY-2004.

XX 13-MAY-2003; 2003WO-US015083.

XX 13-MAY-2002; 2002US-0379994P.

XX (ALEX-) ALEXION PHARM INC.

XX Frederickson S, Hinkel C;

XX WPI; 2004-376022/35.

XX N-PSDB; ADO06850.

XX New humanized antibody or antibody fragment comprising at least one

XX complementary determining region from a non-human antibody and at least

XX one framework region from a human antibody, useful for preventing viral

XX infection.

XX Example; SEQ ID NO 95; 70pp; English.

XX This invention relates to a novel humanised antibody or antibody fragment

XX which binds to an epitope on an envelope glycoprotein of the Venezuelan

XX equine encephalitis virus, and comprises at least one complementary

XX determining region (CDR) from a non-human antibody and at least one

XX framework region from a human antibody. The invention may be useful for

XX the production of compounds with a virucide activity or vaccines. The

XX humanised antibody is useful for preventing or neutralising viral

XX infection. The present sequence is that of a HY4 26 light chain protein

XX which was used in the exemplification of the invention.

```

AA04134
ID  AA04134 standard; protein; 115 AA.
XX
AC  AA04134;
XX
DT  25-MAR-2003 (revised)
DT  06-SEP-1990 (first entry)
XX
DE  Anti-Leu 3a light chain variable region gene product, KOL/206 VL.
XX
KW  HIV; AIDS; anti-Leu3A; vaccine; ds.
XX
OS  Mus musculus.
XX
PN  EP365209-A.
XX
PD  25-APR-1990.
XX
PF  11-OCT-1989; 89EP-00310415.
XX
PR  17-OCT-1988; 88US-00260558.
XX
PA  (BECT ) BECTON DICKINSON CO.
XX
PI  Hinton R, Oi VT;
XX
WPI; 1990-126329/17.
DR  N-PSDB; AAQ04041.
XX
PT  New chimeric variants of murine antibody anti-leucine - contg. human
PT  antibody regions, and DNA encoding sequences.
XX
PS  Claim 4; Fig 4; 12pp; English.
XX
CC  Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be used
CC  to form chimeric mouse-variable, human-constant region Abs suggested as
CC  being useful as a vaccine to HIV. (Updated on 25-MAR-2003 to correct PF
CC  field.)
XX
SQ  Sequence 115 AA;
    Query Match          100.0%; Score 79; DB 2; Length 115;
    Best Local Similarity 100.0%; Pred. No. 4.1e-05;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 KASQSVDDYDGD SYNM 15
Db  27 KASQSVDDYDGD SYNM 41
    |||||
RESULT 43
AA048618
ID  AA048618 standard; protein; 120 AA.
XX
AC  AA048618;
XX
DT  25-MAR-2003 (revised)
DT  03-SEP-1994 (first entry)
XX
DE  Sequence of the monoclonal antibody BAT123 light chain variable region.
XX
KW  Epitope; monoclonal antibody; BAT123; variable light.
XX
OS  Synthetic.
XX
PN  WO9404574-A1.
XX
PD  03-MAR-1994.
XX
PF  24-AUG-1993; 93WO-US007967.
XX
PR  24-AUG-1992; 92WO-US007111.
PR  22-APR-1993; 93US-00039457.

(NISP ) NISSIN SHOKUHN KAISHA LTD.
Ohno T;
WPI; 1994-083117/10.
New humanised antibody specific for epitope on HIV-1 gp 120 - able to
neutralise infection of HG cells, also nucleic acid encoding it, useful
for passive immunisation to treat or prevent HIV-1 infection.
Example; Page 47; 91pp; English.
GPR is a portion of HIV-1 gp120 or gp160 protein. Monoclonal antibodies
(MAbs) that react with this and which have the capacity to neutralise the
infection of H9 cells in culture by live HIV-1 strains MN and IIB are
claimed. Specifically illustrating the invention are the murine MAb
(designated NM-01) produced by hybridoma cell line HB 10726 which is
deposited under ATCC No. HB 10726. The DNA sequences of the variable
regions of the heavy and light chains of MAb NM-01 were cloned by PCR
using cDNA generated from hybridoma HB 10726 cytoplasmic RNA as template.
The DNA was then sequenced. The DNA and deduced AA sequences are given in
AAQ56685/R48613; AAQ56686/R48615. Resequencing the variable regions of
MAb NM-01 resulted in the sequences set out in AAQ56687/R48614 and
AAQ56688/R48616. The heavy chain variable region of NM-01 differs from
that of the MAb BA123, as reported in Liou et al., by 46 AAs out of a
total of 120. The light chain variable regions of these two Abs differ by
23 AAs. Significantly, the three CDRs in the heavy chain (V-H) of the NM-
01 molecule are about 41 to 90% different in sequence from those of
BA123, while the sequences of the three CDRs in the light chain (V-L)
vary by about 29-47% compared to NM-01. (Updated on 25-MAR-2003 to
correct PN field.)
XX
SQ  Sequence 120 AA;
    Query Match          100.0%; Score 79; DB 2; Length 120;
    Best Local Similarity 100.0%; Pred. No. 4.3e-05;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 KASQSVDDYDGD SYNM 15
Db  24 KASQSVDDYDGD SYNM 38
    |||||
RESULT 44
AAP90543
ID  AAP90543 standard; protein; 131 AA.
XX
AC  AAP90543;
XX
DT  24-OCT-2003 (revised)
DT  27-AUG-2003 (revised)
DT  25-MAR-2003 (revised)
DT  20-OCT-1989 (first entry)
XX
DE  Amino acids sequence of a V chi region gene.
XX
KW  V cji region; immunoglobulin; L chain variable region; HIV.
XX
OS  Mus musculus.
XX
PN  EP327000-A.
XX
PD  09-AUG-1989.
XX
PF  30-JAN-1989; 89EP-00101583.
XX
PR  30-JAN-1988; 88JP-00020255.
PR  08-JUL-1988; 88JP-00171385.
XX
PA  (KAGA ) CEMO SERO THERAPEUTIC RES INS.
XX
PI  Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Matsushita S, Hattori T;
```

PI Takatsuki K;
 XX WPI; 1989-229050/32.
 DR N-PSDB; AAN90495.
 XX
 PT Chimeric anti-human immune virus antibodies - contg. mouse variable
 PT regions and human constant regions for diagnosis, treatment and
 PT prevention of AIDS.
 XX
 PS Disclosure; Fig 8; 33pp; English.
 XX
 CC The sequence is encoded by a V chi region gene (see AAN90495). The
 CC sequence from Asp 21 encodes the L chain variable region. (Updated on 25-
 CC MAR-2003 to correct PA field.) (Updated on 27-AUG-2003 to correct OS
 CC field.) (Updated on 24-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 131 AA;
 Query Match 100.0%; Score 79; DB 1; Length 131;
 Best Local Similarity 100.0%; Pred. No. 4.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KASQSVVDYDGD SYMN 15
 DB 44 KASQSVVDYDGD SYMN 58
 RESULT 45
 AAR04132
 ID AAR04132 standard; protein; 131 AA.
 XX
 AC AAR04132;
 XX
 DT 25-MAR-2003 (revised)
 DT 06-SEP-1990 (first entry)
 XX
 DE Anti-Leu 3a light chain variable region gene product, 206 Vx.
 XX
 KW HIV; AIDS; anti-Leu3A; vaccine; ds.
 XX
 OS Mus musculus.
 XX
 FN EP365209-A.
 XX
 PD 25-APR-1990.
 XX
 PF 11-OCT-1989; 89EP-00310415.
 XX
 PR 17-OCT-1988; 88US-00260558.
 XX
 PA (BECT) BECTON DICKINSON CO.
 XX
 PI Hinton R, Oi VT;
 XX
 DR WPI; 1990-126329/17.
 DR N-PSDB; AAQ04039.
 XX
 PT New chimeric variants of murine antibody anti-leucine - contg. human
 PT antibody regions, and DNA encoding sequences.
 XX
 PS Claim 1; Fig 2; 12pp; English.
 XX
 CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be used
 CC to form chimeric mouse-variable, human-constant region Abs suggested as
 CC being useful as a vaccine to HIV. (Updated on 25-MAR-2003 to correct PF
 CC field.)
 XX
 SQ Sequence 131 AA;
 Query Match 100.0%; Score 79; DB 2; Length 131;
 Best Local Similarity 100.0%; Pred. No. 4.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVVDYDGD SYMN 15
 DB 44 KASQSVVDYDGD SYMN 58
 RESULT 46
 AAR70202
 ID AAR70202 standard; protein; 131 AA.
 XX
 AC AAR70202;
 XX
 DT 25-MAR-2003 (revised)
 DT 20-SEP-1995 (first entry)
 XX
 DE Humanized antibody 3B9 light chain.
 XX
 KW Humanized antibody; antibody engineering; monoclonal antibody; MAb;
 KW interleukin-4; IL-4; allergy.
 XX
 OS Homo sapiens.
 XX
 PN WO9507301-A1.
 XX
 PD 16-MAR-1995.
 XX
 PF 07-SEP-1994; 94WO-US010308.
 XX
 PR 07-SEP-1993; 93US-00117366.
 PR 14-OCT-1993; 93US-00136783.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Holmes S, Gross MS, Sylvester DR;
 XX
 DR WPI; 1995-123387/16.
 DR N-PSDB; AAQ83520.
 XX
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from
 PT high affinity mAbs - useful in treatment of IL-4-mediated and IGE-
 PT mediated allergic conditions.
 XX
 PS Disclosure; Page 71-72; 97pp; English.
 XX
 CC A humanized antibody light chain variable region and signal sequence is
 CC given in AAR75355. The signal sequence is also provided in AAR70194. The
 CC sequences of the 3 CDRs are identical to mouse anti-human IL-4 MAb 3B9
 CC light chain CDRs (given in AAR70195-97). (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 131 AA;
 Query Match 100.0%; Score 79; DB 2; Length 131;
 Best Local Similarity 100.0%; Pred. No. 4.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KASQSVVDYDGD SYMN 15
 DB 43 KASQSVVDYDGD SYMN 57
 RESULT 47
 AAR75355
 ID AAR75355 standard; protein; 131 AA.
 XX
 AC AAR75355;
 XX
 DT 25-MAR-2003 (revised)
 DT 20-SEP-1995 (first entry)
 XX
 DE Humanized antibody 3B9 light chain.
 XX
 KW Humanized antibody; antibody engineering; monoclonal antibody; MAb;

```

KW interleukin-4; IL-4; allergy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT Region /label= Sig_peptide
FT 43..57
FT /label= CDR
FT /note= "complementarity determining region"
FT 73..79
FT /label= CDR
FT /note= "complementarity determining region"
FT 112..120
FT /label= CDR
FT /note= "complementarity determining region"
XX
PN WO9507301-A1.
XX
PD 16-MAR-1995.
XX
PF 07-SEP-1994; 94WO-US010308.
XX
PR 07-SEP-1993; 93US-00117366.
PR 14-OCT-1993; 93US-00136783.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Holmes S, Gross MS, Sylvester DR;
XX
DR WPI; 1995-123387/16.
DR N-PSDB; AAQ73986.
XX
XX Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from
PT high affinity mAbs - useful in treatment of IL-4-mediated and IgE-
PT mediated allergic conditions.
XX
PS Disclosure; Fig 5; 97pp; English.
XX
XX A humanized antibody light chain variable region and signal sequence is
CC given in AAR75355. The signal sequence is also provided in AAR70194. The
CC sequences of the first 2 CDRs are identical to mouse anti-human IL-4 mAb
CC 3B9 light chain CDRs (given in AAR70195-96), but the third (AAR70201)
CC differs by a single amino acid from the native mouse CDR (AAR70197).
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 131 AA;
Query Match 100.0%; Score 79; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KASQSVVDYDGD SYNM 15
DB 43 KASQSVVDYDGD SYNM 57
RESULT 48
AAY23771
ID AAY23771 standard; protein; 131 AA.
XX
AC AAY23771;
XX
DT 13-SEP-1999 (first entry)
XX
DE Light chain variable region of humanised murine IL-4 antibody 3B9.
XX
KW Light chain variable region; interleukin-4; IL-4; antibody 3B9;
KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;
KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.

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```

XX Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
PN US5928904-A.
XX
PD 27-JUL-1999.
XX
PF 07-JUN-1995; 95US-00483632.
XX
PR 07-SEP-1993; 93US-00117366.
PR 14-OCT-1993; 93US-00136783.
PR 07-SEP-1994; 94WO-US010308.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Holmes SD, Sylvester DR, Gross MS;
XX
DR WPI; 1999-429500/36.
DR N-PSDB; AAX85888.
XX
XX New DNA molecules encoding recombinant antibodies useful for treating IL4
PT -mediated conditions.
XX
XX Example 3; Fig 5; 50pp; English.
XX
XX The present sequence represents the light chain variable region of a
CC humanised murine interleukin-4 (IL-4) antibody 3B9. The specification
CC describes chimeric and humanised IL-4 monoclonal antibodies. The
CC antibodies of the invention are used in therapeutic and pharmaceutical
CC compositions for treating IL-4 mediated and immunoglobulin E-mediated
CC allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic
CC dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host
CC -versus-graft disease and renal disease. They are also useful in the
CC diagnosis of an allergy or condition associated with excess IL-4
CC production through the measurement e.g. by ELISA of circulating
CC endogenous IL-4 levels in humans
XX
SQ Sequence 131 AA;
Query Match 100.0%; Score 79; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KASQSVVDYDGD SYNM 15
DB 43 KASQSVVDYDGD SYNM 57
RESULT 49
AAY23779
ID AAY23779 standard; protein; 131 AA.
XX
AC AAY23779;
XX
DT 13-SEP-1999 (first entry)
XX
DE Light chain variable region of humanised murine IL-4 antibody 3B9.
XX
KW Light chain variable region; interleukin-4; IL-4; antibody 3B9;
KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;
KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.
XX
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
PN US5928904-A.
XX

```

PD 27-JUL-1999.
 XX
 XX
 XX 07-JUN-1995; 95US-00483632.
 XX
 XX 07-SEP-1993; 93US-00117366.
 PR 14-OCT-1993; 93US-00136783.
 PR 07-SEP-1994; 94WO-US010308.
 XX
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 XX Holmes SD, Sylvester DR, Gross MS;
 XX
 XX WPI; 1999-429500/36.
 DR N-PSDB; AAX85924.
 XX
 XX New DNA molecules encoding recombinant antibodies useful for treating IL4
 PT -mediated conditions.
 PT
 XX Disclosure; Col 61-62; 50pp; English.
 XX
 XX The present sequence represents the light chain variable region of a
 CC humanised murine interleukin-4 (IL-4) antibody 3B9. The specification
 CC describes chimeric and humanised IL-4 monoclonal antibodies. The
 CC antibodies of the invention are used in therapeutic and pharmaceutical
 CC compositions for treating IL-4 mediated and immunoglobulin E-mediated
 CC allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic
 CC dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host
 CC -versus-graft disease and renal disease. They are also useful in the
 CC diagnosis of an allergy or condition associated with excess IL-4
 CC production through the measurement e.g. by ELISA of circulating
 CC endogenous IL-4 levels in humans
 XX
 XX Sequence 131 AA;
 SQ
 Query Match 100.0%; Score 79; DB 2; Length 131;
 Best Local Similarity 100.0%; Pred. No. 4.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KASQSVDDYDGD SYMN 15
 DB 43 KASQSVDDYDGD SYMN 57
 RESULT 50
 AAY18118
 ID AAY18118 standard; protein; 131 AA.
 XX
 XX AAY18118;
 AC
 XX
 XX 11-AUG-1999 (first entry)
 DT
 XX
 DE Light chain sequence for humanised 3B9 antibody.
 XX
 XX Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;
 KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
 KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
 KW autoimmune disease; graft versus host disease.
 XX
 XX Synthetic.
 OS
 XX US5914110-A.
 PN
 XX
 XX 22-JUN-1999.
 PD
 XX
 XX 07-JUN-1995; 95US-00483636.
 PF
 XX
 XX 07-SEP-1993; 93US-00117366.
 PR
 PR 14-OCT-1993; 93US-00136783.
 PR 07-SEP-1994; 94WO-US010308.
 XX
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX

XX Sylvester DR, Holmes SD, Gross MS;
 XX
 XX WPI; 1999-370482/31.
 DR N-PSDB; AAX79517.
 XX
 XX Recombinant IL4 antibodies useful for treatment of allergic rhinitis,
 PT atopic asthma and anaphylactic shock.
 PT
 XX Claim 16; Fig 5; 50pp; English.
 XX
 XX This sequence represents the light chain of the humanised 3B9 antibody of
 CC the invention. The antibody is a chimeric or humanised interleukin-4
 CC (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE)
 CC mediated diseases. The antibodies are useful for the treatment of
 CC allergic disorders such as allergic rhinitis, conjunctivitis, atopic
 CC dermatitis, atopic asthma and anaphylactic shock. The antibodies are also
 CC useful for regulating B and T cell proliferation and as such are useful
 CC in the treatment of autoimmune diseases and graft versus host disease
 XX
 XX Sequence 131 AA;
 SQ
 Query Match 100.0%; Score 79; DB 2; Length 131;
 Best Local Similarity 100.0%; Pred. No. 4.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KASQSVDDYDGD SYMN 15
 DB 43 KASQSVDDYDGD SYMN 57
 Search completed: February 23, 2006, 09:39:30
 Job time : 155.231 secs

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OM protein - protein search, using sw model

Run on: February 23, 2006, 09:41:24 ; Search time 21.2308 Seconds
(without alignments)
67.979 Million cell updates/sec

Title: US-10-723-872-16

Perfect score: 79
Sequence: 1 KASQSVYDGDGYM 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR 80:**

1: pir1:**
2: pir2:**
3: pir3:**
4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 79 | 100.0 | 81 | 2 S42193 | Ig kappa chain V r |
| 2 | 79 | 100.0 | 93 | 2 A38601 | Ig kappa chain V r |
| 3 | 79 | 100.0 | 111 | 1 KVM808 | Ig kappa chain V r |
| 4 | 79 | 100.0 | 111 | 1 KVM543 | Ig kappa chain V r |
| 5 | 79 | 100.0 | 111 | 1 KVM569 | Ig kappa chain V r |
| 6 | 79 | 100.0 | 111 | 1 KVM583 | Ig kappa chain V r |
| 7 | 76 | 96.2 | 110 | 1 KVM510 | Ig kappa chain V r |
| 8 | 76 | 96.2 | 112 | 2 S19971 | Ig kappa chain V r |
| 9 | 76 | 96.2 | 131 | 2 PH1226 | Ig kappa chain pre |
| 10 | 73 | 92.4 | 111 | 2 S09966 | Ig kappa chain V-J |
| 11 | 68 | 86.1 | 111 | 1 KVM581 | Ig kappa chain V r |
| 12 | 65 | 82.3 | 112 | 2 S19976 | Ig kappa chain V r |
| 13 | 51 | 64.6 | 112 | 2 S19972 | Ig kappa chain V r |
| 14 | 48 | 60.8 | 282 | 2 AI0948 | hypothetical prote |
| 15 | 46 | 58.2 | 96 | 2 B49442 | Ig light chain V r |
| 16 | 45 | 57.0 | 109 | 2 PH0093 | Ig kappa chain V r |
| 17 | 43 | 54.4 | 551 | 2 T03793 | calmodulin-binding |
| 18 | 42 | 53.2 | 102 | 2 PH1079 | Ig light chain V r |
| 19 | 42 | 53.2 | 111 | 1 KVM580 | Ig kappa chain V r |
| 20 | 42 | 53.2 | 111 | 2 S09969 | Ig kappa chain V-J |
| 21 | 42 | 53.2 | 115 | 2 S63596 | Ig kappa chain V r |
| 22 | 42 | 53.2 | 120 | 2 S06732 | Ig kappa chain pre |
| 23 | 42 | 53.2 | 303 | 2 A83958 | integrin/recombin |
| 24 | 41 | 51.9 | 91 | 2 S25462 | Ig kappa chain V r |
| 25 | 41 | 51.9 | 107 | 2 S26343 | Ig kappa chain V r |
| 26 | 41 | 51.9 | 107 | 2 S26344 | Ig kappa chain V r |
| 27 | 41 | 51.9 | 108 | 1 KVM554 | Ig kappa chain V r |
| 28 | 41 | 51.9 | 111 | 1 KVM537 | Ig kappa chain V r |
| 29 | 41 | 51.9 | 111 | 2 S09963 | Ig kappa chain V-J |

Ig kappa chain pre
membrane-bound lvt
Ig kappa chain V r
Ig kappa chain V r
Ig kappa chain V r
Ig kappa chain V r
Ig kappa chain V r
Ig kappa chain pre
Ig kappa chain V r
conserved hypothet
vacuolar sorting p
hypothetical prote
hypothetical prote
kinesin-related pr
hypothetical prote
Ig kappa chain V r
Ig kappa chain V r
Ig kappa chain pre
Ig kappa chain V r
Ig kappa chain pre
Ig kappa chain pre
anti-glycoprotein
Ig kappa chain pre
hypothetical prote
E2 protein - bovin
thiamine pyridinyl
hypothetical prote
hypothetical prote
hypothetical prote
endoplasmic reticu
protein disulfide-
protein disulfide-
hypothetical prote
hypothetical prote
small nuclear ribo
proteinase inhibit
proteinase inhibit
Ig kappa chain V r
hypothetical prote
hypothetical prote
protein F21J9.28 l
DAG protein precu
spec-related prote
calcium-binding pr
conserved hypothet
hypothetical prote
Spec-related prote
C0684.5 protein -
mucin hydrolase (
cytochrome c-type
membrane-bound lvt
hypothetical prote
probable AP2 domai
hypothetical prote
protein disulfide-
59K HindIII-C prot
C2L protein - vacc
calmodulin-binding
S-receptor kinase
2C21.2 protein - C
hypothetical prote
hypothetical prote
probable transport
hypothetical prote
U6 snRNA-associate
Ig kappa chain V-I
acetylcoline recep
Ig kappa chain V r
Ig kappa chain V r
Ig kappa chain V r
Ig kappa chain V r
Ig kappa chain V r

| | | | | | | | | | | | | | |
|-----|------|------|------|---|--------|---------------------|-----|----|------|------|---|--------|---------------------|
| 103 | 37 | 46.8 | 112 | 2 | S45715 | Ig kappa chain V r | 176 | 35 | 44.3 | 64 | 2 | F70188 | hypothetical prote |
| 104 | 37 | 46.8 | 128 | 2 | S52448 | Ig kappa chain V r | 177 | 35 | 44.3 | 108 | 2 | C90028 | conserved hypothet |
| 105 | 37 | 46.8 | 128 | 2 | JL0073 | aberrant kappa tra | 178 | 35 | 44.3 | 129 | 2 | D69008 | probable iron-bind |
| 106 | 37 | 46.8 | 137 | 2 | D75427 | hypothetical prote | 179 | 35 | 44.3 | 132 | 2 | B41749 | midgut fatty acid- |
| 107 | 37 | 46.8 | 140 | 2 | PN0446 | Ig kappa chain pre | 180 | 35 | 44.3 | 144 | 2 | T50500 | hypothetical prote |
| 108 | 37 | 46.8 | 210 | 2 | A56169 | Ig kappa chain V r | 181 | 35 | 44.3 | 150 | 2 | H86194 | hypothetical prote |
| 109 | 37 | 46.8 | 233 | 2 | J53322 | p53 specific singl | 182 | 35 | 44.3 | 152 | 2 | T06644 | calmodulin homolog |
| 110 | 37 | 46.8 | 251 | 2 | B84016 | hypothetical prote | 183 | 35 | 44.3 | 173 | 2 | S71812 | RGSI0 protein - hu |
| 111 | 37 | 46.8 | 261 | 2 | T47636 | RNA binding protei | 184 | 35 | 44.3 | 173 | 2 | AH3630 | outer-membrane lip |
| 112 | 37 | 46.8 | 315 | 2 | B82229 | hypothetical prote | 185 | 35 | 44.3 | 181 | 2 | B82908 | inorganic pyrophos |
| 113 | 37 | 46.8 | 319 | 2 | B70194 | conserved hypothet | 186 | 35 | 44.3 | 190 | 2 | H84412 | hypothetical prote |
| 114 | 37 | 46.8 | 362 | 1 | A28517 | severin - slime mo | 187 | 35 | 44.3 | 195 | 2 | F36979 | molecular chaperon |
| 115 | 37 | 46.8 | 405 | 2 | S64052 | 26S proteasome reg | 188 | 35 | 44.3 | 235 | 2 | S23401 | chloride channel p |
| 116 | 37 | 46.8 | 441 | 2 | G01758 | transcription fact | 189 | 35 | 44.3 | 236 | 2 | JC5790 | swelling-induced c |
| 117 | 37 | 46.8 | 506 | 2 | T00926 | hypothetical prote | 190 | 35 | 44.3 | 237 | 2 | JC4135 | chloride conductan |
| 118 | 37 | 46.8 | 560 | 2 | H70645 | serine proteinase | 191 | 35 | 44.3 | 238 | 2 | S67594 | RAP59 protein - ye |
| 119 | 37 | 46.8 | 698 | 2 | D90771 | hypothetical prote | 192 | 35 | 44.3 | 241 | 2 | A53014 | chloride conductan |
| 120 | 37 | 46.8 | 698 | 2 | F64839 | yesH protein presu | 193 | 35 | 44.3 | 241 | 2 | B53014 | chloride channel p |
| 121 | 37 | 46.8 | 835 | 2 | C97322 | probable alpha-ara | 194 | 35 | 44.3 | 245 | 2 | A84289 | hypothetical prote |
| 122 | 37 | 46.8 | 925 | 2 | S50490 | hypothetical prote | 195 | 35 | 44.3 | 246 | 2 | D91186 | probable outer mem |
| 123 | 37 | 46.8 | 1036 | 2 | D70117 | acriflavine resist | 196 | 35 | 44.3 | 246 | 2 | C86033 | probable outer mem |
| 124 | 37 | 46.8 | 1286 | 1 | H36845 | DNA-directed RNA p | 197 | 35 | 44.3 | 248 | 2 | S33756 | granzyme-like prot |
| 125 | 37 | 46.8 | 1286 | 2 | T37366 | RNA polymerase sub | 198 | 35 | 44.3 | 250 | 2 | A69528 | 2-hydroxyhepta-2,4 |
| 126 | 37 | 46.8 | 1286 | 2 | T28521 | DNA-directed RNA p | 199 | 35 | 44.3 | 257 | 2 | AC2406 | 2-hydroxyhepta-2,4 |
| 127 | 37 | 46.8 | 1286 | 2 | A72161 | M6R protein - vari | 200 | 35 | 44.3 | 276 | 2 | S77124 | 5-oxo-1,2,5-tricar |
| 128 | 37 | 46.8 | 1287 | 1 | RNV247 | DNA-directed RNA p | 201 | 35 | 44.3 | 293 | 2 | B97194 | probable protein o |
| 129 | 37 | 46.8 | 1289 | 2 | T30681 | DNA-directed RNA p | 202 | 35 | 44.3 | 302 | 1 | T1RTGK | tissue factor path |
| 130 | 37 | 46.8 | 1329 | 2 | T28203 | probable DNA-direc | 203 | 35 | 44.3 | 323 | 2 | JC2578 | DNA repair protein |
| 131 | 37 | 46.8 | 1920 | 2 | S43721 | lactase (EC 3.2.1.1 | 204 | 35 | 44.3 | 334 | 2 | T23444 | hypothetical prote |
| 132 | 37 | 46.8 | 3951 | 1 | VFIHBI | F1 protein - avian | 205 | 35 | 44.3 | 343 | 1 | G64366 | acetylpolymaine am |
| 133 | 36.5 | 46.2 | 122 | 2 | S40338 | Ig kappa chain - h | 206 | 35 | 44.3 | 348 | 2 | A43358 | macrophage capping |
| 134 | 36.5 | 46.2 | 249 | 2 | S41374 | single chain Fv an | 207 | 35 | 44.3 | 361 | 2 | B85918 | membrane-bound lyt |
| 135 | 36.5 | 46.2 | 1821 | 2 | AG2335 | hypothetical prote | 208 | 35 | 44.3 | 361 | 2 | A65050 | membrane-bound lyt |
| 136 | 36 | 45.6 | 129 | 2 | C72499 | hypothetical prote | 209 | 35 | 44.3 | 361 | 2 | F91073 | membrane-bound lyt |
| 137 | 36 | 45.6 | 135 | 2 | F87396 | conserved hypothet | 210 | 35 | 44.3 | 372 | 2 | T24569 | hypothetical prote |
| 138 | 36 | 45.6 | 146 | 2 | F84777 | probable calmoduli | 211 | 35 | 44.3 | 386 | 2 | B71407 | hypothetical prote |
| 139 | 36 | 45.6 | 187 | 2 | A84532 | probable calmoduli | 212 | 35 | 44.3 | 414 | 1 | TVTRMC | transforming prote |
| 140 | 36 | 45.6 | 230 | 2 | T28330 | hypothetical prote | 213 | 35 | 44.3 | 418 | 2 | H69404 | glutamate-1-semial |
| 141 | 36 | 45.6 | 256 | 2 | T45895 | hypothetical prote | 214 | 35 | 44.3 | 419 | 2 | T04886 | DAG protein homolo |
| 142 | 36 | 45.6 | 311 | 2 | F83871 | multidrug resistan | 215 | 35 | 44.3 | 431 | 2 | J50055 | hypothetical 43.7K |
| 143 | 36 | 45.6 | 336 | 2 | E70628 | hypothetical prote | 216 | 35 | 44.3 | 446 | 2 | C91256 | hypothetical 43.7K |
| 144 | 36 | 45.6 | 336 | 2 | E86942 | hypothetical prote | 217 | 35 | 44.3 | 446 | 2 | G86096 | maltose high-affin |
| 145 | 36 | 45.6 | 359 | 2 | AB0844 | hypothetical prote | 218 | 35 | 44.3 | 462 | 2 | T19652 | hypothetical prote |
| 146 | 36 | 45.6 | 364 | 2 | T33474 | membrane-bound lyt | 219 | 35 | 44.3 | 473 | 2 | S61428 | embryonic abundant |
| 147 | 36 | 45.6 | 367 | 2 | H83088 | hypothetical prote | 220 | 35 | 44.3 | 474 | 2 | T20694 | hypothetical prote |
| 148 | 36 | 45.6 | 368 | 2 | T17195 | hypothetical prote | 221 | 35 | 44.3 | 478 | 2 | H82185 | 6-phospho-beta-glu |
| 149 | 36 | 45.6 | 370 | 2 | AG0359 | probable membrane- | 222 | 35 | 44.3 | 479 | 2 | T23447 | receptor-like prot |
| 150 | 36 | 45.6 | 396 | 2 | I50707 | Sox11 transcriptio | 223 | 35 | 44.3 | 643 | 2 | H88712 | protein C17H12.1 l |
| 151 | 36 | 45.6 | 458 | 2 | S33520 | Lea protein - soyb | 224 | 35 | 44.3 | 645 | 1 | A23723 | protein disulfide- |
| 152 | 36 | 45.6 | 474 | 2 | S68695 | B/K protein - rat | 225 | 35 | 44.3 | 667 | 2 | S63587 | gene pacC protein |
| 153 | 36 | 45.6 | 475 | 2 | T12955 | probable protein k | 226 | 35 | 44.3 | 492 | 2 | T41549 | hypothetical prote |
| 154 | 36 | 45.6 | 531 | 2 | F86432 | T518.16 protein - | 227 | 35 | 44.3 | 541 | 2 | G86151 | hypothetical prote |
| 155 | 36 | 45.6 | 533 | 2 | T15116 | hypothetical prote | 228 | 35 | 44.3 | 602 | 2 | T48697 | hypothetical prote |
| 156 | 36 | 45.6 | 579 | 2 | T24880 | hypothetical prote | 229 | 35 | 44.3 | 642 | 2 | T07862 | receptor-like prot |
| 157 | 36 | 45.6 | 685 | 1 | SXBPT4 | NAD+-protein ADP-r | 230 | 35 | 44.3 | 643 | 2 | H88712 | protein C17H12.1 l |
| 158 | 36 | 45.6 | 688 | 2 | T21641 | hypothetical prote | 231 | 35 | 44.3 | 645 | 1 | A23723 | protein disulfide- |
| 159 | 36 | 45.6 | 691 | 2 | T48506 | hypothetical prote | 232 | 35 | 44.3 | 667 | 2 | S63587 | gene pacC protein |
| 160 | 36 | 45.6 | 698 | 1 | S31630 | NAD+-protein ADP-r | 233 | 35 | 44.3 | 670 | 2 | T09205 | hypothetical prote |
| 161 | 36 | 45.6 | 698 | 1 | S31714 | NAD+-protein ADP-r | 234 | 35 | 44.3 | 670 | 2 | T09274 | hypothetical prote |
| 162 | 36 | 45.6 | 749 | 2 | T44796 | DNA helicase pcra | 235 | 35 | 44.3 | 734 | 2 | B82959 | hypothetical prote |
| 163 | 36 | 45.6 | 823 | 2 | S48986 | probable protein k | 236 | 35 | 44.3 | 740 | 2 | B84741 | hypothetical prote |
| 164 | 36 | 45.6 | 896 | 2 | T07408 | lipoygenase (EC 1 | 237 | 35 | 44.3 | 790 | 2 | T19683 | hypothetical prote |
| 165 | 36 | 45.6 | 1172 | 1 | TSHP2 | thrombospondin 2 p | 238 | 35 | 44.3 | 942 | 1 | JQ1674 | protein kinase TWK |
| 166 | 36 | 45.6 | 1172 | 2 | A42587 | thrombospondin 2 p | 239 | 35 | 44.3 | 1101 | 2 | T21062 | hypothetical prote |
| 167 | 36 | 45.6 | 1335 | 2 | H75511 | DNA polymerase III | 240 | 35 | 44.3 | 1170 | 2 | A40558 | thrombospondin 1 p |
| 168 | 36 | 45.6 | 1395 | 2 | T08851 | Down syndrome cell | 241 | 35 | 44.3 | 1237 | 2 | S86457 | probable RNA helic |
| 169 | 36 | 45.6 | 1976 | 2 | I56555 | sodium channel pro | 242 | 35 | 44.3 | 1277 | 2 | S54451 | hypothetical prote |
| 170 | 35.5 | 44.9 | 87 | 2 | S34094 | Ig kappa chain V r | 243 | 35 | 44.3 | 1363 | 2 | C84346 | hypothetical prote |
| 171 | 35.5 | 44.9 | 133 | 2 | S42611 | HUNKV protein prec | 244 | 35 | 44.3 | 1475 | 2 | AE1530 | probable translati |
| 172 | 35.5 | 44.9 | 140 | 2 | S22658 | Ig kappa chain pre | 245 | 35 | 44.3 | 1666 | 2 | T09072 | hypothetical prote |
| 173 | 35.5 | 44.9 | 142 | 2 | S22902 | Ig kappa chain V r | 246 | 35 | 44.3 | 1918 | 2 | S43719 | lactase (EC 3.2.1.1 |
| 174 | 35.5 | 44.9 | 270 | 2 | JN0767 | homeobox protein H | 247 | 35 | 44.3 | 1926 | 2 | S01169 | beta-glycosidase c |
| 175 | 35 | 44.3 | 57 | 2 | S33824 | gene ng-4 protein | 248 | 35 | 44.3 | 1958 | 2 | T39808 | hypothetical prote |
| | | | | | | | | | | 2399 | 2 | H71879 | toxin-like outer m |

| | | | | | | | | | | | | |
|-----|------|------|------|---|--------|----------------------|-----|------|------|---|--------|----------------------|
| 249 | 35 | 44.3 | 2476 | 2 | T34022 | zonadhesin - pig | 322 | 43.0 | 421 | 2 | G97369 | hypothetical prote |
| 250 | 34.5 | 43.7 | 111 | 2 | S20709 | Ig kappa chain V r | 323 | 43.0 | 422 | 2 | D95948 | probable 4-aminobu |
| 251 | 34.5 | 43.7 | 112 | 2 | PL0273 | Ig kappa chain V r | 324 | 43.0 | 423 | 2 | T07150 | G-box binding fact |
| 252 | 34.5 | 43.7 | 133 | 2 | S23230 | Ig kappa chain pre | 325 | 43.0 | 424 | 2 | T10985 | regulator protein |
| 253 | 34.5 | 43.7 | 255 | 2 | S22534 | seed protein B32E | 326 | 43.0 | 428 | 2 | A89950 | glutamate-1-semial |
| 254 | 34.5 | 43.7 | 4162 | 2 | T42633 | connectin/titin - | 327 | 43.0 | 430 | 2 | D42728 | probable intracell |
| 255 | 34 | 43.0 | 50 | 2 | S56691 | hypothetical prote | 328 | 43.0 | 439 | 2 | C97682 | probable 17.4 protei |
| 256 | 34 | 43.0 | 80 | 2 | B95151 | ribosomal protein | 329 | 43.0 | 442 | 2 | H86276 | hypothetical prote |
| 257 | 34 | 43.0 | 80 | 2 | H98018 | S08 ribosomal prot | 330 | 43.0 | 446 | 2 | G69195 | tubulin beta chain |
| 258 | 34 | 43.0 | 82 | 2 | S65143 | pollen allergen gr | 331 | 43.0 | 447 | 2 | S43426 | hypothetical prote |
| 259 | 34 | 43.0 | 82 | 2 | S65150 | pollen allergen Br | 332 | 43.0 | 448 | 2 | S25324 | hypothetical prote |
| 260 | 34 | 43.0 | 83 | 2 | S65152 | Ig kappa chain V r | 333 | 43.0 | 453 | 2 | A81425 | probable lipoprote |
| 261 | 34 | 43.0 | 111 | 1 | KVMS40 | Ig kappa chain V r | 334 | 43.0 | 465 | 2 | A55518 | hypothetical prote |
| 262 | 34 | 43.0 | 111 | 2 | E53285 | Ig kappa chain V a | 335 | 43.0 | 478 | 2 | AD2888 | two component sens |
| 263 | 34 | 43.0 | 111 | 2 | S09965 | Ig kappa chain V-J | 336 | 43.0 | 478 | 2 | A97664 | probable two-compo |
| 264 | 34 | 43.0 | 112 | 2 | E95905 | hypothetical prote | 337 | 43.0 | 481 | 1 | S77273 | penicillin-binding |
| 265 | 34 | 43.0 | 120 | 1 | GLHUCO | Ig heavy chain V-I | 338 | 43.0 | 490 | 2 | B96952 | sucrase-6-phosphat |
| 266 | 34 | 43.0 | 120 | 1 | MHMS15 | Ig heavy chain V r | 339 | 43.0 | 491 | 2 | E96691 | probable sucrose-p |
| 267 | 34 | 43.0 | 132 | 1 | KVMS32 | Ig kappa chain pre | 340 | 43.0 | 502 | 1 | OXCKAX | acyl-CoA oxidase (|
| 268 | 34 | 43.0 | 150 | 2 | T15596 | hypothetical prote | 341 | 43.0 | 508 | 2 | H64223 | pyruvate kinase (E |
| 269 | 34 | 43.0 | 154 | 2 | G85041 | probable calmoduli | 342 | 43.0 | 509 | 2 | C95900 | probable sugar ABC |
| 270 | 34 | 43.0 | 170 | 2 | A86317 | protein T10022.19 | 343 | 43.0 | 516 | 2 | T09364 | cytochrome P450 ho |
| 271 | 34 | 43.0 | 203 | 2 | T40164 | dna-directed rna p | 344 | 43.0 | 519 | 2 | S71451 | halolysin R4 (fc 3 |
| 272 | 34 | 43.0 | 228 | 2 | C28551 | hypothetical prote | 345 | 43.0 | 520 | 2 | G75141 | beta-mannosidase p |
| 273 | 34 | 43.0 | 239 | 2 | T03783 | caffeoyl-CoA O-met | 346 | 43.0 | 521 | 2 | G96543 | calcium-dependent |
| 274 | 34 | 43.0 | 239 | 2 | T01599 | hypothetical prote | 347 | 43.0 | 530 | 2 | A86433 | hypothetical prote |
| 275 | 34 | 43.0 | 241 | 2 | B90474 | conserved hypothet | 348 | 43.0 | 533 | 2 | F86390 | T518.19 protein - |
| 276 | 34 | 43.0 | 242 | 2 | T03796 | caffeoyl-CoA O-met | 349 | 43.0 | 540 | 2 | T10625 | reticuline oxidase |
| 277 | 34 | 43.0 | 242 | 2 | T03801 | caffeoyl-CoA O-met | 350 | 43.0 | 563 | 2 | S78224 | virulence-associat |
| 278 | 34 | 43.0 | 242 | 2 | T03798 | caffeoyl-CoA O-met | 351 | 43.0 | 569 | 2 | E84904 | probable laccase (|
| 279 | 34 | 43.0 | 244 | 2 | C65016 | hypothetical prote | 352 | 43.0 | 572 | 2 | T22547 | hypothetical prote |
| 280 | 34 | 43.0 | 247 | 2 | T09399 | caffeoyl-CoA O-met | 353 | 43.0 | 591 | 1 | S09498 | virulence-associat |
| 281 | 34 | 43.0 | 249 | 2 | T10731 | caffeoyl-CoA O-met | 354 | 43.0 | 591 | 1 | S22664 | virulence-associat |
| 282 | 34 | 43.0 | 262 | 1 | KLCHI | calcium-binding pr | 355 | 43.0 | 593 | 2 | S15215 | virulence-associat |
| 283 | 34 | 43.0 | 264 | 2 | B96680 | hypothetical prote | 356 | 43.0 | 596 | 2 | B41627 | furin (fc 3.4.21.7 |
| 284 | 34 | 43.0 | 270 | 1 | SYECZ1 | trRNA-pseudouridine | 357 | 43.0 | 602 | 2 | F97057 | cytochrome P450 re |
| 285 | 34 | 43.0 | 270 | 2 | AF0802 | pseudouridylylate sy | 358 | 43.0 | 609 | 2 | T48762 | membrane GTPase le |
| 286 | 34 | 43.0 | 270 | 2 | B91029 | pseudouridylylate sy | 359 | 43.0 | 652 | 2 | S52683 | probable membrane |
| 287 | 34 | 43.0 | 270 | 2 | C85873 | pseudouridylylate sy | 360 | 43.0 | 652 | 2 | T19783 | hypothetical prote |
| 288 | 34 | 43.0 | 274 | 2 | T32736 | hypothetical prote | 361 | 43.0 | 652 | 2 | B84568 | probable calmoduli |
| 289 | 34 | 43.0 | 280 | 2 | T15813 | hypothetical prote | 362 | 43.0 | 668 | 2 | E87756 | protein T01A4.1 [1 |
| 290 | 34 | 43.0 | 288 | 2 | D69099 | pyruvate synthase | 363 | 43.0 | 676 | 2 | G69154 | conserved hypothet |
| 291 | 34 | 43.0 | 295 | 2 | T00725 | hypothetical prote | 364 | 43.0 | 692 | 2 | B64381 | hypothetical prote |
| 292 | 34 | 43.0 | 298 | 1 | C64333 | probable pyruvate | 365 | 43.0 | 699 | 2 | T33375 | hypothetical prote |
| 293 | 34 | 43.0 | 298 | 2 | F90274 | hypothetical prote | 366 | 43.0 | 709 | 1 | OXCKPM | acyl-CoA oxidase (|
| 294 | 34 | 43.0 | 311 | 2 | A75047 | 2-ketovalerate oxi | 367 | 43.0 | 709 | 1 | OXCKX | acyl-CoA oxidase (|
| 295 | 34 | 43.0 | 311 | 2 | T45086 | 2-oxoisovalerate-f | 368 | 43.0 | 709 | 1 | OXCKX4 | acyl-CoA oxidase (|
| 296 | 34 | 43.0 | 311 | 2 | C84101 | hypothetical prote | 369 | 43.0 | 791 | 2 | A53691 | diacylglycerol kin |
| 297 | 34 | 43.0 | 311 | 2 | T21563 | hypothetical prote | 370 | 43.0 | 807 | 2 | C85025 | hypothetical prote |
| 298 | 34 | 43.0 | 313 | 2 | D86219 | protein F22013.19 | 371 | 43.0 | 844 | 1 | ZPECPB | penicillin-binding |
| 299 | 34 | 43.0 | 314 | 2 | B71114 | probable ferredoxi | 372 | 43.0 | 844 | 2 | A85499 | peptidoglycan synt |
| 300 | 34 | 43.0 | 324 | 2 | T34196 | hypothetical prote | 373 | 43.0 | 844 | 2 | A95648 | peptidoglycan synt |
| 301 | 34 | 43.0 | 331 | 2 | T45089 | pyruvate synthase | 374 | 43.0 | 1038 | 2 | D95252 | fucosyltransferase |
| 302 | 34 | 43.0 | 334 | 2 | F75046 | pyruvate synthase | 375 | 43.0 | 1038 | 2 | B98117 | hypothetical prote |
| 303 | 34 | 43.0 | 334 | 2 | F71114 | probable ferredoxi | 376 | 43.0 | 1144 | 2 | D82521 | hypothetical prote |
| 304 | 34 | 43.0 | 335 | 2 | E95216 | galactose operon r | 377 | 43.0 | 1178 | 1 | A39804 | thrombospondin pre |
| 305 | 34 | 43.0 | 335 | 2 | C98080 | hypothetical prote | 378 | 43.0 | 1245 | 2 | D71613 | GAF domain protein |
| 306 | 34 | 43.0 | 336 | 2 | A43260 | glycerolaldehyde-3-p | 379 | 43.0 | 1579 | 2 | T30516 | type II DNA topois |
| 307 | 34 | 43.0 | 340 | 2 | G63181 | adenylosuccinate s | 380 | 43.0 | 1865 | 1 | I48155 | transcription init |
| 308 | 34 | 43.0 | 345 | 2 | S36518 | E2 protein - human | 381 | 43.0 | 2339 | 2 | A45597 | DNA-directed RNA p |
| 309 | 34 | 43.0 | 349 | 2 | C69583 | alcohol dehydrogen | 382 | 43.0 | 2581 | 2 | AF2545 | hypothetical prote |
| 310 | 34 | 43.0 | 350 | 2 | I46608 | MHC PD6-glycoprote | 383 | 43.0 | 1033 | 2 | PH1045 | Ig light chain V r |
| 311 | 34 | 43.0 | 355 | 2 | A83322 | hypothetical prote | 384 | 43.0 | 133 | 2 | S40324 | Ig kappa chain V r |
| 312 | 34 | 43.0 | 365 | 2 | T07151 | G-box binding fact | 385 | 43.0 | 266 | 2 | D84282 | hypothetical prote |
| 313 | 34 | 43.0 | 369 | 2 | T47259 | probable protein d | 386 | 43.0 | 423 | 2 | AH0334 | probable long-chai |
| 314 | 34 | 43.0 | 370 | 1 | W2WL39 | E2 protein - human | 387 | 43.0 | 664 | 2 | T47481 | receptor-like prot |
| 315 | 34 | 43.0 | 377 | 2 | S61892 | polysaccharide exp | 388 | 43.0 | 758 | 2 | T16800 | hypothetical prote |
| 316 | 34 | 43.0 | 378 | 2 | T47407 | hypothetical prote | 389 | 43.0 | 1155 | 2 | B96761 | probable protein k |
| 317 | 34 | 43.0 | 386 | 2 | AE0576 | probable aminotran | 390 | 43.0 | 1157 | 2 | C96761 | hypothetical prote |
| 318 | 34 | 43.0 | 386 | 2 | T32240 | hypothetical prote | 391 | 43.0 | 1187 | 2 | C84568 | hypothetical prote |
| 319 | 34 | 43.0 | 416 | 2 | T23977 | hypothetical prote | 392 | 43.0 | 49 | 2 | S49365 | Ig mu chain trans |
| 320 | 34 | 43.0 | 416 | 2 | G83656 | hypothetical prote | 393 | 43.0 | 82 | 2 | AH0205 | hypothetical prote |
| 321 | 34 | 43.0 | 421 | 2 | AG2587 | lytic murein trans | 394 | 43.0 | 88 | 2 | PC4238 | heat shock protein |

395 33 41.8 89 2 C55587
396 33 41.8 94 2 JCL1479
397 33 41.8 94 2 A49855
398 33 41.8 94 2 A83720
399 33 41.8 108 2 A85844
400 33 41.8 116 2 S06614
401 33 41.8 132 2 H86682
402 33 41.8 146 2 T51473
403 33 41.8 149 1 MCPF
404 33 41.8 149 1 MCTE
405 33 41.8 149 2 S28954
406 33 41.8 149 2 JCL1309
407 33 41.8 150 2 D87652
408 33 41.8 151 2 C95069
409 33 41.8 157 2 JF0075
410 33 41.8 169 2 D84864
411 33 41.8 178 1 TVRTBM
412 33 41.8 187 2 A64542
413 33 41.8 187 2 D71967
414 33 41.8 209 2 T01336
415 33 41.8 226 4 A27279
416 33 41.8 228 2 C87184
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419 33 41.8 241 2 A40975
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421 33 41.8 247 2 T02920
422 33 41.8 247 2 T09757
423 33 41.8 248 2 T14926
424 33 41.8 254 1 G64045
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426 33 41.8 261 1 A34955
427 33 41.8 261 1 KURTB
428 33 41.8 261 1 S00234
429 33 41.8 275 2 T46825
430 33 41.8 276 1 VCMQTN
431 33 41.8 282 2 A52246
432 33 41.8 282 2 F98110
433 33 41.8 282 2 A99205
434 33 41.8 283 2 C64379
435 33 41.8 284 2 T12238
436 33 41.8 286 2 T22444
437 33 41.8 286 2 C64413
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447 33 41.8 316 2 T15395
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454 33 41.8 336 2 F75540
455 33 41.8 339 2 S70218
456 33 41.8 340 2 AG0850
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459 33 41.8 346 2 H96807
460 33 41.8 349 2 S15011
461 33 41.8 350 2 B81803
462 33 41.8 352 1 A39834
463 33 41.8 360 2 JN0921
464 33 41.8 361 2 I48160
465 33 41.8 366 2 D75289
466 33 41.8 367 1 DJPS3P
467 33 41.8 367 2 E81065

acyl carrier prote
heat shock protein
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N5,N10-methylenete
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sidd protein - Sal
pathogenicity isla
ssdp protein - Sal
hypothetical prote
probable endo-1,3-
mbhl protein - mou
probable secreted
actin-capping prot
fimbriin precursor
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hypothetical prote
DNA-directed DNA p
proteinase, probab

468 33 41.8 368 2 J01613
469 33 41.8 372 2 C87268
470 33 41.8 372 2 A83167
471 33 41.8 375 2 F64565
472 33 41.8 382 2 C71861
473 33 41.8 382 2 A84339
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523 33 41.8 551 2 T39092
524 33 41.8 557 2 A56690
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532 33 41.8 595 2 H81044
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536 33 41.8 620 2 T02840
537 33 41.8 621 2 T38467
538 33 41.8 621 2 T48187
539 33 41.8 631 2 T35234
540 33 41.8 631 2 T35234

cyanide hydratase
DNA polymerase III
conserved hypothet
spore coat polysac
probable sugar nuc
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E2 protein - huma
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xylose isomerase (
3-oxoacyl-l-acyl-ca
modification methy
3-isopropylmalate
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glutamate-1-semial
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UDP-N-acetylmurano
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VP5 protein - huma
probable outer mem
probable type III
nucleolar protein
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hypothetical prote
cellulase (EC 3.2.
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hypothetical prote
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hypothetical prote
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penicillin binding
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hypothetical prote
probable membrane
low density lipopr
hypothetical prote
probable secreted

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|-----|------|------|------|---|---------|---------------------|-----|------|------|------|---|--------|----------------------|
| 541 | 33 | 41.8 | 642 | 2 | E89996 | hypothetical prote | 614 | 32.5 | 41.1 | 120 | 2 | A29775 | Ig kappa chain pre |
| 542 | 33 | 41.8 | 646 | 2 | S64115 | hypothetical prote | 615 | 32.5 | 41.1 | 120 | 2 | B29775 | Ig kappa chain pre |
| 543 | 33 | 41.8 | 648 | 2 | A57284 | spermatid perinuc | 616 | 32.5 | 41.1 | 132 | 2 | S40322 | Ig kappa chain - h |
| 544 | 33 | 41.8 | 664 | 2 | S02116 | RNA helicase MSL1 | 617 | 32.5 | 41.1 | 134 | 2 | S40376 | Ig kappa chain - h |
| 545 | 33 | 41.8 | 695 | 2 | A13129 | hypothetical prote | 618 | 32.5 | 41.1 | 164 | 2 | AE1644 | probable cellsurfa |
| 546 | 33 | 41.8 | 697 | 2 | JN0602 | rfb protein - Esch | 619 | 32.5 | 41.1 | 164 | 2 | AF1281 | probable cellsurfa |
| 547 | 33 | 41.8 | 710 | 2 | D96728 | hypothetical prote | 620 | 32.5 | 41.1 | 294 | 2 | T04293 | hypothetical prote |
| 548 | 33 | 41.8 | 715 | 2 | AB2210 | anthranilate synth | 621 | 32.5 | 41.1 | 337 | 2 | AB3440 | acetylpermidine d |
| 549 | 33 | 41.8 | 718 | 2 | D84675 | hypothetical prote | 622 | 32.5 | 41.1 | 343 | 2 | AD0733 | probable bacteriop |
| 550 | 33 | 41.8 | 727 | 2 | H98157 | periplasmic alpha- | 623 | 32.5 | 41.1 | 752 | 2 | F84192 | phosphoenolpyruvat |
| 551 | 33 | 41.8 | 729 | 2 | A37191 | glutamate-ammonia | 624 | 32.5 | 41.1 | 2103 | 1 | QJ1621 | genome polyprotein |
| 552 | 33 | 41.8 | 732 | 1 | JC4655 | acylaminoacyl-pept | 625 | 32.5 | 41.1 | 2167 | 2 | AF1489 | cell wall-associated |
| 553 | 33 | 41.8 | 732 | 1 | JU00132 | acylaminoacyl-pept | 626 | 32.5 | 41.1 | 2910 | 2 | T28156 | DNA-directed RNA p |
| 554 | 33 | 41.8 | 751 | 1 | WMXRGB | probable core prot | 627 | 32 | 40.5 | 63 | 2 | H85778 | hypothetical prote |
| 555 | 33 | 41.8 | 771 | 2 | A87532 | glucoamylase [impo | 628 | 32 | 40.5 | 63 | 2 | D90930 | hypothetical prote |
| 556 | 33 | 41.8 | 778 | 2 | H95046 | MutS2 family prote | 629 | 32 | 40.5 | 63 | 2 | A64929 | hypothetical prote |
| 557 | 33 | 41.8 | 778 | 2 | H97917 | DNA mismatch repai | 630 | 32 | 40.5 | 99 | 2 | D69060 | hypothetical prote |
| 558 | 33 | 41.8 | 797 | 2 | T50072 | hypothetical prote | 631 | 32 | 40.5 | 104 | 2 | T13628 | hypothetical prote |
| 559 | 33 | 41.8 | 800 | 2 | AB1129 | Internalin A [impo | 632 | 32 | 40.5 | 108 | 2 | S31944 | penicillin-binding |
| 560 | 33 | 41.8 | 800 | 2 | S37387 | Internalin A precu | 633 | 32 | 40.5 | 108 | 2 | S31946 | penicillin-binding |
| 561 | 33 | 41.8 | 805 | 2 | T06657 | hypothetical prote | 634 | 32 | 40.5 | 108 | 2 | F85691 | unknown protein en |
| 562 | 33 | 41.8 | 810 | 2 | T00368 | hypothetical prote | 635 | 32 | 40.5 | 108 | 2 | A99822 | hypothetical prote |
| 563 | 33 | 41.8 | 812 | 2 | AG3138 | fimbrial usher pro | 636 | 32 | 40.5 | 111 | 1 | KVMS50 | Ig kappa chain v r |
| 564 | 33 | 41.8 | 812 | 2 | D98149 | hypothetical prote | 637 | 32 | 40.5 | 115 | 1 | K2HUCM | Ig kappa chain v r |
| 565 | 33 | 41.8 | 829 | 2 | S50246 | SIP4 protein - yea | 638 | 32 | 40.5 | 115 | 1 | K3HUI5 | Ig kappa chain pre |
| 566 | 33 | 41.8 | 831 | 2 | T05771 | beta-galactosidase | 639 | 32 | 40.5 | 126 | 2 | S40341 | Ig kappa chain - h |
| 567 | 33 | 41.8 | 837 | 2 | B89583 | protein K07E3.2 [i | 640 | 32 | 40.5 | 129 | 2 | H82735 | hypothetical prote |
| 568 | 33 | 41.8 | 844 | 2 | B71944 | septum formation p | 641 | 32 | 40.5 | 130 | 2 | S40360 | Ig kappa chain - h |
| 569 | 33 | 41.8 | 856 | 2 | T10585 | serine proteinase | 642 | 32 | 40.5 | 133 | 2 | E84669 | hypothetical prote |
| 570 | 33 | 41.8 | 858 | 2 | S56205 | probable membrane | 643 | 32 | 40.5 | 134 | 1 | K4HUI7 | Ig kappa chain pre |
| 571 | 33 | 41.8 | 891 | 2 | H83218 | heme acquisition p | 644 | 32 | 40.5 | 135 | 2 | S78051 | Ig heavy chain pre |
| 572 | 33 | 41.8 | 897 | 1 | A39255 | cytokine receptor | 645 | 32 | 40.5 | 142 | 2 | C39610 | BET1 protein - Yea |
| 573 | 33 | 41.8 | 905 | 2 | G84582 | hypothetical prote | 646 | 32 | 40.5 | 149 | 1 | MC2QF | calmodulin - malar |
| 574 | 33 | 41.8 | 926 | 2 | H84415 | DNA-directed RNA p | 647 | 32 | 40.5 | 151 | 2 | H82654 | single-stranded DN |
| 575 | 33 | 41.8 | 929 | 2 | H84582 | hypothetical prote | 648 | 32 | 40.5 | 151 | 2 | AG1784 | ribose 5-phosphate |
| 576 | 33 | 41.8 | 938 | 2 | AF1772 | hypothetical prote | 649 | 32 | 40.5 | 154 | 2 | C72152 | Bi9L protein - var |
| 577 | 33 | 41.8 | 957 | 2 | H82261 | hemolysin-like pr | 650 | 32 | 40.5 | 155 | 2 | H91284 | hypothetical prote |
| 578 | 33 | 41.8 | 960 | 2 | AF1940 | isoleucyl-tRNA syn | 651 | 32 | 40.5 | 155 | 2 | B86126 | hypothetical prote |
| 579 | 33 | 41.8 | 966 | 2 | F84582 | hypothetical prote | 652 | 32 | 40.5 | 164 | 2 | B97704 | dihydrofolate redu |
| 580 | 33 | 41.8 | 972 | 1 | A33926 | DNA-directed RNA p | 653 | 32 | 40.5 | 167 | 2 | H84812 | hypothetical prote |
| 581 | 33 | 41.8 | 1002 | 2 | D87077 | probable long-chain | 654 | 32 | 40.5 | 167 | 2 | AB2180 | DnaJ protein [impo |
| 582 | 33 | 41.8 | 1070 | 2 | T06733 | kinasin homolog F2 | 655 | 32 | 40.5 | 168 | 2 | A75113 | hypothetical prote |
| 583 | 33 | 41.8 | 1088 | 2 | B85068 | UV-damaged DNA bin | 656 | 32 | 40.5 | 174 | 2 | D54543 | MHC class I histoc |
| 584 | 33 | 41.8 | 1102 | 2 | T04941 | UV-damaged DNA-bin | 657 | 32 | 40.5 | 186 | 2 | D64533 | hypothetical prote |
| 585 | 33 | 41.8 | 1113 | 2 | S48495 | probable membrane | 658 | 32 | 40.5 | 189 | 2 | AG3270 | 16S ribosomal RNA |
| 586 | 33 | 41.8 | 1143 | 2 | T22952 | hypothetical prote | 659 | 32 | 40.5 | 191 | 2 | A81305 | probable purine/py |
| 587 | 33 | 41.8 | 1222 | 2 | S40977 | hypothetical prote | 660 | 32 | 40.5 | 193 | 2 | B83811 | hypothetical prote |
| 588 | 33 | 41.8 | 1238 | 2 | T15919 | hypothetical prote | 661 | 32 | 40.5 | 194 | 2 | H69438 | hypothetical prote |
| 589 | 33 | 41.8 | 1310 | 2 | AD1380 | glycosidase homolo | 662 | 32 | 40.5 | 197 | 1 | A44597 | endo-1,4-beta-xyla |
| 590 | 33 | 41.8 | 1313 | 2 | B96509 | protein F27F5.11 [| 663 | 32 | 40.5 | 199 | 2 | AB2847 | conserved hypotet |
| 591 | 33 | 41.8 | 1408 | 2 | H69068 | cell surface glyco | 664 | 32 | 40.5 | 201 | 2 | D36838 | D13L protein - var |
| 592 | 33 | 41.8 | 1477 | 2 | S64616 | YOR1 protein - yea | 665 | 32 | 40.5 | 204 | 2 | D84809 | hypothetical prote |
| 593 | 33 | 41.8 | 1634 | 1 | JC5500 | phosphoinositide 3 | 666 | 32 | 40.5 | 206 | 2 | AD1644 | probable cellsurfa |
| 594 | 33 | 41.8 | 1744 | 2 | JH0720 | tanabin - African | 667 | 32 | 40.5 | 207 | 2 | BA4994 | eggshell protein 2 |
| 595 | 33 | 41.8 | 1755 | 2 | F82618 | chemotaxis-related | 668 | 32 | 40.5 | 209 | 2 | G10156 | iron-starvation pr |
| 596 | 33 | 41.8 | 1904 | 2 | T13256 | tail-host specific | 669 | 32 | 40.5 | 211 | 2 | S47347 | outer membrane pr |
| 597 | 33 | 41.8 | 2032 | 2 | I39917 | hypothetical prote | 670 | 32 | 40.5 | 212 | 2 | T44321 | hypothetical prote |
| 598 | 33 | 41.8 | 2133 | 2 | T42763 | coagulation factor | 671 | 32 | 40.5 | 212 | 2 | A44994 | eggshell protein 1 |
| 599 | 33 | 41.8 | 2183 | 2 | T37218 | hypothetical prote | 672 | 32 | 40.5 | 212 | 2 | B90035 | hypothetical prote |
| 600 | 33 | 41.8 | 2251 | 2 | T24490 | hypothetical prote | 673 | 32 | 40.5 | 214 | 2 | B96755 | hypothetical prote |
| 601 | 33 | 41.8 | 2610 | 2 | T20968 | hypothetical prote | 674 | 32 | 40.5 | 216 | 2 | JE0241 | Ig kappa chain Am3 |
| 602 | 33 | 41.8 | 2718 | 2 | A23475 | G surface protein | 675 | 32 | 40.5 | 216 | 2 | H87621 | DnaJ-related prote |
| 603 | 33 | 41.8 | 3263 | 2 | E82410 | hypothetical prote | 676 | 32 | 40.5 | 217 | 2 | H72350 | hypothetical prote |
| 604 | 33 | 41.8 | 3535 | 2 | E83641 | probable hemagglut | 677 | 32 | 40.5 | 217 | 2 | QJ1358 | Cl protein - Misca |
| 605 | 33 | 41.8 | 3972 | 2 | S75251 | hypothetical prote | 678 | 32 | 40.5 | 218 | 2 | D75482 | phosphoribosyl-AMP |
| 606 | 33 | 41.8 | 4199 | 2 | S76412 | hypothetical prote | 679 | 32 | 40.5 | 220 | 2 | A75287 | response regulator |
| 607 | 33 | 41.8 | 4767 | 2 | T31345 | hypothetical prote | 680 | 32 | 40.5 | 221 | 2 | T28451 | hypothetical prote |
| 608 | 33 | 41.8 | 5627 | 2 | C83339 | hypothetical prote | 681 | 32 | 40.5 | 226 | 2 | E70809 | hypothetical prote |
| 609 | 32.5 | 41.1 | 85 | 2 | S44901 | ZK652.1 protein - | 682 | 32 | 40.5 | 227 | 1 | IDBP44 | DNA polymerase acc |
| 610 | 32.5 | 41.1 | 88 | 2 | T14082 | hypothetical prote | 683 | 32 | 40.5 | 227 | 2 | B97624 | hypothetical prote |
| 611 | 32.5 | 41.1 | 112 | 1 | KVMS16 | Ig kappa chain v r | 684 | 32 | 40.5 | 229 | 2 | AB0220 | flagellar l-ring p |
| 612 | 32.5 | 41.1 | 113 | 1 | KVMS51 | Ig kappa chain v r | 685 | 32 | 40.5 | 230 | 2 | E81820 | heme utilisation p |
| 613 | 32.5 | 41.1 | 120 | 1 | KVMS67 | Ig kappa chain pre | 686 | 32 | 40.5 | 230 | 2 | B82456 | probable acetyltra |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|--------|--------------------|-----|----|------|-----|---|--------|---------------------|
| 687 | 32 | 40.5 | 231 | 2 | F75600 | CoA transferase, s | 760 | 32 | 40.5 | 414 | 2 | H97601 | hypothetical prote |
| 688 | 32 | 40.5 | 232 | 2 | AE0640 | flagellar L-ring p | 761 | 32 | 40.5 | 414 | 2 | AI2823 | aminotransferase l |
| 689 | 32 | 40.5 | 232 | 2 | AY9811 | flagellar basal bo | 762 | 32 | 40.5 | 414 | 2 | A44654 | dolichyl-diphospho |
| 690 | 32 | 40.5 | 232 | 2 | D64851 | flagellar basal bo | 763 | 32 | 40.5 | 422 | 2 | T16641 | hypothetical prote |
| 691 | 32 | 40.5 | 232 | 2 | E85670 | flagellar basal bo | 764 | 32 | 40.5 | 424 | 2 | D71496 | probable enolase - |
| 692 | 32 | 40.5 | 232 | 2 | A30930 | flagellar basal bo | 765 | 32 | 40.5 | 424 | 2 | E72333 | thiamin biosynthes |
| 693 | 32 | 40.5 | 232 | 2 | S54643 | hypothetical prote | 766 | 32 | 40.5 | 424 | 2 | S11676 | spore coat protein |
| 694 | 32 | 40.5 | 232 | 2 | H87583 | hypothetical prote | 767 | 32 | 40.5 | 427 | 2 | AI3490 | membrane-bound lyt |
| 695 | 32 | 40.5 | 234 | 2 | S28482 | rflB protein - Vib | 768 | 32 | 40.5 | 429 | 2 | S29044 | endoglucanase A pr |
| 696 | 32 | 40.5 | 243 | 1 | OBUNMP | cytochrome-c oxida | 769 | 32 | 40.5 | 433 | 2 | H87660 | peptidoglycan-bind |
| 697 | 32 | 40.5 | 246 | 2 | S47805 | hypothetical prote | 770 | 32 | 40.5 | 435 | 2 | A86195 | hypothetical prote |
| 698 | 32 | 40.5 | 247 | 2 | H82348 | hypothetical prote | 771 | 32 | 40.5 | 439 | 2 | S19656 | protein disulfide- |
| 699 | 32 | 40.5 | 248 | 2 | I39659 | modification methy | 772 | 32 | 40.5 | 442 | 2 | T49906 | hypothetical prote |
| 700 | 32 | 40.5 | 249 | 2 | E63546 | conserved hypothet | 773 | 32 | 40.5 | 444 | 2 | H81437 | trigger factor tig |
| 701 | 32 | 40.5 | 250 | 2 | T18862 | hypothetical prote | 774 | 32 | 40.5 | 448 | 2 | D83145 | hypothetical prote |
| 702 | 32 | 40.5 | 251 | 2 | AI3542 | pseudouridylate sy | 775 | 32 | 40.5 | 452 | 2 | S36482 | E2 protein - human |
| 703 | 32 | 40.5 | 251 | 2 | T24485 | hypothetical prote | 776 | 32 | 40.5 | 453 | 2 | D93760 | conserved hypothet |
| 704 | 32 | 40.5 | 255 | 2 | F90878 | hypothetical prote | 777 | 32 | 40.5 | 454 | 2 | A43501 | sucrose-6-phosphat |
| 705 | 32 | 40.5 | 255 | 2 | D85740 | partial probable o | 778 | 32 | 40.5 | 463 | 2 | F85361 | hypothetical prote |
| 706 | 32 | 40.5 | 261 | 2 | A40579 | trans-activating t | 779 | 32 | 40.5 | 464 | 2 | S50592 | hypothetical prote |
| 707 | 32 | 40.5 | 266 | 2 | T10609 | hypothetical prote | 780 | 32 | 40.5 | 468 | 2 | AC1996 | hypothetical prote |
| 708 | 32 | 40.5 | 271 | 2 | G87071 | hypothetical prote | 781 | 32 | 40.5 | 468 | 2 | T10595 | hypothetical prote |
| 709 | 32 | 40.5 | 273 | 2 | F69903 | D-alanyl-D-alanine | 782 | 32 | 40.5 | 469 | 2 | A35789 | glutamate-1-semial |
| 710 | 32 | 40.5 | 279 | 2 | G70807 | hypothetical prote | 783 | 32 | 40.5 | 469 | 2 | D84857 | hypothetical prote |
| 711 | 32 | 40.5 | 285 | 2 | T15133 | hypothetical prote | 784 | 32 | 40.5 | 472 | 2 | T46217 | glutamate-1-semial |
| 712 | 32 | 40.5 | 286 | 2 | T16241 | hypothetical prote | 785 | 32 | 40.5 | 473 | 1 | T26280 | linoleoyl-CoA desa |
| 713 | 32 | 40.5 | 289 | 1 | S72862 | cysQ homolog - Myc | 786 | 32 | 40.5 | 473 | 2 | S36242 | penicillin-binding |
| 714 | 32 | 40.5 | 293 | 2 | S50109 | vitellogenin gene- | 787 | 32 | 40.5 | 474 | 2 | F97264 | 6-Phospho-Beta-D-G |
| 715 | 32 | 40.5 | 294 | 2 | E86900 | transcription regu | 788 | 32 | 40.5 | 475 | 2 | AC1246 | branched-chain alp |
| 716 | 32 | 40.5 | 298 | 2 | C96690 | unknown protein F2 | 789 | 32 | 40.5 | 484 | 2 | T34504 | hypothetical prote |
| 717 | 32 | 40.5 | 303 | 2 | G02360 | chytotroph embryon | 790 | 32 | 40.5 | 486 | 2 | B35965 | penicillin-binding |
| 718 | 32 | 40.5 | 304 | 2 | C90453 | hypothetical prote | 791 | 32 | 40.5 | 488 | 2 | AI1930 | proteinase [import |
| 719 | 32 | 40.5 | 313 | 2 | G69498 | calcium-binding pr | 792 | 32 | 40.5 | 489 | 2 | A45988 | dentin matrix acid |
| 720 | 32 | 40.5 | 313 | 2 | A41524 | transcription fact | 793 | 32 | 40.5 | 491 | 2 | T50950 | hypothetical prote |
| 721 | 32 | 40.5 | 315 | 2 | T10613 | hypothetical prote | 794 | 32 | 40.5 | 499 | 2 | G82753 | two-component syst |
| 722 | 32 | 40.5 | 317 | 2 | S54548 | hypothetical prote | 795 | 32 | 40.5 | 500 | 2 | G71836 | anthranilate synth |
| 723 | 32 | 40.5 | 323 | 2 | H89923 | hypothetical prote | 796 | 32 | 40.5 | 500 | 2 | B64680 | anthranilate synth |
| 724 | 32 | 40.5 | 325 | 2 | S57089 | hypothetical prote | 797 | 32 | 40.5 | 509 | 2 | T29303 | hypothetical prote |
| 725 | 32 | 40.5 | 326 | 2 | AF2024 | hypothetical prote | 798 | 32 | 40.5 | 509 | 2 | D86146 | F22i4.11 protein - |
| 726 | 32 | 40.5 | 328 | 2 | S73860 | 6-phosphofructokin | 799 | 32 | 40.5 | 510 | 2 | T30420 | hypothetical prote |
| 727 | 32 | 40.5 | 333 | 2 | H82245 | glyceraldehide 3-p | 800 | 32 | 40.5 | 515 | 2 | H72455 | hypothetical prote |
| 728 | 32 | 40.5 | 336 | 2 | T44605 | F420-dependent glu | 801 | 32 | 40.5 | 515 | 2 | T45644 | hypothetical prote |
| 729 | 32 | 40.5 | 337 | 2 | T43372 | Chromo domain prot | 802 | 32 | 40.5 | 518 | 2 | E71663 | protein-export mem |
| 730 | 32 | 40.5 | 340 | 2 | T05120 | hypothetical prote | 803 | 32 | 40.5 | 520 | 2 | T41709 | BRC domain contai |
| 731 | 32 | 40.5 | 345 | 2 | AG3500 | phosphate-binding | 804 | 32 | 40.5 | 523 | 2 | A82233 | anthranilate synth |
| 732 | 32 | 40.5 | 345 | 2 | A24587 | membrane antigen t | 805 | 32 | 40.5 | 530 | 2 | A42605 | halolysin (EC 3.4. |
| 733 | 32 | 40.5 | 346 | 2 | T51728 | hypothetical prote | 806 | 32 | 40.5 | 532 | 2 | C96514 | hypothetical prote |
| 734 | 32 | 40.5 | 348 | 2 | C70417 | phosphate starvati | 807 | 32 | 40.5 | 533 | 1 | S71778 | calcium-dependent |
| 735 | 32 | 40.5 | 350 | 2 | S61426 | late embryogenesis | 808 | 32 | 40.5 | 537 | 2 | F90465 | medium-chain-fatty |
| 736 | 32 | 40.5 | 354 | 2 | H70608 | probable succinyl- | 809 | 32 | 40.5 | 576 | 2 | B84386 | glycine-tRNA synth |
| 737 | 32 | 40.5 | 360 | 2 | S06287 | fragmin - slime mo | 810 | 32 | 40.5 | 586 | 1 | VGWNB | nonstructural glyco |
| 738 | 32 | 40.5 | 361 | 2 | B59099 | hypothetical prote | 811 | 32 | 40.5 | 598 | 2 | T42070 | protein serine/thr |
| 739 | 32 | 40.5 | 370 | 2 | S36558 | E2 protein - human | 812 | 32 | 40.5 | 600 | 2 | S76764 | hypothetical prote |
| 740 | 32 | 40.5 | 371 | 2 | S70728 | mxg protein - Shi | 813 | 32 | 40.5 | 600 | 2 | T39516 | threonine ammonia- |
| 741 | 32 | 40.5 | 375 | 2 | S70960 | rflQRS protein - V | 814 | 32 | 40.5 | 601 | 2 | S57962 | cspC protein - Clo |
| 742 | 32 | 40.5 | 376 | 2 | D84316 | hypothetical prote | 815 | 32 | 40.5 | 605 | 1 | FWSYBA | beta-conglycinin a |
| 743 | 32 | 40.5 | 377 | 2 | C64888 | outer membrane por | 816 | 32 | 40.5 | 605 | 2 | S20007 | beta-conglycinin a |
| 744 | 32 | 40.5 | 382 | 2 | G85234 | hypothetical prote | 817 | 32 | 40.5 | 608 | 2 | S51790 | centromere protein |
| 745 | 32 | 40.5 | 383 | 2 | A55739 | (MIC) protein MHC | 818 | 32 | 40.5 | 612 | 2 | C90419 | glucan 1,4 alpha g |
| 746 | 32 | 40.5 | 383 | 2 | H71714 | deoxyguanosinetrip | 819 | 32 | 40.5 | 614 | 2 | B41935 | spat protein - Bac |
| 747 | 32 | 40.5 | 383 | 2 | E90285 | hypothetical prote | 820 | 32 | 40.5 | 624 | 2 | T19630 | hypothetical prote |
| 748 | 32 | 40.5 | 384 | 2 | F97711 | hypothetical prote | 821 | 32 | 40.5 | 625 | 2 | E98009 | type II site-speci |
| 749 | 32 | 40.5 | 397 | 2 | AH3494 | DNA-directed DNA p | 822 | 32 | 40.5 | 625 | 2 | G95141 | type II restrictio |
| 750 | 32 | 40.5 | 397 | 2 | E82860 | hypothetical prote | 823 | 32 | 40.5 | 626 | 1 | RGBY23 | cell division cont |
| 751 | 32 | 40.5 | 398 | 2 | T21766 | hypothetical prote | 824 | 32 | 40.5 | 627 | 1 | A35836 | L-plastin - human |
| 752 | 32 | 40.5 | 398 | 2 | C83499 | probable transglyc | 825 | 32 | 40.5 | 627 | 2 | I49445 | 65K macrophage pro |
| 753 | 32 | 40.5 | 399 | 2 | T03375 | hypothetical prote | 826 | 32 | 40.5 | 635 | 2 | T00011 | ccal protein - rat |
| 754 | 32 | 40.5 | 401 | 2 | D87368 | imidazolonepropion | 827 | 32 | 40.5 | 637 | 2 | T04552 | hypothetical prote |
| 755 | 32 | 40.5 | 402 | 1 | S70969 | bundle-forming pil | 828 | 32 | 40.5 | 640 | 2 | AF0100 | general secretion |
| 756 | 32 | 40.5 | 410 | 1 | I40755 | trigger factor 2 [| 829 | 32 | 40.5 | 649 | 2 | A49512 | alpha-amylase (EC |
| 757 | 32 | 40.5 | 411 | 1 | HY5NFA | fibrolase (EC 3.4. | 830 | 32 | 40.5 | 658 | 1 | A65079 | arginine decarboxy |
| 758 | 32 | 40.5 | 411 | 2 | F97760 | hypothetical prote | 831 | 32 | 40.5 | 658 | 2 | AG0876 | arginine decarboxy |
| 759 | 32 | 40.5 | 414 | 2 | D97827 | ATP-dependent RNA | 832 | 32 | 40.5 | 658 | 2 | F91105 | biosynthetic argin |

| | | | | | | | | | | | | |
|-----|----|------|------|---|--------|-----|------|------|------|---|--------|---------------------|
| 833 | 32 | 40.5 | 658 | 2 | A85951 | 906 | 32 | 40.5 | 1101 | 2 | S15271 | endoglucanase C (E |
| 834 | 32 | 40.5 | 672 | 1 | KIBOC | 907 | 32 | 40.5 | 1117 | 2 | S33851 | fibronectin-bindin |
| 835 | 32 | 40.5 | 672 | 1 | KIHUCA | 908 | 32 | 40.5 | 1127 | 2 | E71156 | endopeptidase La h |
| 836 | 32 | 40.5 | 672 | 1 | KIMSCA | 909 | 32 | 40.5 | 1137 | 2 | JC5950 | integrin alpha-7 c |
| 837 | 32 | 40.5 | 672 | 1 | KIRBC | 910 | 32 | 40.5 | 1142 | 2 | T35103 | probable negative |
| 838 | 32 | 40.5 | 672 | 1 | KIRTC | 911 | 32 | 40.5 | 1178 | 2 | S30431 | MSP-300 protein - |
| 839 | 32 | 40.5 | 674 | 2 | S78570 | 912 | 32 | 40.5 | 1198 | 2 | T49726 | hypothetical prote |
| 840 | 32 | 40.5 | 676 | 2 | C97775 | 913 | 32 | 40.5 | 1216 | 2 | T09224 | spindle assembly c |
| 841 | 32 | 40.5 | 679 | 2 | S06000 | 914 | 32 | 40.5 | 1268 | 2 | B36502 | insulin receptor-r |
| 842 | 32 | 40.5 | 680 | 2 | G95194 | 915 | 32 | 40.5 | 1274 | 2 | A89599 | hypothetical prote |
| 843 | 32 | 40.5 | 685 | 2 | D84232 | 916 | 32 | 40.5 | 1282 | 2 | JE0120 | glycoprotein A - m |
| 844 | 32 | 40.5 | 685 | 2 | D98061 | 917 | 32 | 40.5 | 1300 | 2 | A36502 | insulin receptor-r |
| 845 | 32 | 40.5 | 694 | 2 | T01504 | 918 | 32 | 40.5 | 1357 | 2 | S57052 | hypothetical prote |
| 846 | 32 | 40.5 | 715 | 2 | G86239 | 919 | 32 | 40.5 | 1360 | 2 | F96596 | hypothetical prote |
| 847 | 32 | 40.5 | 715 | 2 | G86239 | 920 | 32 | 40.5 | 1378 | 2 | T30173 | zinc finger protei |
| 848 | 32 | 40.5 | 718 | 1 | VCPIVM | 921 | 32 | 40.5 | 1399 | 2 | G83112 | DNA-directed RNA p |
| 849 | 32 | 40.5 | 732 | 1 | S07624 | 922 | 32 | 40.5 | 1401 | 2 | G82336 | DNA-directed RNA p |
| 850 | 32 | 40.5 | 733 | 2 | AD2444 | 923 | 32 | 40.5 | 1406 | 2 | AB0456 | DNA-directed RNA p |
| 851 | 32 | 40.5 | 745 | 2 | G72453 | 924 | 32 | 40.5 | 1407 | 1 | RNECC | DNA-directed RNA p |
| 852 | 32 | 40.5 | 755 | 2 | AG3069 | 925 | 32 | 40.5 | 1407 | 2 | H84933 | DNA-directed RNA p |
| 853 | 32 | 40.5 | 755 | 2 | C98217 | 926 | 32 | 40.5 | 1407 | 2 | AD0933 | DNA-directed RNA p |
| 854 | 32 | 40.5 | 765 | 2 | B75288 | 927 | 32 | 40.5 | 1407 | 2 | G91242 | DNA-directed RNA p |
| 855 | 32 | 40.5 | 767 | 2 | A82882 | 928 | 32 | 40.5 | 1407 | 2 | D86090 | RNA polymerase, be |
| 856 | 32 | 40.5 | 767 | 2 | S63182 | 929 | 32 | 40.5 | 1407 | 2 | A42239 | adenylate cyclase |
| 857 | 32 | 40.5 | 775 | 2 | C95921 | 930 | 32 | 40.5 | 1438 | 2 | A48216 | neurexin III-alpha |
| 858 | 32 | 40.5 | 775 | 2 | E84828 | 931 | 32 | 40.5 | 1470 | 2 | B48218 | neurexin III-alpha |
| 859 | 32 | 40.5 | 777 | 2 | AD0982 | 932 | 32 | 40.5 | 1490 | 2 | S32373 | DNA-binding protei |
| 860 | 32 | 40.5 | 781 | 2 | T18693 | 933 | 32 | 40.5 | 1510 | 2 | C84727 | probable glucan sy |
| 861 | 32 | 40.5 | 783 | 2 | T37457 | 934 | 32 | 40.5 | 1560 | 2 | T09202 | probable tail comp |
| 862 | 32 | 40.5 | 784 | 2 | E84785 | 935 | 32 | 40.5 | 1571 | 2 | T14155 | zinc finger protei |
| 863 | 32 | 40.5 | 788 | 2 | C82595 | 936 | 32 | 40.5 | 1578 | 2 | A48216 | neurexin III-alpha |
| 864 | 32 | 40.5 | 789 | 2 | T45762 | 937 | 32 | 40.5 | 1626 | 2 | T09271 | phage-related prot |
| 865 | 32 | 40.5 | 796 | 2 | E88029 | 938 | 32 | 40.5 | 1645 | 2 | F96907 | probable tail comp |
| 866 | 32 | 40.5 | 800 | 2 | A84293 | 939 | 32 | 40.5 | 1650 | 2 | S53457 | dominant autoantig |
| 867 | 32 | 40.5 | 802 | 2 | G89893 | 940 | 32 | 40.5 | 1661 | 2 | S64800 | probable membrane |
| 868 | 32 | 40.5 | 808 | 1 | JQ2043 | 941 | 32 | 40.5 | 1664 | 2 | T18216 | integrin-like prot |
| 869 | 32 | 40.5 | 818 | 2 | H82165 | 942 | 32 | 40.5 | 1687 | 2 | T39072 | DNA2-NAM7 helicase |
| 870 | 32 | 40.5 | 828 | 1 | T00534 | 943 | 32 | 40.5 | 1707 | 2 | S77910 | hypothetical prote |
| 871 | 32 | 40.5 | 831 | 2 | G87620 | 944 | 32 | 40.5 | 1721 | 2 | T12114 | hypothetical prote |
| 872 | 32 | 40.5 | 832 | 2 | S55396 | 945 | 32 | 40.5 | 1780 | 2 | A85045 | probable glucan sy |
| 873 | 32 | 40.5 | 840 | 2 | AG0526 | 946 | 32 | 40.5 | 1878 | 2 | E86189 | hypothetical prote |
| 874 | 32 | 40.5 | 845 | 1 | B71255 | 947 | 32 | 40.5 | 1946 | 2 | AE1449 | hypothetical prote |
| 875 | 32 | 40.5 | 849 | 2 | T46253 | 948 | 32 | 40.5 | 1963 | 2 | T49914 | callose synthase c |
| 876 | 32 | 40.5 | 851 | 2 | B40671 | 949 | 32 | 40.5 | 1999 | 1 | S21801 | myosin heavy chain |
| 877 | 32 | 40.5 | 851 | 2 | S11508 | 950 | 32 | 40.5 | 2055 | 2 | T31110 | extracellular matr |
| 878 | 32 | 40.5 | 862 | 2 | S51493 | 951 | 32 | 40.5 | 2254 | 2 | T09053 | low voltage-activa |
| 879 | 32 | 40.5 | 863 | 2 | T49709 | 952 | 32 | 40.5 | 2334 | 2 | S32920 | cell wall-associat |
| 880 | 32 | 40.5 | 864 | 2 | A40671 | 953 | 32 | 40.5 | 2352 | 2 | T43431 | alpha-glucan synth |
| 881 | 32 | 40.5 | 866 | 2 | A11880 | 954 | 32 | 40.5 | 2551 | 2 | B98047 | hypothetical prote |
| 882 | 32 | 40.5 | 868 | 2 | AF3204 | 955 | 32 | 40.5 | 3224 | 1 | S58884 | Ran-binding protei |
| 883 | 32 | 40.5 | 879 | 2 | F96558 | 956 | 32 | 40.5 | 3248 | 2 | T17414 | TipC protein - eli |
| 884 | 32 | 40.5 | 885 | 2 | S61189 | 957 | 32 | 40.5 | 4096 | 2 | A57099 | DNA-activated prot |
| 885 | 32 | 40.5 | 888 | 2 | E71280 | 958 | 32 | 40.5 | 4660 | 2 | T42737 | gp330 protein prec |
| 886 | 32 | 40.5 | 894 | 2 | T20625 | 959 | 32 | 40.5 | 5105 | 2 | T32650 | hypothetical prote |
| 887 | 32 | 40.5 | 903 | 2 | T00358 | 960 | 31.5 | 39.9 | 101 | 2 | S34153 | IG kappa chain V-I |
| 888 | 32 | 40.5 | 919 | 1 | RNV2CA | 961 | 31.5 | 39.9 | 124 | 2 | S20633 | IG kappa chain - h |
| 889 | 32 | 40.5 | 923 | 2 | T41350 | 962 | 31.5 | 39.9 | 124 | 2 | S03876 | IG kappa chain V-I |
| 890 | 32 | 40.5 | 930 | 2 | G02083 | 963 | 31.5 | 39.9 | 133 | 1 | A24452 | IG kappa chain pre |
| 891 | 32 | 40.5 | 940 | 2 | H82159 | 964 | 31.5 | 39.9 | 271 | 2 | S30230 | homoeotic protein H |
| 892 | 32 | 40.5 | 946 | 2 | A84133 | 965 | 31.5 | 39.9 | 274 | 2 | G86276 | L-lactate permease |
| 893 | 32 | 40.5 | 958 | 2 | T51148 | 966 | 31.5 | 39.9 | 282 | 2 | F84267 | F14117.2 protein - |
| 894 | 32 | 40.5 | 963 | 2 | A57238 | 967 | 31.5 | 39.9 | 348 | 1 | T26381 | purple acid phosph |
| 895 | 32 | 40.5 | 965 | 2 | T50670 | 968 | 31.5 | 39.9 | 354 | 2 | S33309 | GTP-binding regula |
| 896 | 32 | 40.5 | 971 | 2 | H71719 | 969 | 31.5 | 39.9 | 388 | 2 | T43183 | probable 26S prote |
| 897 | 32 | 40.5 | 976 | 2 | A97104 | 970 | 31.5 | 39.9 | 409 | 2 | T37976 | probable proteasom |
| 898 | 32 | 40.5 | 980 | 2 | T05414 | 971 | 31.5 | 39.9 | 430 | 2 | B83633 | hypothetical prote |
| 899 | 32 | 40.5 | 985 | 2 | G87351 | 972 | 31.5 | 39.9 | 463 | 1 | T26378 | acid phosphatase (|
| 900 | 32 | 40.5 | 1001 | 2 | T28897 | 973 | 31.5 | 39.9 | 483 | 2 | H97246 | UDP-N-acetylmuram |
| 901 | 32 | 40.5 | 1012 | 2 | T23160 | 974 | 31.5 | 39.9 | 497 | 2 | S31477 | finger protein zfp |
| 902 | 32 | 40.5 | 1023 | 2 | T30257 | 975 | 31.5 | 39.9 | 522 | 2 | H72267 | conserved hypothet |
| 903 | 32 | 40.5 | 1026 | 2 | T19631 | 976 | 31.5 | 39.9 | 536 | 2 | H72268 | conserved hypothet |
| 904 | 32 | 40.5 | 1035 | 2 | G87373 | 977 | 31.5 | 39.9 | 586 | 2 | JQ0184 | old protein - phag |
| 905 | 32 | 40.5 | 1091 | 2 | T48444 | 978 | 31.5 | 39.9 | 666 | 2 | S56781 | hypothetical prote |

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979 31.5 39.9 941 2 I40772
980 31.5 39.9 946 2 F81361
981 31.5 39.9 953 2 T01093
982 31.5 39.9 1025 2 S50293
983 31.5 39.9 1175 2 S39951
984 31.5 39.9 1434 2 C90109
985 31.5 39.9 1446 2 T10916
986 31.5 39.9 1689 2 J50080
987 31.5 39.9 2037 2 S37178
988 31 39.2 63 2 A86910
989 31 39.2 67 2 I39617
990 31 39.2 74 2 B85600
991 31 39.2 74 2 F90749
992 31 39.2 74 2 H64826
993 31 39.2 83 2 S66246
994 31 39.2 90 2 S15149
995 31 39.2 95 2 S76543
996 31 39.2 96 4 I38165
997 31 39.2 98 1 F8EF
998 31 39.2 98 1 FESG
999 31 39.2 98 1 FESGAL
1000 31 39.2 100 2 S55163

hypotheical prote
probable cell divi
luminiddependens pr
probable membrane
chitin synthase (E
DNA-directed RNA p
carboxypeptidase D
DNA-directed RNA p
fatty-acyl-CoA syn
hypotheical prote
cold shock protein
cold shock protein
nuclear factor int
hypotheical prote
hypotheical RLF/M
ferredoxin [2Fe-2S
ferredoxin [2Fe-2S
hypotheical prote

ALIGNMENTS

RESULT 1
S42193
Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 07-Oct-1994 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C:Accession: S42193
R:Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec
A:Reference number: S42176; MUID:94009207; PMID:7691608
A:Accession: S42193
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-81 <MOJ>
A:Cross-references: UNIPARC:UPI0000116566; EMBL:Z25456; NID:G407846; PIDN:CAA80943.1; PI
A:Note: the authors translated the codon GTT for residue 36 as Ala
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 79; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVYDGDGYNN 15
Db 6 KASQSVYDGDGYNN 20

RESULT 2
A38601
Ig kappa chain V region (IG3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
C:Accession: A38601
R:Goshorn, S.C.; Retzel, E.; Jemerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same antigen
A:Reference number: A38601; MUID:91115823; PMID:1703527
A:Accession: A38601
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-93 <GOS>
A:Cross-references: UNIPARC:UPI0000115175; GB:M57978; NID:G196402; PIDN:AAA63359.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
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Query Match 100.0%; Score 79; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVYDGDGYNN 15
Db 5 KASQSVYDGDGYNN 19

RESULT 3
KVMS08
Ig kappa chain V region (PC6308) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: C01937; A01937
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152; PMID:103003
A:Accession: C01937
A:Molecule type: protein
A:Residues: 1-111 <WEI>
A:Cross-references: UNIPROT:P01667; UNIPARC:UPI000002A102
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (Kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 79; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVYDGDGYNN 15
Db 24 KASQSVYDGDGYNN 38

RESULT 4
KVMS43
Ig kappa chain V region (PC7043) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C:Accession: A01937; S42187; S42194; S42190; S42189; S42188; S42191; S42192
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152; PMID:103003
A:Accession: A01937
A:Molecule type: protein
A:Residues: 1-111 <WEI>
A:Cross-references: UNIPROT:P01665; UNIPARC:UPI000002A100
R:Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec
A:Reference number: S42176; MUID:94009207; PMID:7691608
A:Accession: S42187
A:Molecule type: DNA
A:Residues: 10-99 <MOJ>
A:Cross-references: UNIPARC:UPI000011655C; EMBL:Z25444; NID:G407832; PIDN:CAA80931.1; PI
A:Note: V-kappa-21B; anti-collagen
A:Accession: S42194
A:Molecule type: DNA
A:Residues: 12-99 <MOW>
A:Cross-references: UNIPARC:UPI000011655E; EMBL:Z25458; NID:G407844; PIDN:CAA80945.1; PI
A:Note: V-kappa-21E; anti-collagen
A:Accession: S42190
A:Molecule type: DNA
A:Residues: 13-99 <MOF>
A:Cross-references: UNIPARC:UPI0000116562; EMBL:Z25450; NID:G407838; PIDN:CAA80937.1; PI
A:Note: V-kappa-21B; anti-collagen
A:Accession: S42189
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A.Molecule type: DNA
A.Residues: 15-99 <MOA>
A:Cross-references: UNIPARC:UPI0000116560; EMBL:Z25448; NID:G407836; PIDN:CAA80935.1; PI
A>Note: V-kappa-21E; anti-collagen
A.Accession: S42188
A.Molecule type: DNA
A.Residues: 12-99 <MOZ>
A:Cross-references: UNIPARC:UPI000011655E; EMBL:Z25446; NID:G407834; PIDN:CAA80933.1; PI
A>Note: V-kappa-21E; anti-collagen
A.Accession: S42191
A.Molecule type: DNA
A.Residues: 10-99 <MOY>
A:Cross-references: UNIPARC:UPI000011655C; EMBL:Z25452; NID:G407840; PIDN:CAA80939.1; PI
A>Note: V-kappa-21E; anti-collagen
A.Accession: S42192
A.Molecule type: DNA
A.Residues: 10-99 <MOO>
A:Cross-references: UNIPARC:UPI000011655C; EMBL:Z25454; NID:G407842; PIDN:CAA80941.1; PI
A>Note: V-kappa-21E; anti-collagen
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 79; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDPDGDSDSYN 15
DB 24 KASQSVDPDGDSDSYN 38
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RESULT 5
KWS69
Ig kappa chain V region (PC7769) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C.Accession: E01937; A01937
R.Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A>Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152; PMID:103003
A.Accession: E01937
A.Molecule type: protein
A.Residues: 1-111 <WEI>
A:Cross-references: UNIPROT:P01669; UNIPARC:UPI000002A104
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 79; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDPDGDSDSYN 15
DB 24 KASQSVDPDGDSDSYN 38
|||||:|||||

RESULT 6
KWS83
Ig kappa chain V region (PC7183) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C.Accession: E01937; A01937
R.Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978

Query Match 100.0%; Score 79; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDPDGDSDSYN 15
DB 24 KASQSVDPDGDSDSYN 38
|||||:|||||

RESULT 7
KWS10
Ig kappa chain V region (PC7210) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C.Accession: D01937; A01937
R.Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A>Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152; PMID:103003
A.Accession: D01937
A.Molecule type: protein
A.Residues: 1-110 <WEI>
A:Cross-references: UNIPROT:P01668; UNIPARC:UPI000002A103
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 96.2%; Score 76; DB 1; Length 110;
Best Local Similarity 93.3%; Pred. No. 1.5e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDPDGDSDSYN 15
DB 24 KASQSLDVPDGDSDSYN 38
|||||:|||||

RESULT 8
S19971
Ig kappa chain V region (CD4 mAb clone M-T310 and others) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C.Accession: S19971; S19973
R.Weissenhorn, W.; Riettmueller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: S19963
A.Accession: S19971
A.Molecule type: mRNA
A.Residues: 1-112 <WEI>
A:Cross-references: UNIPARC:UPI0000116030; EMBL:X65091; NID:G52288; PIDN:CAA46219.1; PI
A:Experimental source: clone M-T310
A.Accession: S19973
A.Molecule type: mRNA
A.Residues: 1-112 <WEW>
A:Cross-references: UNIPARC:UPI0000116030; EMBL:X65092; NID:G52292; PIDN:CAA46220.1; PI
A:Experimental source: M-T404
C:Superfamily: immunoglobulin V region; immunoglobulin homology

A>Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152; PMID:103003
A.Accession: B01937
A.Molecule type: protein
A.Residues: 1-111 <WEI>
A:Cross-references: UNIPROT:P01666; UNIPARC:UPI000002A101
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 79; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDPDGDSDSYN 15
DB 24 KASQSVDPDGDSDSYN 38
|||||:|||||

RESULT 7
KWS10
Ig kappa chain V region (PC7210) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C.Accession: D01937; A01937
R.Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A>Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152; PMID:103003
A.Accession: D01937
A.Molecule type: protein
A.Residues: 1-110 <WEI>
A:Cross-references: UNIPROT:P01668; UNIPARC:UPI000002A103
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 96.2%; Score 76; DB 1; Length 110;
Best Local Similarity 93.3%; Pred. No. 1.5e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDPDGDSDSYN 15
DB 24 KASQSLDVPDGDSDSYN 38
|||||:|||||

RESULT 8
S19971
Ig kappa chain V region (CD4 mAb clone M-T310 and others) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C.Accession: S19971; S19973
R.Weissenhorn, W.; Riettmueller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: S19963
A.Accession: S19971
A.Molecule type: mRNA
A.Residues: 1-112 <WEI>
A:Cross-references: UNIPARC:UPI0000116030; EMBL:X65091; NID:G52288; PIDN:CAA46219.1; PI
A:Experimental source: clone M-T310
A.Accession: S19973
A.Molecule type: mRNA
A.Residues: 1-112 <WEW>
A:Cross-references: UNIPARC:UPI0000116030; EMBL:X65092; NID:G52292; PIDN:CAA46220.1; PI
A:Experimental source: M-T404
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>

Query Match 96.2%; Score 76; DB 2; Length 112;
Best Local Similarity 93.3%; Pred. No. 1.5e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSDVDGDSYNN 15
|||||:|||||
Db 24 KASQSLDYDGDYNN 38

RESULT 9

PH1226

Ig kappa chain precursor V region (M-T310) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000

C;Accession: PH1226

R;Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; Lenz

Gene 121, 271-278, 1992

A;Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and on

A;Reference number: PH1224; MUID:93077041; PMID:1446824

A;Accession: PH1226

A;Molecule type: mRNA

A;Residues: 1-131 <WEI>

A;Cross-references: UNIPARC:UPI00001153EE; GB:S50265; NID:g260765; PIDN:AAB24320.1; PID:

A;Note: this mouse sequence was hybridized and fused with a human constant region gene

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-131/Product: Ig light chain V region #status predicted <MAT>

F;16-114/Domain: immunoglobulin homology <IMM>

Query Match 96.2%; Score 76; DB 2; Length 131;
Best Local Similarity 93.3%; Pred. No. 1.8e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSDVDGDSYNN 15
|||||:|||||
Db 44 KASQSLDYDGDYNN 58

RESULT 10

S09966

Ig kappa chain V-J region (1E10) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000

C;Accession: S09966

R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.

Eur. J. Immunol. 20, 771-777, 1990

A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie

A;Reference number: S09955; MUID:90269328; PMID:2347362

A;Accession: S09966

A;Molecule type: mRNA

A;Residues: 1-111 <REI>

A;Cross-references: UNIPARC:UPI0000115B65; EMBL:X51854; NID:g55397; PIDN:CAA36147.1; PID

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;16-94/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 73; DB 2; Length 111;
Best Local Similarity 93.3%; Pred. No. 4.7e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KASQSDVDGDSYNN 15
|||||:|||||
Db 24 KASXSDVDYDGDYNN 38

RESULT 11

KWMSC1

Ig kappa chain V region (CBPC 101) - mouse (tentative sequence)

C;Species: Mus musculus (house mouse)

C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 09-Jul-2004
C;Accession: A01936

R;McKean, D.J.; Bell, M.; Potter, M.

Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978

A;Title: Mechanisms of antibody diversity: multiple genes encode structurally related m

A;Reference number: A93822; MUID:79012520; PMID:99744

A;Accession: A01936

A;Molecule type: protein

A;Residues: 1-111 <MCK>

A;Cross-references: UNIPROT:P01664; UNIPARC:UPI000002A0FF

C;Comment: This chain was isolated from a myeloma protein.

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka

tain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into le

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer

F;16-94/Domain: immunoglobulin homology <IMM>

F;23-92/Disulfide bonds: #status predicted

Query Match 86.1%; Score 68; DB 1; Length 111;
Best Local Similarity 86.7%; Pred. No. 0.00032;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KASQSDVDGDSYNN 15
|||||:|||||
Db 24 KASQSDVDYTGDSYNN 38

RESULT 12

S19976

Ig kappa chain V region (M-T413) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000

C;Accession: S19976

R;Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.

submitted to the EMBL Data Library, March 1992

A;Description: Structural characterization of CD4 mAb.

A;Reference number: S19963

A;Accession: S19976

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-112 <WEI>

A;Cross-references: UNIPARC:UPI0000116031; EMBL:X65093; NID:g52298; PIDN:CAA46221.1; PI

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;16-94/Domain: immunoglobulin homology <IMM>

Query Match 82.3%; Score 65; DB 2; Length 112;
Best Local Similarity 80.0%; Pred. No. 0.001;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KASQSDVDGDSYNN 15
|||||:|||||
Db 24 KASQSLDYDADSYNN 38

RESULT 13

S19972

Ig kappa chain V region (M-T321) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000

C;Accession: S19972

R;Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.

submitted to the EMBL Data Library, March 1992

A;Description: Structural characterization of CD4 mAb.

A;Reference number: S19963

A;Accession: S19972

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-112 <WEI>

A;Cross-references: UNIPARC:UPI0000116032; EMBL:X65094; NID:g52290; PIDN:CAA46222.1; PI

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;16-94/Domain: immunoglobulin homology <IMM>

Query Match 64.6%; Score 51; DB 2; Length 112;
 Best Local Similarity 66.7%; Pred. No. 0.22;
 Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASQSVYDGDGYMN 15
 :|||||: |||:
 DB 24 RASQSVYDGYNAISYMH 38

RESULT 14
 AI0948
 hypothetical protein STY3863 [imported] - Salmonella enterica subsp. enterica serovar Typhimurium
 C:Species: Salmonella enterica subsp. enterica serovar Typhi
 A:Note: this species has also been called Salmonella typhi
 C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C:Accession: AI0948
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; Karpman, A.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, J.; Mouton, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; White, N.; Farrar, J.
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhimurium
 A:Reference number: AB0502; MUID:21534947; PMID:11677608
 A:Accession: AI0948
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-282 <PAR>
 A:Cross-references: UNIPARC:UPI000005A655; GB:AL513382; PIDN:CAD09611.1; PID:g16504722;
 C:Genetics:
 A:Gene: STY3863

Query Match 60.8%; Score 48; DB 2; Length 282;
 Best Local Similarity 60.0%; Pred. No. 1.8;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KASQSVYDGDGYMN 15
 :||: ||||| |||
 DB 263 EALEPDDYDGDYMN 277

RESULT 15
 B49442
 Ig light chain V region (50.1) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
 C:Accession: B49442
 R:Stura, E.A.; Stanfield, R.L.; Fieser, G.G.; Silver, S.; Roguska, M.; Hincapié, L.M.; Suck, D.
 Proteins 14, 499-508, 1992
 A:Title: Crystallization, sequence, and preliminary crystallographic data for an antipeptide fragment of the mouse Ig light chain V region
 A:Reference number: A49442; MUID:93066166; PMID:1438187
 A:Accession: B49442
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-96 <STU>
 A:Cross-references: UNIPARC:UPI0000176D6E
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:8-86/Domain: immunoglobulin homology <IMM>

Query Match 58.2%; Score 46; DB 2; Length 96;
 Best Local Similarity 53.3%; Pred. No. 1.3;
 Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVYDGDGYMN 15
 :|||||: |||:
 DB 16 RASESVDDGNSFLN 30

RESULT 16
 PH0093
 Ig kappa chain V region (anti-cyclosporin E) - mouse (fragment)
 C:Species: Mus musculus (house mouse)

C>Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 21-Jan-2000
 C:Accession: PH0093
 R:Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Kocher, H.P.; Quesniaux, V.F.J.; Mol. Immunol. 27, 1029-1038, 1990
 A:Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine.
 A:Reference number: PH0087; MUID:91042649; PMID:2122240
 A:Accession: PH0093
 A:Molecule type: mRNA
 A:Residues: 1-109 <SCH>
 A:Cross-references: UNIPARC:UPI00001767BF
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:16-94/Domain: immunoglobulin homology <IMM>
 F:24-38/Region: complementarity-determining 1
 F:54-60/Region: complementarity-determining 2
 F:93-101/Region: complementarity-determining 3

Query Match 57.0%; Score 45; DB 2; Length 109;
 Best Local Similarity 60.0%; Pred. No. 2.2;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KASQSVYDGDGYMN 15
 :||: ||||| |||:
 DB 24 RASESVDDGNSFLN 38

RESULT 17
 T03793
 calmodulin-binding protein TCB60 - common tobacco
 C:Species: Nicotiana tabacum (common tobacco)
 C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 31-Dec-2004
 C:Accession: T03793
 R:Dash, S.; Lu, Y.; Harrington, H.M.
 submitted to the EMBL Data Library, May 1996
 A:Description: Molecular cloning and characterization of a tobacco calmodulin-binding protein
 A:Reference number: Z15090
 A:Accession: T03793
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-551 <DAS>
 A:Cross-references: UNIPROT:P93370; UNIPARC:UPI00000A2388; EMBL:U58971; NID:g1698547; P:1
 A:Experimental source: strain Wisconsin 38
 C:Genetics:
 A:Gene: TCB60
 C:Superfamily: Calmodulin-binding protein

Query Match 54.4%; Score 43; DB 2; Length 551;
 Best Local Similarity 53.8%; Pred. No. 25;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 SQSVYDGDGYMN 15
 :||: ||||| |||:
 DB 292 NOVVEYDGSFLN 304

RESULT 18
 PH1079
 Ig light chain V region (clone 202.38m) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
 C:Accession: PH1079
 R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell clones
 A:Reference number: PH0971; MUID:92381444; PMID:1512540
 A:Accession: PH1079
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-102 <TIL>
 A:Cross-references: UNIPARC:UPI00001767CE
 A:Experimental source: B cell, strain [NZB x NZW]F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin

F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 53.2%; Score 42; DB 2; Length 102;
Best Local Similarity 60.0%; Pred. No. 6.4;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KASQSDVDYDGDSDYNN 15
:||:||||| | | | |
Db 24 RASESDVDNYGISFMN 38

RESULT 19

KWMS80

Ig kappa chain V regions (PC2880, PC1229, PC7132, 70) - mouse (tentative sequence)

C:Species: Mus musculus (house mouse)

C:Date: 01-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 09-Jul-2004

C:Accession: B93204; B94239; A01930

R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.

Nature 276, 785-790, 1978

A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.

A:Reference number: A93204; MUID:79073152; PMID:103003

A:Contents: PC2880, PC1229, and PC7132

A:Accession: B93204

A:Molecule type: protein

A:Residues: 1-111 <WEI>

A:Cross-references: UNIPROT:P01654; UNIPARC:UPI000002A0E8

A>Note: the PC2880 and PC1229 sequences are identical

R:Gray, W.R.; Dreyer, W.J.; Hood, L.

Science 155, 465-467, 1967

A:Title: Mechanism of antibody synthesis: size differences between mouse kappa chains.

A:Reference number: A94239; MUID:67056897; PMID:4162931

A:Contents: 70

A:Accession: B94239

A:Molecule type: protein

A:Residues: 1-31, 'S', 33-111 <GRA>

A:Cross-references: UNIPARC:UPI000002A0EB

A>Note: this is a Bence Jones protein

C:Comment: The PC2880 sequence is shown.

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger complexes.

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer

F:16-94/Domain: immunoglobulin homology <IMM>

F:23-92/Disulfide bonds: #status predicted

Query Match 53.2%; Score 42; DB 1; Length 111;
Best Local Similarity 60.0%; Pred. No. 7;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KASQSDVDYDGDSDYNN 15
:||:||||| | | | |
Db 24 RASESDVDNYGISFMN 38

RESULT 20

S09969

Ig kappa chain V-J region (34-3C) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000

C:Accession: S09969

R:Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jatton, J.C.; Izui, S.

Eur. J. Immunol. 20, 771-777, 1990

A:Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies

A:Reference number: S09955; MUID:90269328; PMID:2347362

A:Accession: S09969

A:Molecule type: mRNA

A:Residues: 1-111 <REI>

A:Cross-references: UNIPARC:UPI0000115868; EMBL:X51857; NID:G55404; PIDN:CAA36150.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 53.2%; Score 42; DB 2; Length 111;
Best Local Similarity 60.0%; Pred. No. 7;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KASQSDVDYDGDSDYNN 15
:||:||||| | | | |
Db 24 RASESDVDNYGISFMN 38

RESULT 21

S63596

Ig kappa chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000

C:Accession: S63596

R:Verdaguer, N.; Mateu, M.G.; Bravo, J.; Domingo, E.; Fita, I.

J. Mol. Biol. 256, 364-376, 1996

A:Title: Induced pocket to accommodate the cell attachment Arg-Gly-Asp motif in a neutralizing antibody.

A:Reference number: S63596; MUID:96174482; PMID:8594203

A:Accession: S63596

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-115 <VER>

A:Cross-references: UNIPARC:UPI00001154DD; GB:S81196; NID:G1336821; PIDN:AAB36171.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 53.2%; Score 42; DB 2; Length 115;
Best Local Similarity 53.3%; Pred. No. 7.3;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KASQSDVDYDGDSDYNN 15
:||:||||| | | | |
Db 24 RASESDVDSSGHSMH 38

RESULT 22

S06732

Ig kappa chain precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000

C:Accession: S06732

R:Alanen, A.; Weiss, S.

Eur. J. Immunol. 19, 1961-1963, 1989

A:Title: Sequence and linkage of the V(kappa)21A and G germ-line gene segments in the mouse

A:Reference number: S06731; MUID:90060210; PMID:2583230

A:Accession: S06732

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-120 <ALA>

A:Cross-references: UNIPARC:UPI0000176796; EMBL:X16954

C:Genetics:

A:Introns: 18/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:37-115/Domain: immunoglobulin homology <IMM>

Query Match 53.2%; Score 42; DB 2; Length 120;
Best Local Similarity 60.0%; Pred. No. 7.6;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KASQSDVDYDGDSDYNN 15
:||:||||| | | | |
Db 45 RASESDVDNYGISFMN 59

RESULT 23

A83958

integrase/recombinase codV [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C:Accession: A83958

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira

Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: A83958
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-303 <STO>
A;Cross-references: UNIPROT:Q9KA25; UNIPARC:UPI00000C3F01; GB:AP001515; GB:BA000004; NID
A;Experimental source: strain C-125
C;Genetics:
A;Gene: codV
C;Superfamily: probable site-specific integrase/recombinase XerC

Query Match 53.2%; Score 42; DB 2; Length 303;
Best Local Similarity 53.3%; Pred. No. 20;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 KASQSVDDYDGD SYMN 15
||:|||||:|:
Db 204 KKSQSVDDLPGLFLN 218

RESULT 24
S25462
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
A;Accession: S25462
R;Monstier, M.; Easy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
submitted to the EMBL Data Library, July 1992
A;Description: Structure and binding properties of monoclonal antibodies to core histone
A;Reference number: S25174
A;Accession: S25462
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-91 <MON>
A;Cross-references: UNIPARC:UPI00001160C5; EMBL:X67623; NID:G52188; PIDN:CAA47881.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 51.9%; Score 41; DB 2; Length 91;
Best Local Similarity 53.3%; Pred. No. 8.3;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASQSVDDYDGD SYMN 15
||:|||||:|:
Db 24 RASESVDSYGN SFMH 38

RESULT 25
S26343
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
A;Accession: S26343
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e
A;Reference number: S26343
A;Accession: S26343
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <STA>
A;Cross-references: UNIPARC:UPI0000115F8A; EMBL:X59207; NID:G52334; PIDN:CAA41917.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-93/Domain: immunoglobulin homology <IMM>

Query Match 51.9%; Score 41; DB 2; Length 107;
Best Local Similarity 53.3%; Pred. No. 9.9;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASQSVDDYDGD SYMN 15

Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: A83958
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-303 <STO>
A;Cross-references: UNIPROT:Q9KA25; UNIPARC:UPI00000C3F01; GB:AP001515; GB:BA000004; NID
A;Experimental source: strain C-125
C;Genetics:
A;Gene: codV
C;Superfamily: probable site-specific integrase/recombinase XerC

Query Match 53.2%; Score 42; DB 2; Length 303;
Best Local Similarity 53.3%; Pred. No. 20;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 KASQSVDDYDGD SYMN 15
||:|||||:|:
Db 204 KKSQSVDDLPGLFLN 218

RESULT 24
S25462
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
A;Accession: S25462
R;Monstier, M.; Easy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
submitted to the EMBL Data Library, July 1992
A;Description: Structure and binding properties of monoclonal antibodies to core histone
A;Reference number: S25174
A;Accession: S25462
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-91 <MON>
A;Cross-references: UNIPARC:UPI00001160C5; EMBL:X67623; NID:G52188; PIDN:CAA47881.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 51.9%; Score 41; DB 2; Length 91;
Best Local Similarity 53.3%; Pred. No. 8.3;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASQSVDDYDGD SYMN 15
||:|||||:|:
Db 24 RASESVDSYGN SFMH 38

RESULT 25
S26343
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
A;Accession: S26343
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e
A;Reference number: S26343
A;Accession: S26343
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <STA>
A;Cross-references: UNIPARC:UPI0000115F8A; EMBL:X59207; NID:G52334; PIDN:CAA41917.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-93/Domain: immunoglobulin homology <IMM>

Query Match 51.9%; Score 41; DB 2; Length 107;
Best Local Similarity 53.3%; Pred. No. 9.9;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASQSVDDYDGD SYMN 15

Db 23 RASESVDSYGN SFMH 37
||:|||||:|:
RESULT 26
S26344
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
A;Accession: S26344
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26344
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <STA>
A;Cross-references: UNIPARC:UPI0000115F8C; EMBL:X59209; NID:G52336; PIDN:CAA41919.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-93/Domain: immunoglobulin homology <IMM>

Query Match 51.9%; Score 41; DB 2; Length 107;
Best Local Similarity 53.3%; Pred. No. 9.9;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASQSVDDYDGD SYMN 15
||:|||||:|:
Db 23 RASESVDSYGN SFMH 37

RESULT 27
KWS54
Ig kappa chain V region (PC2154) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
A;Accession: A01940
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
A;Accession: A01940
A;Molecule type: protein
A;Residues: 1-108 <WEI>
A;Cross-references: UNIPROT:P01674; UNIPARC:UPI000002A10F
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k) h
ain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-94/Domain: immunoglobulin homology <IMM>
F;23-92/Disulfide bonds: #status predicted

Query Match 51.9%; Score 41; DB 1; Length 108;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KASQSVDDYDGD SYMN 15
||:|||||:|:
Db 24 RASQSVSTSGYSYMH 38

RESULT 28
KWS37
Ig kappa chain V regions (PC3741, T111) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
A;Accession: A93204; A93822; A01934
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
A;Contents: PC3741

A;Accession: A93204
A;Molecule type: protein
A;Residues: 1-111 <WEI>
A;Cross-references: UNIPROT:P01660; UNIPARC:UPI000002A0FB
R;McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A;Title: Mechanisms of antibody diversity: multiple genes encode structurally related m
A;Reference number: A93822; MUID:79012520; PMID:99744
A;Contents: T111
A;Accession: A93822
A;Molecule type: protein
A;Residues: 1-111 <MCK>
A;Cross-references: UNIPARC:UPI000002A0FB
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-94/Domain: immunoglobulin homology <IMM>
F;23-92/Disulfide bonds: #status predicted

Query Match 51.9%; Score 41; DB 1; Length 111;
Best Local Similarity 53.3%; Pred. No. 10;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASQSDYDGDGSDYMN 15
:||||| :|:|:
24 RASESDVDSYGNFSFMH 38

RESULT 29
S09963
Ig kappa chain V-J region (103-78) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
A;Accession: S09963
R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jatton, J.C.; Izui, S.
Eur. J. Immunol. 20, 771-777, 1990
A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie
A;Reference number: S09955; MUID:90269328; PMID:2347362
A;Accession: S09963
A;Molecule type: mRNA
A;Residues: 1-111 <REI>
A;Cross-references: UNIPROT:Q920E9; UNIPARC:UPI00001767C4; EMBL:X51851
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>

Query Match 51.9%; Score 41; DB 2; Length 111;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KASQSDYDGDGSDYMN 15
:||||| :|:|:
24 RASQSVSSSGSYGMH 38

RESULT 30
KYM5M6
Ig kappa chain precursor V regions (M63, AB22, PC9245, PC4050) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C;Accession: B90412; B90374; B93822; C93204; D93204; PH1078; A01935
R;Burstein, Y.; Schechter, I.
Biochemistry 17, 2392-2400, 1978
A;Title: Primary structures of N-terminal extra peptide segments linked to the variable
expression of immunoglobulin genes.
A;Reference number: A90412; MUID:78235887; PMID:98179
A;Contents: M63
A;Accession: B90412
A;Molecule type: protein
A;Residues: 1-35 <BUR>
A;Cross-references: UNIPROT:P01661; UNIPARC:UPI000017371A
R;McKean, D.; Potter, M.; Hood, L.

Biochemistry 12, 760-771, 1973
A;Title: Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains v
A;Reference number: A90374; MUID:73140225; PMID:4691517
A;Contents: M63
A;Accession: B90374
A;Molecule type: protein
A;Residues: 21-46, Q', 48-53, B', 55-57, Z', 59-86, F', 88-131 <MCK>
A;Cross-references: UNIPARC:UPI000017371B
A;Note: This sequence has since been revised in reference A93822
R;McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A;Title: Mechanisms of antibody diversity: multiple genes encode structurally related m
A;Reference number: A93822; MUID:79012520; PMID:99744
A;Contents: M63; AB22
A;Accession: B93822
A;Molecule type: protein
A;Residues: 1-53; 69-107 <MC2>
A;Cross-references: UNIPARC:UPI000017371C; UNIPARC:UPI000017371D
A;Accession: C93822
A;Molecule type: protein
A;Residues: 21-119, Y', 121-131 <MC3>
A;Cross-references: UNIPARC:UPI000017371C; UNIPARC:UPI000017371D
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
A;Contents: PC9245; PC4050
A;Accession: C93204
A;Molecule type: protein
A;Residues: 21-119, Y', 121-131 <WEI>
A;Cross-references: UNIPARC:UPI000002A0FD
A;Accession: D93204
A;Molecule type: protein
A;Residues: 21-119, L', 121-123, A', 125-129, L', 131 <WE2>
A;Cross-references: UNIPARC:UPI000002A0FD
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IGM and IGA anti-DNA antibodies are the products of clonally selective B
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1078
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 21-122 <TIL>
A;Cross-references: UNIPARC:UPI000017371E
A;Experimental source: B cell, strain [NZB x NZW]F1, clone 17p.73
C;Comment: The M63 precursor sequence is shown.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status experimental <SIG>
F;21-131/Domain: Ig kappa chain precursor V region #status experimental <MAT>
F;36-114/Domain: immunoglobulin homology <IMM>
F;43-112/Disulfide bonds: #status predicted

Query Match 51.9%; Score 41; DB 1; Length 131;
Best Local Similarity 53.3%; Pred. No. 12;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASQSDYDGDGSDYMN 15
:||||| :|:|:
44 RASESDVDSYGNFSFMH 58

Db

RESULT 31
E83146
membrane-bound lytic transglycosylase PA4001 [imported] - Pseudomonas aeruginosa (strain
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 05-Oct-2004
C;Accession: E83146
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bi
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.

```
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
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Query Match 51.3%; Score 40.5; DB 2; Length 101;
Best Local Similarity 56.2%; Pred. No. 13;
Matches 9; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

Qy 1 KASQS-VYDGDGYMN 15
| : | | : | | : | |
Db 24 KSSQSLSDSGKTYLN 39

RESULT 34
A36259
ig kappa chain V region (TE34) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 21-Jan-2000
C;Accession: A36259
R;Zilber, B.; Scherf, T.; Levitt, M.; Anglister, J.
Biochemistry 29, 10032-10041, 1990
A;Title: NMR-derived model for a peptide-antibody complex.
A;Reference number: A36259; MUID:91104915; PMID:2271636
A;Accession: A36259
A>Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-112 <ZIL>
A;Cross-references: UNIPARC:UPI0000176AFD; GB:M30458; GB:M30459; GB:M30480; GB:M30481; GB:M30482; GB:M30483; GB:M30484; GB:M30485; GB:M30486; GB:M30487; GB:M30488; GB:M30489; GB:M30490; GB:M30491; GB:M30492; GB:M30493; GB:M30494; GB:M30495; GB:M30496; GB:M30497; GB:M30498; GB:M30499; GB:M30500; GB:M30501; GB:M30502; GB:M30503; GB:M30504; GB:M30505; GB:M30506; GB:M30507; GB:M30508; GB:M30509; GB:M30510; GB:M30511; GB:M30512; GB:M30513; GB:M30514; GB:M30515; GB:M30516; GB:M30517; GB:M30518; GB:M30519; GB:M30520; GB:M30521; GB:M30522; GB:M30523; GB:M30524; GB:M30525; GB:M30526; GB:M30527; GB:M30528; GB:M30529; GB:M30530; GB:M30531; GB:M30532; GB:M30533; GB:M30534; GB:M30535; GB:M30536; GB:M30537; GB:M30538; GB:M30539; GB:M30540; GB:M30541; GB:M30542; GB:M30543; GB:M30544; GB:M30545; GB:M30546; GB:M30547; GB:M30548; GB:M30549; GB:M30550; GB:M30551; GB:M30552; GB:M30553; GB:M30554; GB:M30555; GB:M30556; GB:M30557; GB:M30558; GB:M30559; GB:M30560; GB:M30561; GB:M30562; GB:M30563; GB:M30564; 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GB:M30929; GB:M30930; GB:M30931; GB:M30932; GB:M3

C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
A;Accession: C32513
R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.; J. Clin. Invest. 82, 852-860, 1988
A;Title: Immunoglobulin kappa light chain variable region gene complex organization and A;Reference number: A94689; MUID:08331394; PMID:3138286
A;Accession: C32513
A;Molecule type: DNA
A;Residues: 1-132 <KOF>
A;Cross-references: UNIPARC:UPI0000114D99; GB:M20830; NID:g196939; PIDN:AAA38844.1; PID: F;16-115/Domain: immunoglobulin homology <IMM>

Query Match 51.3%; Score 40.5; DB 2; Length 132;
Best Local Similarity 56.2%; Pred. No. 15;
Matches 9; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

Qy 1 KASQS-VYDGDGYMN 15
:|||||:|||||:
Db 44 KSSQLSDGKTYLN 59
:

RESULT 37
S37202
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
A;Accession: S37202
R;Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
submitted to the EMBL Data Library, August 1993
A;Description: Production and cloning of TMV-specific monoclonal antibodies.
A;Reference number: S37200
A;Accession: S37202
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-111 <FIS>
A;Cross-references: UNIPARC:UPI00001161AF; EMBL:X74590; NID:g402595; PID:g402596
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-94/Domain: immunoglobulin homology <IMM>

Query Match 50.6%; Score 40; DB 2; Length 111;
Best Local Similarity 60.0%; Pred. No. 15;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KASQSVYDGDGYMN 15
:|||||:|||||:
Db 24 RASESVDDLGFNM 38
:

RESULT 38
A69012
conserved hypothetical protein MTH1091 - Methanobacterium thermoautotrophicum (strain De C;Species: Methanobacterium thermoautotrophicum
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
A;Accession: A69012
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: A69012
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-154 <MTH>
A;Cross-references: UNIPROT:Q27163; UNIPARC:UPI0000066529; GB:AE000666; NID A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1091
A;Start codon: GTG
C;Superfamily: Uncharacterized conserved protein

Query Match 50.6%; Score 40; DB 1; Length 154;
Best Local Similarity 75.0%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 DYDGDGYMN 14
|||||:
Db 84 DYDGYL 91
:

RESULT 39
T43335
vacuolar sorting protein Vps29 homolog - fission yeast (Schizosaccharomyces pombe) (frag C;Species: Schizosaccharomyces pombe
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
A;Accession: T43335
R;Kawakuni, M.
submitted to the EMBL Data Library, March 1998
A;Description: S.Pombe vps29 homolog.
A;Reference number: Z22436
A;Accession: T43335
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-176 <KAW>
A;Cross-references: UNIPROT:O42711; UNIPARC:UPI000006A333; EMBL:AB011824; PIDN:BA25106. C;Superfamily: VPS29-like phosphatase-related protein

Query Match 50.6%; Score 40; DB 2; Length 176;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ASQSVYDGDGYMN 15
:|||||:|:
Db 51 AVQAVEYDGRFFLN 64
:

RESULT 40
H84590
hypothetical protein Atg20570 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
A;Accession: H84590
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: H84590
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-406 <STO>
A;Cross-references: UNIPROT:Q9SIV3; UNIPARC:UPI000017A778; GB:AE002093; NID:g4512654; PI C;Genetics:
A;Gene: Atg20570
A;Map position: 2

Query Match 50.6%; Score 40; DB 2; Length 406;
Best Local Similarity 63.6%; Pred. No. 58;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASQSVYDGDGS 12
:|||||:
Db 118 AAETVYDGS 128
:

RESULT 41
H85633
hypothetical protein ymcA [imported] - Escherichia coli (strain O157:H7, substrain EDL93 C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
A;Accession: H85633
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: H85633

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-698 <STO>
 A:Cross-references: UNIPROT:Q8X542; UNIPARC:UPI0000165752; GB:AE005174; NID:g12514249; F
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: ymcA
 C:Superfamily: Vibrio cholerae otnG protein

Query Match 50.6%; Score 40; DB 2; Length 698;
 Best Local Similarity 50.0%; Pred. No. 1e+02;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 VDYDGSYNN 15
 :::|||:|
 Db 222 LEYDGBNYQN 231

RESULT 42

A44259
 Kinesin-related protein KIF2 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
 C:Accession: A44259; S27871
 R:Alizawa, H.; Sekine, Y.; Takemura, R.; Zhang, Z.; Nangaku, M.; Hirokawa, N. J. Cell Biol. 119, 1287-1296, 1992
 A:Title: Kinesin family in murine central nervous system.
 A:Reference number: A44259; MUID:93077686; PMID:1447303

A:Accession: A44259
 A:Molecule type: mRNA
 A:Residues: 1-716 <AIZ>

A:Cross-references: UNIPROT:P28740; UNIPARC:UPI0000028DD8; EMBL:D12644; NID:g220467; PID
 A:Experimental source: brain
 A:Note: sequence extracted from NCBI backbone (NCBIP:118908)
 C:Superfamily: kinesin-related protein KIF2; kinesin motor domain homology
 C:Keywords: ATP; microtubule binding; nucleotide binding; P-loop
 F:196-531/Domain: kinesin motor domain homology <XMOY>
 F:285-292/Region: nucleotide-binding motif A [P-loop]
 F:291/Binding site: ATP (Lys) #status predicted

Query Match 50.6%; Score 40; DB 1; Length 716;
 Best Local Similarity 63.6%; Pred. No. 1.1e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 SOSVDYDGSY 13
 :::|||
 Db 659 TREVDYDVS 669

RESULT 43

T14513
 hypothetical protein C18G5.10 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: T14513
 R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X
 submitted to the Protein Sequence Database, August 1999
 A:Reference number: Z18120

A:Accession: T14513
 A:Molecule type: DNA
 A:Residues: 1-808 <BEV>

A:Cross-references: UNIPROT:Q9SW62; UNIPARC:UPI000009C9E7; EMBL:AL110116
 A:Experimental source: cultivar Columbia; BAC clone C18G5

C:Genetics:
 A:Gene: ATSP:C18G5.10
 A:Map position: 4
 A:Introns: 202/1; 243/3; 333/3; 541/2; 577/3

Query Match 50.6%; Score 40; DB 2; Length 808;
 Best Local Similarity 77.8%; Pred. No. 1.2e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 VDYDGSYNN 14
 :|||:
 Db 132 VKYDGSYV 140

RESULT 44

S34095
 Ig kappa chain V region - human
 C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 31-Dec-2004
 C:Accession: S34095
 R:Wagner, S.D.; Luzzatto, L. Eur. J. Immunol. 23, 391-397, 1993
 A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
 A:Reference number: S34076; MUID:93170387; PMID:8436174

A:Accession: S34095
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-83 <WAG>

A:Cross-references: UNIPROT:Q8TCD0; UNIPARC:UPI0000176B14; EMBL:X67179
 C:Superfamily: immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-80/Domain: immunoglobulin homology <IMW>

Query Match 50.0%; Score 39.5; DB 2; Length 83;
 Best Local Similarity 50.0%; Pred. No. 13;
 Matches 8; Conservative 6; Mismatches 1; Indels 1; Gaps 1;

QY 1 KASQSDY-DGDSYNN 15
 :::|||:|
 Db 9 RSSQLVSDGNTYLN 24

RESULT 45

B25155
 Ig kappa chain V region (SM1.5) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 28-Dec-1987 #sequence_revision 02-Jun-1988 #text_change 16-Aug-1996
 C:Accession: B25155

R:Robbins, P.F.; Rosen, E.M.; Haba, S.; Nisonoff, A. Proc. Natl. Acad. Sci. U.S.A. 83, 1050-1054, 1986
 A:Title: Relationship of V(H) and V(L) genes encoding three idiotypic families of anti-F
 A:Reference number: A94083; MUID:86149212; PMID:3081888

A:Accession: B25155
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA

A:Residues: 1-89 <ROB>
 A:Cross-references: UNIPARC:UPI00001769ED
 C:Comment: this chain is expressed in an IgM with anti-arsenate activity.
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 50.0%; Score 39.5; DB 2; Length 89;
 Best Local Similarity 56.2%; Pred. No. 14;
 Matches 9; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 KASQS-VDYDGSYNN 15
 :|||:|
 Db 2 KXSQSLDSDGKTYLN 17

RESULT 46

S49572
 Ig kappa chain precursor - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 06-Mar-1995 #sequence_revision 14-Jul-1995 #text_change 21-Jan-2000
 C:Accession: S49572
 R:Giachino, C.; Padovan, E.; Lanzavecchia, A.

submitted to the EMBL Data Library, November 1994

A:Description: k+l+ dual receptor B cells are present in the human peripheral repertoire
A:Reference number: S49571
A:Accession: S49572
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-114 <GIA>
A:Cross-references: UNIPARC:UPI0000116709; EMBL:Z46626; NID:G575261; PIDN:CAA86596.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 50.0%; Score 39.5; DB 2; Length 114;
Best Local Similarity 50.0%; Pred. No. 19;
Matches 8; Conservative 6; Mismatches 1; Indels 1; Gaps 1;

QY 1 KASQSDVY-DGDSYNN 15
::|||:| ||:|:|
Db 24 RSSQSLVYSDGNTYLN 39

RESULT 47
S42268
Ig kappa chain V region (A17) - human
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 31-Dec-2004
C:Accession: S42268
R:Lautner-Rieske, A.; Huber, C.; Meindl, A.; Pargent, W.; Schaeble, K.F.; Thiebe, R.; Z
Eur. J. Immunol. 22, 1023-1029, 1992
A:Title: The human immunoglobulin kappa locus. Characterization of the duplicated A regi
A:Reference number: A49043; MUID:92201291; PMID:1551402
A:Accession: S42268
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-120 <LAU>
A:Cross-references: UNIPROT:Q8TCD0; UNIPARC:UPI0000176EB9; EMBL:X63403
C:Genetics:
A:Introns: 17/1
C:Superfamily: immunoglobulin homology
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 50.0%; Score 39.5; DB 2; Length 120;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 8; Conservative 6; Mismatches 1; Indels 1; Gaps 1;

QY 1 KASQSDVY-DGDSYNN 15
::|||:| ||:|:|
Db 44 RSSQSLVYSDGNTYLN 59

RESULT 48
S42267
Ig kappa chain V region (A1) - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 31-Dec-2004
C:Accession: S42267
R:Lautner-Rieske, A.; Huber, C.; Meindl, A.; Pargent, W.; Schaeble, K.F.; Thiebe, R.; Z
Eur. J. Immunol. 22, 1023-1029, 1992
A:Title: The human immunoglobulin kappa locus. Characterization of the duplicated A regi
A:Reference number: A49043; MUID:92201291; PMID:1551402
A:Accession: S42267
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-120 <LAU>
A:Cross-references: UNIPROT:Q8TCD0; UNIPARC:UPI0000176997; EMBL:X63402
C:Genetics:
A:Introns: 17/3
C:Superfamily: immunoglobulin homology
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 50.0%; Score 39.5; DB 2; Length 120;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 8; Conservative 6; Mismatches 1; Indels 1; Gaps 1;

QY 1 KASQSDVY-DGDSYNN 15

Db 44 RSSQSLVYSDGNTYLN 59
::|||:| ||:|:|

RESULT 49
K2HURP
Ig kappa chain precursor V-II region (RPWI) - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: A01890
R:Klobeck, H.G.; Meindl, A.; Combriato, G.; Solomon, A.; Zachau, H.G.
Nucleic Acids Res. 13, 6499-6513, 1985
A:Title: Human immunoglobulin kappa light chain genes of subgroups II and III.
A:Reference number: A93588; MUID:86041852; PMID:2997711
A:Accession: A01890
A:Molecule type: DNA
A:Residues: 1-133 <KLO>
A:Cross-references: UNIPROT:P06310; UNIPARC:UPI000012E159
A>Note: the sequence was determined from the differentiated gene
C:Genetics:
A:Gene: GDB:IGKV2
A:Cross-references: GDB:136265
A:Map position: 2p12-2p12
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-133/Product: Ig kappa chain V-II region (RPWI) #status predicted <MAT>
F:21-43/Region: framework 1
F:36-115/Domain: immunoglobulin homology <IMM>
F:44-59/Region: complementarity-determining 1
F:60-74/Region: framework 2
F:75-81/Region: complementarity-determining 2
F:82-113/Region: framework 3
F:114-122/Region: complementarity-determining 3
F:123-133/Region: framework 4
F:43-113/Disulfide bonds: #status predicted

Query Match 50.0%; Score 39.5; DB 1; Length 133;
Best Local Similarity 50.0%; Pred. No. 22;
Matches 8; Conservative 6; Mismatches 1; Indels 1; Gaps 1;

QY 1 KASQSDVY-DGDSYNN 15
::|||:| ||:|:|
Db 44 RSSQSLVYSDGNTYLN 59

RESULT 50
D45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 109) - mouse (f
C:Species: Mus musculus (house mouse)
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: D45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu
J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on h
A:Reference number: A45722; MUID:93100833; PMID:7677958
A:Accession: D45722
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-111 <SIM>
A:Cross-references: UNIPARC:UPI0000176D43
A>Note: sequence extracted from NCBI backbone (NCBIF:120592)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 49.4%; Score 39; DB 2; Length 111;
Best Local Similarity 53.3%; Pred. No. 22;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: February 23, 2006, 09:29:34 ; Search time 60.3077 Seconds
(without alignments)
50.999 Million cell updates/sec

Title: US-10-723-872-18

Perfect score: 31

Sequence: 1 AASNLES 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 31 | 100.0 | 7 | 2 | AAR70196 MAb 3B9 1 |
| 2 | 31 | 100.0 | 7 | 2 | AAW83028 Anti-Fas |
| 3 | 31 | 100.0 | 7 | 2 | AAY23773 CDR of th |
| 4 | 31 | 100.0 | 7 | 2 | AAY18115 |
| 5 | 31 | 100.0 | 7 | 3 | AAB14745 Mouse ant |
| 6 | 31 | 100.0 | 7 | 3 | AAY51137 Murine CD |
| 7 | 31 | 100.0 | 7 | 3 | AAW90895 Murine an |
| 8 | 31 | 100.0 | 7 | 3 | AAY59260 Antibody |
| 9 | 31 | 100.0 | 7 | 5 | AAO18540 Murine Ma |
| 10 | 31 | 100.0 | 7 | 5 | ABB74910 Humanised |
| 11 | 31 | 100.0 | 7 | 5 | AAU70353 Mouse Kap |
| 12 | 31 | 100.0 | 7 | 5 | ABB74864 Humanised |
| 13 | 31 | 100.0 | 7 | 5 | AAU99854 Mouse AC1 |
| 14 | 31 | 100.0 | 7 | 6 | AAE37723 Mouse ant |
| 15 | 31 | 100.0 | 7 | 7 | AAO29928 Mouse ant |
| 16 | 31 | 100.0 | 7 | 8 | ADJ87916 Mouse AC1 |
| 17 | 31 | 100.0 | 7 | 9 | ADY93300 mAb CG10 |
| 18 | 31 | 100.0 | 15 | 2 | AAW86144 |
| 19 | 31 | 100.0 | 41 | 3 | AAW91015 1F7 antib |
| 20 | 31 | 100.0 | 103 | 3 | AAW51140 Murine de |
| 21 | 31 | 100.0 | 103 | 3 | AAW59263 Antibody |
| 22 | 31 | 100.0 | 105 | 6 | AAE37732 MT413 mod |
| 23 | 31 | 100.0 | 106 | 2 | AAR33309 MaE15 lig |
| 24 | 31 | 100.0 | 106 | 3 | AAY85197 Light cha |

| | | | | | |
|----|----|-------|-----|---|---------------------|
| 25 | 31 | 100.0 | 110 | 5 | AAO18536 |
| 26 | 31 | 100.0 | 111 | 1 | AAP90541 Immunoglo |
| 27 | 31 | 100.0 | 111 | 1 | AAS5123 Mouse ant |
| 28 | 31 | 100.0 | 111 | 2 | AAR55127 Mouse-hum |
| 29 | 31 | 100.0 | 111 | 2 | AAR60302 Anti HIV |
| 30 | 31 | 100.0 | 111 | 2 | AAR60306 Chimeric |
| 31 | 31 | 100.0 | 111 | 2 | AAY23781 Light cha |
| 32 | 31 | 100.0 | 111 | 2 | AAY18123 Light cha |
| 33 | 31 | 100.0 | 111 | 3 | AAY51146 Murine de |
| 34 | 31 | 100.0 | 111 | 3 | AAY51144 Murine de |
| 35 | 31 | 100.0 | 111 | 3 | AAY59267 Antibody |
| 36 | 31 | 100.0 | 111 | 5 | AAU99852 Mouse AC1 |
| 37 | 31 | 100.0 | 111 | 7 | AAO29926 Mouse ant |
| 38 | 31 | 100.0 | 111 | 7 | ADC27439 TMEFF2#10 |
| 39 | 31 | 100.0 | 111 | 8 | ADJ87912 Mouse AC1 |
| 40 | 31 | 100.0 | 111 | 9 | ADY85020 Human HMG |
| 41 | 31 | 100.0 | 111 | 9 | AEI13680 Human vfk |
| 42 | 31 | 100.0 | 111 | 9 | AEI13684 Human ant |
| 43 | 31 | 100.0 | 111 | 9 | AEI13678 Human lig |
| 44 | 31 | 100.0 | 111 | 9 | AEI13682 Human ant |
| 45 | 31 | 100.0 | 111 | 9 | AEI13683 Human ant |
| 46 | 31 | 100.0 | 112 | 2 | AAR24575 Human x m |
| 47 | 31 | 100.0 | 112 | 6 | ABO10750 Variable |
| 48 | 31 | 100.0 | 112 | 6 | ABR44694 Murine Ku |
| 49 | 31 | 100.0 | 112 | 8 | ADU67960 Mouse Kab |
| 50 | 31 | 100.0 | 113 | 4 | AAB71895 Monoclonal |
| 51 | 31 | 100.0 | 113 | 8 | ADI26494 Human ECL |
| 52 | 31 | 100.0 | 113 | 8 | ADO06847 Virucidal |
| 53 | 31 | 100.0 | 113 | 8 | ADO06796 Virucidal |
| 54 | 31 | 100.0 | 113 | 8 | ADO06849 Virucidal |
| 55 | 31 | 100.0 | 113 | 8 | ADO06851 Virucidal |
| 56 | 31 | 100.0 | 113 | 8 | ADQ090832 Kabat sub |
| 57 | 31 | 100.0 | 115 | 2 | AAR04134 Anti-Leu |
| 58 | 31 | 100.0 | 126 | 9 | AEI14798 Light cha |
| 59 | 31 | 100.0 | 126 | 9 | AEI14799 Light cha |
| 60 | 31 | 100.0 | 131 | 1 | AAP90543 Amino aci |
| 61 | 31 | 100.0 | 131 | 2 | AAR04132 Anti-Leu |
| 62 | 31 | 100.0 | 131 | 2 | AAR32123 Anti-CD4 |
| 63 | 31 | 100.0 | 131 | 2 | AAR70202 Humanized |
| 64 | 31 | 100.0 | 131 | 2 | AAR75355 Humanized |
| 65 | 31 | 100.0 | 131 | 2 | AAW34516 Variable |
| 66 | 31 | 100.0 | 131 | 2 | AAY23771 Light cha |
| 67 | 31 | 100.0 | 131 | 2 | AAY23779 Light cha |
| 68 | 31 | 100.0 | 131 | 2 | AAY18118 Light cha |
| 69 | 31 | 100.0 | 131 | 2 | AAY18126 Light cha |
| 70 | 31 | 100.0 | 132 | 2 | AAR70189 Mouse Mab |
| 71 | 31 | 100.0 | 132 | 2 | AAY23767 Light cha |
| 72 | 31 | 100.0 | 132 | 2 | AAW18120 Light cha |
| 73 | 31 | 100.0 | 218 | 2 | AAW13563 Humanised |
| 74 | 31 | 100.0 | 218 | 6 | ABP96773 TSH recep |
| 75 | 31 | 100.0 | 218 | 6 | ABP96774 TSH recep |
| 76 | 31 | 100.0 | 220 | 8 | ADO06858 Virucidal |
| 77 | 31 | 100.0 | 220 | 8 | ADO06856 Virucidal |
| 78 | 31 | 100.0 | 222 | 2 | AAW01751 MHI monocl |
| 79 | 31 | 100.0 | 238 | 2 | AAW83035 Anti-Fas |
| 80 | 31 | 100.0 | 238 | 2 | AAW83042 Anti-Fas |
| 81 | 31 | 100.0 | 238 | 2 | AAW83034 Anti-Fas |
| 82 | 31 | 100.0 | 238 | 2 | AAW83033 Anti-Fas |
| 83 | 31 | 100.0 | 238 | 2 | AAW83032 Anti-Fas |
| 84 | 31 | 100.0 | 238 | 3 | AAW83031 Anti-Fas |
| 85 | 31 | 100.0 | 238 | 3 | AAW83042 Anti-Fas |
| 86 | 31 | 100.0 | 238 | 3 | AAW83034 Anti-Fas |
| 87 | 31 | 100.0 | 238 | 3 | AAW83033 Anti-Fas |
| 88 | 31 | 100.0 | 238 | 3 | AAW83032 Anti-Fas |
| 89 | 31 | 100.0 | 238 | 3 | AAW83031 Anti-Fas |
| 90 | 31 | 100.0 | 238 | 3 | AAW83032 Anti-Fas |
| 91 | 31 | 100.0 | 238 | 3 | AAW83031 Anti-Fas |
| 92 | 31 | 100.0 | 238 | 3 | AAW83032 Anti-Fas |
| 93 | 31 | 100.0 | 238 | 3 | AAW83031 Anti-Fas |
| 94 | 31 | 100.0 | 238 | 3 | AAW83032 Anti-Fas |
| 95 | 31 | 100.0 | 238 | 3 | AAW83031 Anti-Fas |
| 96 | 31 | 100.0 | 238 | 3 | AAW83032 Anti-Fas |
| 97 | 31 | 100.0 | 238 | 3 | AAW83031 Anti-Fas |

| | | | | | | | | | | | | | | | |
|-----|----|-------|------|---|-----------|----------|------------|-----|----|------|-----|---|-----------|----------|------------|
| 98 | 31 | 100.0 | 238 | 3 | AAW90922 | Aaw90922 | Humanised | 171 | 28 | 90.3 | 114 | 8 | ADG25816 | Adg25816 | Anti-CD30 |
| 99 | 31 | 100.0 | 238 | 3 | AAW90930 | Aaw90930 | Humanised | 172 | 28 | 90.3 | 115 | 8 | ADW3243 | Adw3243 | Pgp-resis |
| 100 | 31 | 100.0 | 238 | 5 | AAE18371 | Aae18371 | Human pen | 173 | 28 | 90.3 | 120 | 2 | AAR48618 | Aar48618 | Sequence |
| 101 | 31 | 100.0 | 238 | 5 | ABE74937 | AbE74937 | Humanised | 174 | 28 | 90.3 | 131 | 2 | AAR30881 | Aar30881 | Antibody |
| 102 | 31 | 100.0 | 238 | 5 | ABB74938 | Abb74938 | Humanised | 175 | 28 | 90.3 | 135 | 7 | ADD25689 | Add25689 | Binding d |
| 103 | 31 | 100.0 | 238 | 5 | ABB74939 | Abb74939 | Humanised | 176 | 28 | 90.3 | 135 | 9 | ADY21663 | Ady21663 | Antibody |
| 104 | 31 | 100.0 | 238 | 5 | ABB74942 | Abb74942 | Humanised | 177 | 28 | 90.3 | 147 | 2 | AAy34312 | Aay34312 | IgM antib |
| 105 | 31 | 100.0 | 238 | 5 | ABB74943 | Abb74943 | Humanised | 178 | 28 | 90.3 | 165 | 7 | ADD28245 | Add28245 | Human het |
| 106 | 31 | 100.0 | 238 | 5 | ABB74913 | Abb74913 | Humanised | 179 | 28 | 90.3 | 165 | 9 | ADV86832 | Adv86832 | Bacillus |
| 107 | 31 | 100.0 | 238 | 5 | ABB74897 | Abb74897 | Humanised | 180 | 28 | 90.3 | 215 | 8 | ADH10328 | Adh10328 | Anti-HIV- |
| 108 | 31 | 100.0 | 238 | 5 | ABB74899 | Abb74899 | Humanised | 181 | 28 | 90.3 | 234 | 8 | ADS84458 | Ads84458 | Human ant |
| 109 | 31 | 100.0 | 238 | 5 | ABB74867 | Abb74867 | Humanised | 182 | 28 | 90.3 | 234 | 8 | ADJ68600 | Adj68600 | Human ant |
| 110 | 31 | 100.0 | 238 | 5 | ABB74900 | Abb74900 | Humanised | 183 | 28 | 90.3 | 240 | 6 | ABJ38595 | Abj38595 | Hepatitis |
| 111 | 31 | 100.0 | 238 | 5 | ABB74892 | Abb74892 | Humanised | 184 | 28 | 90.3 | 240 | 6 | ABJ38592 | Abj38592 | Hepatitis |
| 112 | 31 | 100.0 | 238 | 5 | ABB74893 | Abb74893 | Humanised | 185 | 28 | 90.3 | 247 | 8 | ADG28588 | Adg28588 | Paramyxov |
| 113 | 31 | 100.0 | 238 | 5 | ABB74891 | Abb74891 | Humanised | 186 | 28 | 90.3 | 271 | 7 | ADD25693 | Add25693 | Binding d |
| 114 | 31 | 100.0 | 238 | 5 | ABB74896 | Abb74896 | Humanised | 187 | 28 | 90.3 | 271 | 9 | ADY21667 | Ady21667 | Single ch |
| 115 | 31 | 100.0 | 238 | 5 | ABB74901 | Abb74901 | Humanised | 188 | 28 | 90.3 | 272 | 2 | AAW16688 | Aaw16688 | Murine an |
| 116 | 31 | 100.0 | 238 | 5 | ABG76346 | Abg76346 | Mouse DAV | 189 | 28 | 90.3 | 287 | 6 | ABR42057 | AbR42057 | Costimula |
| 117 | 31 | 100.0 | 238 | 9 | ABE96755 | AbE96755 | DAV-1 ant | 190 | 28 | 90.3 | 299 | 4 | AAAG63657 | AaG63657 | Amino aci |
| 118 | 31 | 100.0 | 305 | 3 | AAy51142 | Aay51142 | Murine de | 191 | 28 | 90.3 | 299 | 4 | AAAG63660 | AaG63660 | Amino aci |
| 119 | 31 | 100.0 | 305 | 3 | AAy51141 | Aay51141 | Murine de | 192 | 28 | 90.3 | 302 | 4 | AAAB82483 | AaB82483 | Cotton tr |
| 120 | 31 | 100.0 | 305 | 3 | AAy59264 | Aay59264 | Antibody | 193 | 28 | 90.3 | 467 | 6 | ADA36223 | Ada36223 | Acinetoba |
| 121 | 31 | 100.0 | 305 | 3 | AAy59265 | Aay59265 | Antibody | 194 | 28 | 90.3 | 543 | 7 | ADD12876 | Add12876 | CD28/mela |
| 122 | 31 | 100.0 | 308 | 8 | AQ96330 | Aq96330 | T cell ac | 195 | 28 | 90.3 | 556 | 9 | ADY21677 | Ady21677 | Binding d |
| 123 | 31 | 100.0 | 331 | 6 | AAE37727 | Aae37727 | Chemokine | 196 | 28 | 90.3 | 556 | 9 | ADY21677 | Ady21677 | Antibody |
| 124 | 31 | 100.0 | 331 | 6 | AAE37733 | Aae37733 | Chemokine | 197 | 28 | 90.3 | 556 | 9 | ADY22063 | Ady22063 | Antibody |
| 125 | 31 | 100.0 | 339 | 6 | AAE37728 | Aae37728 | Chemokine | 198 | 28 | 90.3 | 556 | 9 | ADY21752 | Ady21752 | Antibody |
| 126 | 31 | 100.0 | 499 | 5 | AAO22598 | Aao22598 | 499-mer S | 199 | 28 | 90.3 | 573 | 9 | ADY21807 | Ady21807 | Antibody |
| 127 | 31 | 100.0 | 522 | 6 | ABJ26394 | Abj26394 | Aspergill | 200 | 28 | 90.3 | 573 | 9 | ADY22071 | Ady22071 | Antibody |
| 128 | 31 | 100.0 | 522 | 6 | ABJ25794 | Abj25794 | Aspergill | 201 | 28 | 90.3 | 632 | 2 | AAW55684 | Aaw55684 | H. pylori |
| 129 | 31 | 100.0 | 629 | 8 | AQ96326 | Aq96326 | T cell ac | 202 | 28 | 90.3 | 634 | 2 | AAy21548 | Aay21548 | Human hep |
| 130 | 31 | 100.0 | 942 | 8 | ADN19844 | Adn19844 | Bacterial | 203 | 28 | 90.3 | 648 | 9 | ADY21809 | Ady21809 | Antibody |
| 131 | 31 | 100.0 | 1208 | 8 | ADQ96328 | Adq96328 | Human pro | 204 | 28 | 90.3 | 663 | 9 | ADY22107 | Ady22107 | Antibody |
| 132 | 31 | 100.0 | 1208 | 8 | ADQ96328 | Adq96328 | T cell ac | 205 | 28 | 90.3 | 715 | 9 | ADY22075 | Ady22075 | Antibody |
| 133 | 31 | 100.0 | 1208 | 9 | ADY15794 | Ady15794 | PRO polyyp | 206 | 28 | 90.3 | 715 | 9 | ADY22073 | Ady22073 | Antibody |
| 134 | 31 | 100.0 | 1208 | 9 | ADY15792 | Ady15792 | PRO polyyp | 207 | 28 | 90.3 | 716 | 9 | ADY22105 | Ady22105 | Antibody |
| 135 | 31 | 100.0 | 1213 | 5 | AAO22597 | Aao22597 | 1213-mer | 208 | 28 | 90.3 | 716 | 9 | ADY22103 | Ady22103 | Antibody |
| 136 | 28 | 90.3 | 7 | 4 | AAAG63642 | Aag63642 | Complemen | 209 | 28 | 90.3 | 784 | 4 | ABB71112 | Abb71112 | Drosophil |
| 137 | 28 | 90.3 | 7 | 6 | AAAG63651 | Aag63651 | Complemen | 210 | 28 | 90.3 | 787 | 9 | ADY22091 | Ady22091 | Antibody |
| 138 | 28 | 90.3 | 7 | 6 | ABJ38600 | Abj38600 | Hepatitis | 211 | 28 | 90.3 | 787 | 9 | ADY22079 | Ady22079 | Antibody |
| 139 | 28 | 90.3 | 7 | 6 | ABJ38609 | Abj38609 | Hepatitis | 212 | 28 | 90.3 | 787 | 9 | ADY22093 | Ady22093 | Antibody |
| 140 | 28 | 90.3 | 7 | 8 | ADU38488 | Adu38488 | Mouse ant | 213 | 28 | 90.3 | 789 | 9 | ADY22081 | Ady22081 | Antibody |
| 141 | 28 | 90.3 | 7 | 9 | AEA45061 | Aea45061 | Apolipop | 214 | 28 | 90.3 | 989 | 9 | ADY22101 | Ady22101 | Antibody |
| 142 | 28 | 90.3 | 7 | 9 | AEA45067 | Aea45067 | Apolipop | 215 | 28 | 90.3 | 989 | 9 | ADY22099 | Ady22099 | Antibody |
| 143 | 28 | 90.3 | 7 | 9 | AEA45183 | Aea45183 | Apolipop | 216 | 28 | 90.3 | 990 | 9 | ADY22085 | Ady22085 | Antibody |
| 144 | 28 | 90.3 | 40 | 6 | ABJ25316 | Abj25316 | SAC isola | 217 | 28 | 90.3 | 990 | 9 | ADY22087 | Ady22087 | Antibody |
| 145 | 28 | 90.3 | 102 | 9 | ADY33945 | Ady33945 | Anti-Tie | 218 | 27 | 87.1 | 7 | 2 | AAr75490 | Aar75490 | Mouse ant |
| 146 | 28 | 90.3 | 104 | 2 | AAW62804 | Aaw62804 | Amino aci | 219 | 27 | 87.1 | 7 | 2 | AAr75489 | Aar75489 | Mouse ant |
| 147 | 28 | 90.3 | 105 | 2 | AAW52239 | Aaw52239 | Antibody | 220 | 27 | 87.1 | 7 | 2 | AAW01148 | Aaw01148 | MAB 1.4 l |
| 148 | 28 | 90.3 | 107 | 8 | ADP22236 | Adp22236 | Human ant | 221 | 27 | 87.1 | 7 | 2 | AAW27345 | Aaw27345 | CDR2 from |
| 149 | 28 | 90.3 | 107 | 8 | ADS84406 | Ads84406 | Human ant | 222 | 27 | 87.1 | 7 | 2 | AAW44171 | Aaw44171 | Monoclonal |
| 150 | 28 | 90.3 | 107 | 8 | ADR68548 | Adr68548 | Anti-EPO- | 223 | 27 | 87.1 | 7 | 3 | AAAB09999 | Aab09999 | H. pylori |
| 151 | 28 | 90.3 | 107 | 9 | ADW96639 | Adw96639 | Human ant | 224 | 27 | 87.1 | 7 | 4 | AAAB98264 | Aab98264 | Anti-A33 |
| 152 | 28 | 90.3 | 107 | 9 | ADW80211 | Adw80211 | Human ant | 225 | 27 | 87.1 | 7 | 4 | AAAB75184 | Aab75184 | A33 anti |
| 153 | 28 | 90.3 | 108 | 2 | AAK42633 | Aak42633 | Light cha | 226 | 27 | 87.1 | 7 | 5 | AAE28153 | Aae28153 | Murine 3F |
| 154 | 28 | 90.3 | 108 | 2 | AAK80942 | Aak80942 | Antibody | 227 | 27 | 87.1 | 7 | 5 | AAU99862 | Aau99862 | Mouse Hep |
| 155 | 28 | 90.3 | 108 | 9 | AEA45202 | Aea45202 | Apolipop | 228 | 27 | 87.1 | 7 | 7 | AAO29936 | Aao29936 | Mouse ant |
| 156 | 28 | 90.3 | 108 | 9 | AEA45114 | Aea45114 | Apolipop | 229 | 27 | 87.1 | 7 | 8 | ADE25806 | AdE25806 | Anti-alph |
| 157 | 28 | 90.3 | 111 | 2 | AAW07441 | Aaw07441 | Anti-DNA | 230 | 27 | 87.1 | 7 | 8 | ADJ87932 | Adj87932 | Mouse Hep |
| 158 | 28 | 90.3 | 111 | 4 | AAAG63656 | Aag63656 | Amino aci | 231 | 27 | 87.1 | 7 | 8 | ADM78100 | Adm78100 | Human SJB |
| 159 | 28 | 90.3 | 111 | 4 | AAAG63653 | Aag63653 | Amino aci | 232 | 27 | 87.1 | 7 | 8 | AQC37235 | Aqc37235 | Mouse mon |
| 160 | 28 | 90.3 | 111 | 6 | ABJ38612 | Abj38612 | Hepatitis | 233 | 27 | 87.1 | 7 | 8 | ADR89797 | Adr89797 | Anti-CD70 |
| 161 | 28 | 90.3 | 111 | 6 | ABJ38615 | Abj38615 | Hepatitis | 234 | 27 | 87.1 | 7 | 8 | ADR90816 | Adr90816 | LC-CDR2 f |
| 162 | 28 | 90.3 | 111 | 8 | ADR38688 | Adr38688 | Mouse lig | 235 | 27 | 87.1 | 7 | 8 | ADR90825 | Adr90825 | LC-CDR2 f |
| 163 | 28 | 90.3 | 112 | 4 | ABE84296 | AbE84296 | Amino aci | 236 | 27 | 87.1 | 7 | 8 | ADR90824 | Adr90824 | LC-CDR2 f |
| 164 | 28 | 90.3 | 112 | 6 | ABO27164 | AbO27164 | Mouse ant | 237 | 27 | 87.1 | 7 | 8 | ADR90827 | Adr90827 | LC-CDR2 f |
| 165 | 28 | 90.3 | 112 | 8 | ADR38690 | Adr38690 | Mouse lig | 238 | 27 | 87.1 | 7 | 8 | ADR90834 | Adr90834 | LC-CDR2 f |
| 166 | 28 | 90.3 | 113 | 2 | AAK79892 | Aak79892 | Anti-EGFR | 239 | 27 | 87.1 | 7 | 8 | ADR90840 | Adr90840 | LC-CDR2 f |
| 167 | 28 | 90.3 | 113 | 2 | AAK79882 | Aak79882 | Anti-EGFR | 240 | 27 | 87.1 | 7 | 8 | ADR90819 | Adr90819 | LC-CDR2 f |
| 168 | 28 | 90.3 | 113 | 2 | AAK79891 | Aak79891 | Anti-EGFR | 241 | 27 | 87.1 | 7 | 8 | ADR90831 | Adr90831 | LC-CDR2 f |
| 169 | 28 | 90.3 | 114 | 7 | ADD28276 | Add28276 | Human het | 242 | 27 | 87.1 | 7 | 8 | ADR90832 | Adr90832 | LC-CDR2 f |
| 170 | 28 | 90.3 | 114 | 8 | ADG25819 | Adg25819 | Anti-CD30 | 243 | 27 | 87.1 | 7 | 8 | ADR90817 | Adr90817 | LC-CDR2 f |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|----------|-----------|-----|----|------|-----|---|----------|------------|
| 244 | 27 | 87.1 | 7 | 8 | ADR90822 | LC-CDR2 f | 317 | 27 | 87.1 | 109 | 4 | AAB98233 | Humanised |
| 245 | 27 | 87.1 | 7 | 8 | ADR90835 | LC-CDR2 f | 318 | 27 | 87.1 | 109 | 4 | AAB98237 | Humanised |
| 246 | 27 | 87.1 | 7 | 8 | ADR90821 | LC-CDR2 f | 319 | 27 | 87.1 | 109 | 4 | AAB98231 | Rabbit an |
| 247 | 27 | 87.1 | 7 | 8 | ADR90826 | LC-CDR2 f | 320 | 27 | 87.1 | 109 | 4 | AAB98239 | Humanised |
| 248 | 27 | 87.1 | 7 | 8 | ADR90836 | LC-CDR2 f | 321 | 27 | 87.1 | 109 | 4 | AAB98238 | Humanised |
| 249 | 27 | 87.1 | 7 | 8 | ADR90837 | LC-CDR2 f | 322 | 27 | 87.1 | 109 | 4 | AAB98235 | Humanised |
| 250 | 27 | 87.1 | 7 | 8 | ADR90838 | LC-CDR2 f | 323 | 27 | 87.1 | 109 | 4 | AAB98236 | Humanised |
| 251 | 27 | 87.1 | 7 | 8 | ADT75152 | Murine li | 324 | 27 | 87.1 | 109 | 4 | AAB75157 | Human ant |
| 252 | 27 | 87.1 | 7 | 8 | ADU38474 | Mouse ant | 325 | 27 | 87.1 | 109 | 4 | AAB75154 | Human ant |
| 253 | 27 | 87.1 | 7 | 9 | ADW95702 | Anti-hil- | 326 | 27 | 87.1 | 109 | 4 | AAB75152 | Humanised |
| 254 | 27 | 87.1 | 7 | 9 | ADX15707 | Mouse ant | 327 | 27 | 87.1 | 109 | 4 | AAB75155 | Human ant |
| 255 | 27 | 87.1 | 7 | 9 | AEA46185 | Apolipop | 328 | 27 | 87.1 | 109 | 4 | AAB75149 | Rabbit an |
| 256 | 27 | 87.1 | 7 | 9 | ABE21455 | Mouse ant | 329 | 27 | 87.1 | 109 | 4 | AAB75153 | Human ant |
| 257 | 27 | 87.1 | 7 | 9 | ABE31213 | Antibody | 330 | 27 | 87.1 | 109 | 4 | AAB75158 | Human ant |
| 258 | 27 | 87.1 | 8 | 8 | ADT75084 | Murine li | 331 | 27 | 87.1 | 109 | 4 | AAB75156 | Human ant |
| 259 | 27 | 87.1 | 11 | 2 | ADR95164 | Mouse ant | 332 | 27 | 87.1 | 109 | 8 | ADT74994 | Light cha |
| 260 | 27 | 87.1 | 17 | 2 | AAR85179 | GM-CSF re | 333 | 27 | 87.1 | 109 | 8 | ADT75009 | Light cha |
| 261 | 27 | 87.1 | 20 | 5 | AAU70785 | Hepatitis | 334 | 27 | 87.1 | 109 | 8 | ADT74995 | Light cha |
| 262 | 27 | 87.1 | 20 | 5 | AAU70784 | Hepatitis | 335 | 27 | 87.1 | 109 | 9 | AEA16579 | Protein o |
| 263 | 27 | 87.1 | 20 | 7 | ADC85038 | HBV HBCAg | 336 | 27 | 87.1 | 110 | 7 | AAR60810 | Light cha |
| 264 | 27 | 87.1 | 20 | 7 | ADC85039 | HBV HBCAg | 337 | 27 | 87.1 | 110 | 7 | ADC27443 | TMFPF2#18 |
| 265 | 27 | 87.1 | 20 | 8 | ADK14595 | Hepatitis | 338 | 27 | 87.1 | 111 | 2 | AAR25721 | Humanised |
| 266 | 27 | 87.1 | 20 | 8 | ADK14596 | Hepatitis | 339 | 27 | 87.1 | 111 | 2 | AAR47494 | Murine an |
| 267 | 27 | 87.1 | 55 | 5 | ABB79679 | Chronic l | 340 | 27 | 87.1 | 111 | 2 | AAR53930 | Light cha |
| 268 | 27 | 87.1 | 55 | 5 | ABB79678 | Chronic l | 341 | 27 | 87.1 | 111 | 2 | AAR60528 | Light cha |
| 269 | 27 | 87.1 | 55 | 8 | ADR90769 | CDR's fro | 342 | 27 | 87.1 | 111 | 2 | AAR48622 | Sequence |
| 270 | 27 | 87.1 | 55 | 8 | ADR90780 | CDR's fro | 343 | 27 | 87.1 | 111 | 2 | AAR65172 | Sequence |
| 271 | 27 | 87.1 | 57 | 5 | ABB79672 | Chronic l | 344 | 27 | 87.1 | 111 | 2 | AAR65174 | Murine NM |
| 272 | 27 | 87.1 | 57 | 5 | ABB79666 | Chronic l | 345 | 27 | 87.1 | 111 | 2 | AAR85236 | Region pr |
| 273 | 27 | 87.1 | 57 | 5 | ABB79667 | Chronic l | 346 | 27 | 87.1 | 111 | 2 | AAR85236 | Murine 20 |
| 274 | 27 | 87.1 | 57 | 5 | ABB79681 | Chronic l | 347 | 27 | 87.1 | 111 | 2 | AAR85242 | Humanised |
| 275 | 27 | 87.1 | 57 | 8 | ADR90771 | CDR's fro | 348 | 27 | 87.1 | 111 | 3 | AAB10019 | Humanised |
| 276 | 27 | 87.1 | 57 | 8 | ADR90775 | CDR's fro | 349 | 27 | 87.1 | 111 | 4 | AAB59662 | H. pylori |
| 277 | 27 | 87.1 | 57 | 8 | ADR90762 | CDR's fro | 350 | 27 | 87.1 | 111 | 4 | AAB59662 | Humanised |
| 278 | 27 | 87.1 | 57 | 8 | ADR90766 | CDR's fro | 351 | 27 | 87.1 | 111 | 4 | AAB59661 | Murine Fd |
| 279 | 27 | 87.1 | 58 | 5 | ABB79668 | Chronic l | 352 | 27 | 87.1 | 111 | 5 | AAU99860 | Mouse Hef |
| 280 | 27 | 87.1 | 58 | 5 | ADR90763 | CDR's fro | 353 | 27 | 87.1 | 111 | 7 | AAO29934 | Mouse ant |
| 281 | 27 | 87.1 | 59 | 5 | ABB79669 | Chronic l | 354 | 27 | 87.1 | 111 | 8 | ADT25831 | Anti-alpha |
| 282 | 27 | 87.1 | 59 | 5 | ABB79676 | Chronic l | 355 | 27 | 87.1 | 111 | 8 | ADT25830 | Anti-alpha |
| 283 | 27 | 87.1 | 60 | 6 | ABU56880 | BONT/A Hc | 356 | 27 | 87.1 | 111 | 8 | ADJ87928 | Mouse Hef |
| 284 | 27 | 87.1 | 60 | 6 | ABU56875 | BONT/A Hc | 357 | 27 | 87.1 | 111 | 8 | ADT47765 | Humanised |
| 285 | 27 | 87.1 | 60 | 6 | ABU56876 | BONT/A Hc | 358 | 27 | 87.1 | 111 | 8 | ADT47709 | Humanised |
| 286 | 27 | 87.1 | 60 | 6 | ABU56879 | BONT/A Hc | 359 | 27 | 87.1 | 111 | 8 | ADT47764 | Mouse Fd7 |
| 287 | 27 | 87.1 | 60 | 6 | ABU56879 | BONT/A Hc | 360 | 27 | 87.1 | 111 | 8 | ADT47708 | Mouse Fd7 |
| 288 | 27 | 87.1 | 61 | 5 | ABB79661 | Chronic l | 361 | 27 | 87.1 | 111 | 8 | ADQ37211 | Mouse mon |
| 289 | 27 | 87.1 | 61 | 5 | ABB79673 | CDR's fro | 362 | 27 | 87.1 | 111 | 8 | ADQ37216 | Mouse mon |
| 290 | 27 | 87.1 | 62 | 5 | ABB79663 | Chronic l | 363 | 27 | 87.1 | 111 | 8 | ADQ37217 | Mouse mon |
| 291 | 27 | 87.1 | 62 | 5 | ABB79664 | Chronic l | 364 | 27 | 87.1 | 111 | 8 | ADQ37217 | Mouse mon |
| 292 | 27 | 87.1 | 62 | 8 | ADR90774 | CDR's fro | 365 | 27 | 87.1 | 111 | 8 | ADT15140 | Mouse ant- |
| 293 | 27 | 87.1 | 62 | 8 | ADR90760 | CDR's fro | 366 | 27 | 87.1 | 111 | 8 | ADT15140 | Mouse ant- |
| 294 | 27 | 87.1 | 63 | 5 | ABB79659 | Chronic l | 367 | 27 | 87.1 | 111 | 9 | ADT16641 | Humanized |
| 295 | 27 | 87.1 | 63 | 5 | ABB79658 | Chronic l | 368 | 27 | 87.1 | 112 | 2 | AAR10539 | Chimeric |
| 296 | 27 | 87.1 | 63 | 8 | ADR90757 | CDR's fro | 369 | 27 | 87.1 | 112 | 2 | AAR13089 | Murine 1B |
| 297 | 27 | 87.1 | 63 | 8 | ADR90772 | CDR's fro | 370 | 27 | 87.1 | 112 | 2 | AAR80272 | VI region |
| 298 | 27 | 87.1 | 67 | 5 | ABB79676 | Chronic l | 371 | 27 | 87.1 | 112 | 2 | AAR75431 | Human thy |
| 299 | 27 | 87.1 | 67 | 5 | ADR90768 | CDR's fro | 372 | 27 | 87.1 | 112 | 2 | AAR79156 | Human IGE |
| 300 | 27 | 87.1 | 68 | 5 | ABB79677 | Chronic l | 373 | 27 | 87.1 | 112 | 2 | AAR79158 | Human IGE |
| 301 | 27 | 87.1 | 68 | 5 | ADR90779 | CDR's fro | 374 | 27 | 87.1 | 112 | 2 | AAR79249 | Light cha |
| 302 | 27 | 87.1 | 70 | 5 | ABB79675 | Chronic l | 375 | 27 | 87.1 | 112 | 2 | AAR79249 | Light cha |
| 303 | 27 | 87.1 | 70 | 5 | ADR90778 | CDR's fro | 376 | 27 | 87.1 | 112 | 2 | AAW27358 | Light cha |
| 304 | 27 | 87.1 | 71 | 5 | ABB79673 | Chronic l | 377 | 27 | 87.1 | 112 | 5 | ABB77332 | Mouse 1B4 |
| 305 | 27 | 87.1 | 71 | 8 | ADR90767 | CDR's fro | 378 | 27 | 87.1 | 112 | 5 | ABB77331 | Veneered |
| 306 | 27 | 87.1 | 85 | 6 | ABR41597 | Human DIT | 379 | 27 | 87.1 | 112 | 6 | ABB98910 | Variable |
| 307 | 27 | 87.1 | 103 | 2 | AAR47933 | Light cha | 380 | 27 | 87.1 | 112 | 8 | ADG25827 | Anti-CD30 |
| 308 | 27 | 87.1 | 103 | 2 | AAW89349 | Mouse 23F | 381 | 27 | 87.1 | 112 | 8 | ADR38676 | Mouse lig |
| 309 | 27 | 87.1 | 107 | 2 | AAW27353 | Light cha | 382 | 27 | 87.1 | 112 | 8 | ADR38689 | Mouse lig |
| 310 | 27 | 87.1 | 108 | 2 | AAV13949 | VL chain | 383 | 27 | 87.1 | 112 | 8 | ADR38675 | Mouse lig |
| 311 | 27 | 87.1 | 108 | 8 | ADT74998 | Light cha | 384 | 27 | 87.1 | 112 | 8 | ADR38681 | Mouse lig |
| 312 | 27 | 87.1 | 108 | 8 | ADT75001 | Light cha | 385 | 27 | 87.1 | 112 | 8 | ADR38680 | Mouse lig |
| 313 | 27 | 87.1 | 109 | 4 | AAB98230 | Rabbit an | 386 | 27 | 87.1 | 112 | 8 | ADR38679 | Mouse lig |
| 314 | 27 | 87.1 | 109 | 4 | AAB98235 | Humanised | 387 | 27 | 87.1 | 112 | 8 | ADT75130 | Light cha |
| 315 | 27 | 87.1 | 109 | 4 | AAB98234 | Humanised | 388 | 27 | 87.1 | 112 | 8 | ADT75138 | Light cha |
| 316 | 27 | 87.1 | 109 | 4 | AAB98236 | Humanised | 389 | 27 | 87.1 | 112 | 8 | ADT75123 | Light cha |

| | | | | | | | | | | | | | | | |
|-----|----|------|-----|---|----------|----------|------------|-----|----|------|------|------|-----------|------------|-----------|
| 390 | 27 | 87.1 | 112 | 8 | ADT75139 | Adt75139 | Light cha | 463 | 27 | 87.1 | 230 | 2 | AAR06610 | Intact no | |
| 391 | 27 | 87.1 | 112 | 8 | ADT75137 | Adt75137 | Light cha | 464 | 27 | 87.1 | 230 | 2 | AAR59801 | Fusarium | |
| 392 | 27 | 87.1 | 112 | 8 | ADT75136 | Adt75136 | Light cha | 465 | 27 | 87.1 | 230 | 2 | AAR46295 | F. solani | |
| 393 | 27 | 87.1 | 112 | 9 | ADV77267 | Adv77267 | Murine an | 466 | 27 | 87.1 | 230 | 2 | AAR59796 | Fusarium | |
| 394 | 27 | 87.1 | 112 | 9 | ADV77266 | Adv77266 | Veneered | 467 | 27 | 87.1 | 237 | 2 | AAW73873 | Human ant | |
| 395 | 27 | 87.1 | 112 | 9 | ADM95700 | Adm95700 | Mouse ant | 468 | 27 | 87.1 | 238 | 6 | ADA47339 | TRX1 ligh | |
| 396 | 27 | 87.1 | 112 | 9 | ADX15705 | Adx15705 | Mouse ant | 469 | 27 | 87.1 | 238 | 6 | ADA47330 | TRX1 ligh | |
| 397 | 27 | 87.1 | 112 | 9 | ADY28849 | Ady28849 | Murine an | 470 | 27 | 87.1 | 238 | 6 | ADA47338 | TRX1 ligh | |
| 398 | 27 | 87.1 | 112 | 9 | AEb21444 | Aeb21444 | Anti-IL13 | 471 | 27 | 87.1 | 238 | 6 | ADA47332 | TRX1 ligh | |
| 399 | 27 | 87.1 | 112 | 9 | AEb21446 | Aeb21446 | Anti-IL13 | 472 | 27 | 87.1 | 238 | 6 | ADP88434 | Antibody | |
| 400 | 27 | 87.1 | 112 | 9 | AEb21493 | Aeb21493 | Anti-IL13 | 473 | 27 | 87.1 | 238 | 8 | ADP88442 | Antibody | |
| 401 | 27 | 87.1 | 112 | 9 | AEb21495 | Aeb21495 | Anti-IL13 | 474 | 27 | 87.1 | 238 | 8 | ADP88450 | Antibody | |
| 402 | 27 | 87.1 | 112 | 9 | AEb21448 | Aeb21448 | Anti-IL13 | 475 | 27 | 87.1 | 238 | 8 | ADP88426 | Antibody | |
| 403 | 27 | 87.1 | 112 | 9 | AEb21501 | Aeb21501 | Anti-IL13 | 476 | 27 | 87.1 | 238 | 8 | ADQ87972 | Light cha | |
| 404 | 27 | 87.1 | 112 | 9 | AEb31253 | Aeb31253 | Antibody | 477 | 27 | 87.1 | 238 | 8 | ADQ87976 | Light cha | |
| 405 | 27 | 87.1 | 112 | 9 | AEb31259 | Aeb31259 | Antibody | 478 | 27 | 87.1 | 238 | 8 | ADQ87964 | Light cha | |
| 406 | 27 | 87.1 | 112 | 9 | AEb31204 | Aeb31204 | Antibody | 479 | 27 | 87.1 | 238 | 8 | ADQ87968 | Light cha | |
| 407 | 27 | 87.1 | 112 | 9 | AEb31206 | Aeb31206 | Antibody | 480 | 27 | 87.1 | 238 | 9 | ADY30114 | Human Igg | |
| 408 | 27 | 87.1 | 112 | 9 | AEb31251 | Aeb31251 | Antibody | 481 | 27 | 87.1 | 240 | 2 | AAW73875 | Human ant | |
| 409 | 27 | 87.1 | 112 | 9 | AEb31202 | Aeb31202 | Antibody | 482 | 27 | 87.1 | 241 | 8 | ADP79577 | Plasmiid p | |
| 410 | 27 | 87.1 | 113 | 8 | ADG25823 | Adg25823 | Anti-CD30 | 483 | 27 | 87.1 | 243 | 9 | ADW95686 | Anti-IL-6 | |
| 411 | 27 | 87.1 | 113 | 8 | ADT75140 | Adt75140 | Light cha | 484 | 27 | 87.1 | 243 | 9 | ADX15691 | Mouse ant | |
| 412 | 27 | 87.1 | 113 | 8 | ADT75131 | Adt75131 | Light cha | 485 | 27 | 87.1 | 248 | 9 | AEb21503 | Anti-IL13 | |
| 413 | 27 | 87.1 | 113 | 8 | ADT75129 | Adt75129 | Light cha | 486 | 27 | 87.1 | 248 | 9 | AEb31261 | Monoclonal | |
| 414 | 27 | 87.1 | 113 | 8 | ADT75127 | Adt75127 | Light cha | 487 | 27 | 87.1 | 249 | 4 | AAAB20436 | Anti-FIX/ | |
| 415 | 27 | 87.1 | 113 | 8 | ADT75056 | Adt75056 | Light cha | 488 | 27 | 87.1 | 249 | 4 | AAAB20435 | Anti-FIX/ | |
| 416 | 27 | 87.1 | 113 | 8 | ADT75135 | Adt75135 | Light cha | 489 | 27 | 87.1 | 252 | 2 | AAW02294 | Yeast-FvK | |
| 417 | 27 | 87.1 | 113 | 8 | ADT75141 | Adt75141 | Light cha | 490 | 27 | 87.1 | 256 | 5 | ABG77309 | Selected | |
| 418 | 27 | 87.1 | 113 | 9 | AEb21354 | Aeb21354 | Mouse ant | 491 | 27 | 87.1 | 259 | 9 | ADY84995 | Lawsonia | |
| 419 | 27 | 87.1 | 113 | 9 | AEb31112 | Aeb31112 | Antibody | 492 | 27 | 87.1 | 260 | 2 | ADY77617 | Anti-C5 M | |
| 420 | 27 | 87.1 | 114 | 5 | AAE28148 | Aae28148 | Humanised | 493 | 27 | 87.1 | 271 | 2 | AAW02293 | FvK-II-K | |
| 421 | 27 | 87.1 | 114 | 5 | AAE28146 | Aae28146 | Murine 9F | 494 | 27 | 87.1 | 285 | 8 | ADX66246 | Plant ful | |
| 422 | 27 | 87.1 | 117 | 8 | ADM78053 | Adm78053 | Human SKB | 495 | 27 | 87.1 | 291 | 4 | AAAB20443 | Antibody | |
| 423 | 27 | 87.1 | 120 | 2 | AAK48620 | Aak48620 | Sequence | 496 | 27 | 87.1 | 291 | 6 | ABR42054 | Newcastle | |
| 424 | 27 | 87.1 | 120 | 8 | ADR30761 | Adr30761 | Mouse B2G | 497 | 27 | 87.1 | 294 | 4 | AAAB20442 | Anti-FIX/ | |
| 425 | 27 | 87.1 | 120 | 9 | AEA88776 | Aea88776 | Murine SA | 498 | 27 | 87.1 | 310 | 5 | ABJ04709 | Mycobacte | |
| 426 | 27 | 87.1 | 121 | 2 | AAK33346 | Aak33346 | Sequence | 499 | 27 | 87.1 | 322 | 4 | AAAB20440 | Antibody | |
| 427 | 27 | 87.1 | 121 | 2 | AAK48615 | Aak48615 | Sequence | 500 | 27 | 87.1 | 325 | 4 | AAAB20438 | Anti-FIX/ | |
| 428 | 27 | 87.1 | 121 | 2 | AAW09259 | Aaw09259 | Monoclonal | 501 | 27 | 87.1 | 329 | 4 | AAAB70840 | SNV-env 1 | |
| 429 | 27 | 87.1 | 121 | 2 | AAW09274 | Aaw09274 | MAB NM-01 | 502 | 27 | 87.1 | 380 | 5 | ABJ11281 | Yeast sel | |
| 430 | 27 | 87.1 | 125 | 2 | AAK15440 | Aak15440 | Light cha | 503 | 27 | 87.1 | 396 | 5 | ABB48811 | Listeria | |
| 431 | 27 | 87.1 | 129 | 5 | AAU70767 | Aau70767 | Hepatitis | 504 | 27 | 87.1 | 396 | 6 | ABU32470 | Protein e | |
| 432 | 27 | 87.1 | 129 | 7 | ADC85021 | Adc85021 | HBV HBcAg | 505 | 27 | 87.1 | 437 | 2 | AAW37738 | Nucleotid | |
| 433 | 27 | 87.1 | 129 | 8 | ADK14578 | Adk14578 | Hepatitis | 506 | 27 | 87.1 | 438 | 5 | ABJ10971 | Yeast sel | |
| 434 | 27 | 87.1 | 130 | 6 | ABJ36932 | Abj36932 | Anti-CD40 | 507 | 27 | 87.1 | 439 | 3 | AAAG32105 | Arabidops | |
| 435 | 27 | 87.1 | 131 | 2 | AAK28668 | Aak28668 | p12-k2. 3 | 508 | 27 | 87.1 | 468 | 3 | AAK45381 | Arabidops | |
| 436 | 27 | 87.1 | 131 | 2 | AAK29008 | Aak29008 | p64-k4 pr | 509 | 27 | 87.1 | 468 | 3 | AAK21096 | Arabidops | |
| 437 | 27 | 87.1 | 131 | 2 | AAW01143 | Aaw01143 | MAB 1.4.1 | 510 | 27 | 87.1 | 486 | 6 | ABR53424 | Protein s | |
| 438 | 27 | 87.1 | 131 | 2 | AAW30278 | Aaw30278 | Light cha | 511 | 27 | 87.1 | 486 | 7 | ADK64682 | Disease t | |
| 439 | 27 | 87.1 | 131 | 2 | AAW30274 | Aaw30274 | Light cha | 512 | 27 | 87.1 | 495 | 4 | AAAB72414 | Double-he | |
| 440 | 27 | 87.1 | 131 | 2 | AAW44168 | Aaw44168 | Monoclonal | 513 | 27 | 87.1 | 512 | 5 | ABJ11211 | Yeast sel | |
| 441 | 27 | 87.1 | 132 | 2 | AAK10920 | Aak10920 | kappa lig | 514 | 27 | 87.1 | 619 | 4 | AAE10890 | Rickettsi | |
| 442 | 27 | 87.1 | 132 | 2 | AAW03723 | Aaw03723 | Anti-huma | 515 | 27 | 87.1 | 623 | 9 | AEA99706 | Human CAB | |
| 443 | 27 | 87.1 | 132 | 8 | ADP88791 | Adp88791 | Anti-CD70 | 516 | 27 | 87.1 | 729 | 4 | AAAB20439 | Antibody | |
| 444 | 27 | 87.1 | 135 | 5 | ABG77379 | Abg77379 | Selected | 517 | 27 | 87.1 | 732 | 4 | AAAB20437 | Anti-FIX/ | |
| 445 | 27 | 87.1 | 147 | 4 | AAW87796 | Aaw87796 | Human imm | 518 | 27 | 87.1 | 762 | 9 | ABEC08408 | ScFv-B2-F | |
| 446 | 27 | 87.1 | 149 | 2 | AAW02292 | Aaw02292 | FvK-II V | 519 | 27 | 87.1 | 856 | 4 | ABEB68808 | Drosophil | |
| 447 | 27 | 87.1 | 177 | 8 | ADS44631 | Ada44631 | Bacterial | 520 | 27 | 87.1 | 856 | 7 | ADJ37949 | D melanog | |
| 448 | 27 | 87.1 | 179 | 8 | ADK17745 | Adk17745 | Anti-CEA | 521 | 27 | 87.1 | 1040 | 8 | ADJ17749 | Rat major | |
| 449 | 27 | 87.1 | 199 | 6 | AAE34647 | Aae34647 | Fusarium | 522 | 27 | 87.1 | 1072 | 8 | ADJ17747 | Human maj | |
| 450 | 27 | 87.1 | 214 | 8 | ADN98361 | Adn98361 | Human Igg | 523 | 27 | 87.1 | 1127 | 8 | ADJ17789 | Polylysins | |
| 451 | 27 | 87.1 | 214 | 8 | ADU86568 | Adu86568 | Immunoglo | 524 | 27 | 87.1 | 1159 | 8 | ADJ17787 | Polylysins | |
| 452 | 27 | 87.1 | 214 | 8 | ADU86567 | Adu86567 | Immunoglo | 525 | 27 | 87.1 | 1206 | 8 | ADJ17763 | GALA + ra | |
| 453 | 27 | 87.1 | 215 | 2 | AAK74781 | Aak74781 | Light cha | 526 | 27 | 87.1 | 1238 | 8 | ADJ17761 | GALA + hu | |
| 454 | 27 | 87.1 | 218 | 2 | AAK75459 | Aak75459 | Mouse ant | 527 | 27 | 87.1 | 1273 | 8 | ADJ17777 | MS2 pepti | |
| 455 | 27 | 87.1 | 218 | 2 | AAK75457 | Aak75457 | Mouse ant | 528 | 27 | 87.1 | 2188 | 6 | ADA36476 | Acinetoba | |
| 456 | 27 | 87.1 | 218 | 5 | AAW49204 | Aaw49204 | Humanised | 529 | 27 | 87.1 | 3096 | 4 | AAAB46770 | PANCIP3 p | |
| 457 | 27 | 87.1 | 218 | 6 | ABP96770 | Abp96770 | TSH recep | 530 | 27 | 87.1 | 7 | 5 | AAU070326 | Human Kap | |
| 458 | 27 | 87.1 | 218 | 6 | ABP96769 | Abp96769 | TSR recep | 531 | 27 | 87.1 | 26 | 83.9 | 8 | AAK52530 | 3D6 light |
| 459 | 27 | 87.1 | 218 | 8 | ADP88435 | Adp88435 | Antibody | 532 | 27 | 87.1 | 26 | 83.9 | 8 | ABR51454 | Synthetic |
| 460 | 27 | 87.1 | 218 | 8 | ADP88427 | Adp88427 | Antibody | 533 | 27 | 87.1 | 26 | 83.9 | 24 | AAW88887 | Polypepti |
| 461 | 27 | 87.1 | 218 | 8 | ADP88451 | Adp88451 | Antibody | 534 | 27 | 87.1 | 26 | 83.9 | 24 | ABB50955 | Human sec |
| 462 | 27 | 87.1 | 218 | 8 | ADP88443 | Adp88443 | Antibody | 535 | 27 | 87.1 | 26 | 83.9 | 24 | ABO45212 | Novel hum |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|----------|-----------|-----|----|------|------|---|----------|-----------|
| 536 | 26 | 83.9 | 24 | 7 | ABO26692 | Protein a | 609 | 26 | 83.9 | 258 | 8 | ADS07642 | Staphyloc |
| 537 | 26 | 83.9 | 45 | 2 | Aaw88894 | Polypepti | 610 | 26 | 83.9 | 262 | 6 | ABU70836 | Human adi |
| 538 | 26 | 83.9 | 45 | 4 | ABBS0962 | Human sec | 611 | 26 | 83.9 | 263 | 2 | Aaw97889 | Kabat con |
| 539 | 26 | 83.9 | 45 | 6 | ABO45219 | Novel hum | 612 | 26 | 83.9 | 264 | 5 | ABG70161 | Human pre |
| 540 | 26 | 83.9 | 45 | 7 | ABO26699 | Protein a | 613 | 26 | 83.9 | 265 | 6 | ABU70644 | Human adi |
| 541 | 26 | 83.9 | 71 | 8 | Aam89776 | Human imm | 614 | 26 | 83.9 | 280 | 6 | AAI20071 | B. burgdo |
| 542 | 26 | 83.9 | 98 | 8 | ADQ75211 | Adg75211 | 615 | 26 | 83.9 | 283 | 5 | ABU75160 | Kabat con |
| 543 | 26 | 83.9 | 101 | 7 | ADL91311 | VL chain | 616 | 26 | 83.9 | 283 | 5 | ABG73148 | Kabat con |
| 544 | 26 | 83.9 | 101 | 8 | ADO36338 | Intracell | 617 | 26 | 83.9 | 283 | 6 | ABG73868 | Kabat con |
| 545 | 26 | 83.9 | 105 | 4 | AAE06076 | Human gen | 618 | 26 | 83.9 | 292 | 4 | ABR71496 | Drosophil |
| 546 | 26 | 83.9 | 105 | 5 | ABG33898 | Human sec | 619 | 26 | 83.9 | 302 | 2 | AAI20070 | B. burgdo |
| 547 | 26 | 83.9 | 106 | 3 | AAV87099 | Human sec | 620 | 26 | 83.9 | 316 | 4 | AAM93216 | Human pol |
| 548 | 26 | 83.9 | 107 | 2 | AAR30770 | Consensus | 621 | 26 | 83.9 | 316 | 8 | ADL30587 | Human pro |
| 549 | 26 | 83.9 | 107 | 4 | AAAB6040 | Human VI | 622 | 26 | 83.9 | 320 | 4 | ABG01510 | Novel hum |
| 550 | 26 | 83.9 | 107 | 4 | AAAB6040 | Consensus | 623 | 26 | 83.9 | 327 | 6 | ABU70403 | Human adi |
| 551 | 26 | 83.9 | 107 | 7 | ABG61585 | Human var | 624 | 26 | 83.9 | 337 | 6 | ABU70453 | Human adi |
| 552 | 26 | 83.9 | 107 | 7 | ADG75564 | Humanised | 625 | 26 | 83.9 | 361 | 9 | ABE45604 | Maize rar |
| 553 | 26 | 83.9 | 107 | 8 | ADG71454 | Human ant | 626 | 26 | 83.9 | 366 | 4 | ABG07923 | Novel hum |
| 554 | 26 | 83.9 | 107 | 8 | ADJ88008 | Human var | 627 | 26 | 83.9 | 367 | 8 | ADQ37151 | OsSgr1 pr |
| 555 | 26 | 83.9 | 107 | 8 | ADN12054 | Variable | 628 | 26 | 83.9 | 367 | 8 | ADQ15735 | Rice stre |
| 556 | 26 | 83.9 | 107 | 8 | ADP43328 | Human mon | 629 | 26 | 83.9 | 377 | 8 | ADT60325 | Plant pol |
| 557 | 26 | 83.9 | 107 | 8 | ADP22172 | Human ant | 630 | 26 | 83.9 | 388 | 8 | ADY05347 | Plant ful |
| 558 | 26 | 83.9 | 107 | 9 | ADW21305 | Human kap | 631 | 26 | 83.9 | 390 | 8 | ADY05389 | Plant ful |
| 559 | 26 | 83.9 | 108 | 2 | AAW70622 | Human con | 632 | 26 | 83.9 | 393 | 8 | ADY05397 | Plant ful |
| 560 | 26 | 83.9 | 108 | 3 | AAW82345 | Human con | 633 | 26 | 83.9 | 407 | 4 | ABBS0235 | Human tra |
| 561 | 26 | 83.9 | 108 | 4 | AAE12062 | Human ant | 634 | 26 | 83.9 | 408 | 3 | AAI86199 | Nuclear t |
| 562 | 26 | 83.9 | 108 | 5 | ABP61191 | Human ant | 635 | 26 | 83.9 | 412 | 7 | ADP28111 | Human NTR |
| 563 | 26 | 83.9 | 108 | 8 | ADG38991 | Human con | 636 | 26 | 83.9 | 416 | 8 | ADY10021 | Plant ful |
| 564 | 26 | 83.9 | 108 | 8 | ADR03366 | Human sub | 637 | 26 | 83.9 | 454 | 2 | AAW75854 | Human sec |
| 565 | 26 | 83.9 | 108 | 8 | ADP79572 | Human kap | 638 | 26 | 83.9 | 454 | 2 | AAW75854 | Human sec |
| 566 | 26 | 83.9 | 109 | 2 | AAK30764 | Consensus | 639 | 26 | 83.9 | 456 | 7 | ADP40443 | Human cho |
| 567 | 26 | 83.9 | 109 | 2 | AAK47041 | Sequence | 640 | 26 | 83.9 | 464 | 3 | ABE12447 | Human 149 |
| 568 | 26 | 83.9 | 109 | 5 | AAU74544 | Human sub | 641 | 26 | 83.9 | 492 | 8 | ADP28313 | Human KPP |
| 569 | 26 | 83.9 | 109 | 9 | AEA38745 | Human VL | 642 | 26 | 83.9 | 493 | 8 | ADQ37139 | Cell prol |
| 570 | 26 | 83.9 | 110 | 5 | AAE28149 | Human con | 643 | 26 | 83.9 | 498 | 8 | ADQ15723 | Rice stre |
| 571 | 26 | 83.9 | 111 | 2 | AAW95652 | Mus muscu | 644 | 26 | 83.9 | 498 | 8 | ADW41531 | Rice hist |
| 572 | 26 | 83.9 | 111 | 4 | AAW76941 | Variable | 645 | 26 | 83.9 | 506 | 4 | AAI73377 | Moraxella |
| 573 | 26 | 83.9 | 111 | 8 | ADN07028 | Humiii va | 646 | 26 | 83.9 | 507 | 5 | AAO17567 | M catarrh |
| 574 | 26 | 83.9 | 111 | 9 | ADW00650 | Human hum | 647 | 26 | 83.9 | 510 | 8 | ADL05974 | M catarr |
| 575 | 26 | 83.9 | 112 | 8 | ADP66618 | Anti-RAS | 648 | 26 | 83.9 | 510 | 8 | ADM41532 | Rice hist |
| 576 | 26 | 83.9 | 112 | 8 | ADP96650 | Anti-RAS | 649 | 26 | 83.9 | 510 | 8 | ADM41532 | Rice hist |
| 577 | 26 | 83.9 | 112 | 8 | ADO79342 | Antibody | 650 | 26 | 83.9 | 510 | 8 | ADP68855 | Rice hist |
| 578 | 26 | 83.9 | 112 | 9 | ABE21888 | Human DC- | 651 | 26 | 83.9 | 547 | 4 | ABE69125 | Drosophil |
| 579 | 26 | 83.9 | 114 | 8 | ADR40434 | Human kap | 652 | 26 | 83.9 | 585 | 7 | ADL90060 | Ubiqulin |
| 580 | 26 | 83.9 | 114 | 8 | ADR40352 | Human kap | 653 | 26 | 83.9 | 589 | 4 | ABY74670 | Human pro |
| 581 | 26 | 83.9 | 124 | 4 | ABG02537 | Novel hum | 654 | 26 | 83.9 | 589 | 4 | ABY5205 | Human pro |
| 582 | 26 | 83.9 | 125 | 6 | ABG71755 | Variable | 655 | 26 | 83.9 | 589 | 4 | ABY5205 | Human pro |
| 583 | 26 | 83.9 | 125 | 9 | ADY58503 | Consensus | 656 | 26 | 83.9 | 589 | 4 | ABY94311 | Human pro |
| 584 | 26 | 83.9 | 126 | 2 | AAV17492 | Consensus | 657 | 26 | 83.9 | 589 | 4 | ABU52717 | Human bra |
| 585 | 26 | 83.9 | 126 | 2 | AAV08702 | Human lig | 658 | 26 | 83.9 | 589 | 4 | ABE62194 | Human SAP |
| 586 | 26 | 83.9 | 126 | 2 | AAV08702 | Human lig | 659 | 26 | 83.9 | 589 | 7 | ADP59377 | Human sto |
| 587 | 26 | 83.9 | 126 | 3 | AAV08701 | Human con | 660 | 26 | 83.9 | 589 | 7 | ADL90052 | Human ubi |
| 588 | 26 | 83.9 | 126 | 3 | AAV83645 | Conserved | 661 | 26 | 83.9 | 589 | 9 | ADY17996 | PRO polyP |
| 589 | 26 | 83.9 | 126 | 5 | ABBO4943 | Human CD2 | 662 | 26 | 83.9 | 589 | 9 | ADY54104 | Anino aci |
| 590 | 26 | 83.9 | 126 | 5 | AAU10768 | Amino aci | 663 | 26 | 83.9 | 589 | 9 | ADY70288 | Human bet |
| 591 | 26 | 83.9 | 126 | 6 | ABG71656 | Consensus | 664 | 26 | 83.9 | 595 | 7 | ADL90050 | Human ubi |
| 592 | 26 | 83.9 | 126 | 6 | ABG71769 | Variable | 665 | 26 | 83.9 | 596 | 4 | AAE64210 | Murine HS |
| 593 | 26 | 83.9 | 126 | 7 | ADP00054 | Human con | 666 | 26 | 83.9 | 601 | 7 | ADL18594 | Human dis |
| 594 | 26 | 83.9 | 128 | 5 | ABBO4947 | CD28 synt | 667 | 26 | 83.9 | 604 | 4 | ABG16557 | Novel hum |
| 595 | 26 | 83.9 | 128 | 5 | AAU10774 | Light cha | 668 | 26 | 83.9 | 615 | 4 | ABG04678 | Novel hum |
| 596 | 26 | 83.9 | 129 | 6 | ABG71751 | Antibody | 669 | 26 | 83.9 | 624 | 4 | ABE47122 | Human Cha |
| 597 | 26 | 83.9 | 130 | 5 | AAU10776 | Light cha | 670 | 26 | 83.9 | 624 | 5 | ABY97373 | Novel Hum |
| 598 | 26 | 83.9 | 131 | 6 | ABG71753 | Antibody | 671 | 26 | 83.9 | 624 | 5 | ABY73446 | Candida a |
| 599 | 26 | 83.9 | 161 | 7 | ABO82934 | Pseudomon | 672 | 26 | 83.9 | 624 | 7 | ADC35081 | Human bre |
| 600 | 26 | 83.9 | 201 | 6 | ABU70523 | Human adi | 673 | 26 | 83.9 | 624 | 7 | ADL90057 | Ubiqulin |
| 601 | 26 | 83.9 | 214 | 6 | ABU70502 | Human adi | 674 | 26 | 83.9 | 632 | 4 | ABG04680 | Novel hum |
| 602 | 26 | 83.9 | 236 | 9 | AEA41031 | Human ant | 675 | 26 | 83.9 | 638 | 7 | ADL90059 | Ubiqulin |
| 603 | 26 | 83.9 | 237 | 8 | ADX66125 | Plant ful | 676 | 26 | 83.9 | 664 | 5 | ABY92106 | Herbicida |
| 604 | 26 | 83.9 | 239 | 2 | AAV79866 | Anti-EGFR | 677 | 26 | 83.9 | 721 | 4 | AAE78364 | GRR1 homo |
| 605 | 26 | 83.9 | 254 | 4 | AAE81904 | S. epider | 678 | 26 | 83.9 | 748 | 6 | ADB12089 | Allolococ |
| 606 | 26 | 83.9 | 257 | 8 | ADX72897 | Plant ful | 679 | 26 | 83.9 | 761 | 6 | ADB12087 | Allolococ |
| 607 | 26 | 83.9 | 258 | 8 | ADX72869 | Plant ful | 680 | 26 | 83.9 | 801 | 4 | ABE62287 | Drosophil |
| 608 | 26 | 83.9 | 258 | 5 | ABP39759 | Staphyloc | 681 | 26 | 83.9 | 1261 | 7 | ADB70301 | C. neofo |

| | | | | | | | | | | | | | | | |
|-----|----|------|-------|---|-----------|-----------|------------|-----|----|------|-----|---|----------|-----------|-----------|
| 682 | 26 | 83.9 | 1957 | 6 | ABM66683 | Abm66683 | Photorhab | 755 | 25 | 80.6 | 331 | 8 | ADP24901 | Adp24901 | PRO polyp |
| 683 | 26 | 83.9 | 2056 | 4 | ABB59344 | Abb59344 | Drosophil | 756 | 25 | 80.6 | 334 | 4 | AA999943 | Aab999943 | Rat chond |
| 684 | 26 | 83.9 | 2854 | 6 | ABM69174 | Abm69174 | Photorhab | 757 | 25 | 80.6 | 334 | 4 | ADT66643 | Adt66643 | Rat Prote |
| 685 | 26 | 83.9 | 3497 | 6 | ABM68681 | Abm68681 | Photorhab | 758 | 25 | 80.6 | 334 | 8 | ADT66643 | Adt66643 | Rat chond |
| 686 | 26 | 83.9 | 3673 | 6 | ABM68688 | Abm68688 | Photorhab | 759 | 25 | 80.6 | 334 | 8 | ADT66643 | Adt66643 | Rat chond |
| 687 | 26 | 83.9 | 15281 | 2 | AA444929 | Aar444929 | T. niveum | 760 | 25 | 80.6 | 344 | 3 | AA944995 | Aay944995 | Human eec |
| 688 | 25 | 80.6 | 7 | 7 | AD69245 | Add69245 | Human lig | 761 | 25 | 80.6 | 344 | 3 | AA944896 | Aay944896 | Human pro |
| 689 | 25 | 80.6 | 7 | 7 | AD69242 | Add69242 | Human lig | 762 | 25 | 80.6 | 344 | 3 | AA944896 | Aay944896 | Human pro |
| 690 | 25 | 80.6 | 7 | 7 | ADD93797 | Add93797 | Antibody | 763 | 25 | 80.6 | 344 | 8 | AA888374 | Aab888374 | Human mem |
| 691 | 25 | 80.6 | 7 | 8 | AD524339 | Ad524339 | Fab target | 764 | 25 | 80.6 | 344 | 8 | ADQ95926 | Adq95926 | T cell ac |
| 692 | 25 | 80.6 | 7 | 9 | AEA45439 | Aea45439 | Apollipop | 765 | 25 | 80.6 | 344 | 8 | ADQ95924 | Adq95924 | T cell ac |
| 693 | 25 | 80.6 | 7 | 9 | AEA40642 | Aea40642 | Anti-VSGF | 766 | 25 | 80.6 | 344 | 8 | ADQ95928 | Adq95928 | T cell ac |
| 694 | 25 | 80.6 | 7 | 9 | ABE28764 | Aeb28764 | Human CDR | 767 | 25 | 80.6 | 344 | 9 | ADW63113 | Adw63113 | Human clo |
| 695 | 25 | 80.6 | 40 | 6 | ABU25331 | Abu25331 | SAC isola | 768 | 25 | 80.6 | 345 | 9 | ADW18350 | Adw18350 | Eucalyptu |
| 696 | 25 | 80.6 | 94 | 9 | ADY54708 | Ady54708 | Rabbit VL | 769 | 25 | 80.6 | 351 | 3 | AA806147 | Aag06147 | Arabidops |
| 697 | 25 | 80.6 | 95 | 7 | ADP09971 | Adp09971 | Antibody | 770 | 25 | 80.6 | 353 | 4 | AA932119 | Aab93219 | Human pro |
| 698 | 25 | 80.6 | 95 | 7 | ADP09970 | Adp09970 | Antibody | 771 | 25 | 80.6 | 355 | 8 | ADX50396 | Adx50396 | Human KIF |
| 699 | 25 | 80.6 | 95 | 7 | ADP10076 | Adp10076 | Antibody | 772 | 25 | 80.6 | 355 | 8 | ADX66661 | Adx66661 | Plant ful |
| 700 | 25 | 80.6 | 95 | 7 | ADP10178 | Adp10178 | Antibody | 773 | 25 | 80.6 | 355 | 8 | ADX95777 | Adx95777 | Plant ful |
| 701 | 25 | 80.6 | 95 | 7 | ADP10177 | Adp10177 | Antibody | 774 | 25 | 80.6 | 362 | 7 | ADC61396 | Adc61396 | Hordeum v |
| 702 | 25 | 80.6 | 95 | 7 | ADP10075 | Adp10075 | VEGF anti | 775 | 25 | 80.6 | 365 | 2 | AAW89557 | Aaw89557 | Trifolium |
| 703 | 25 | 80.6 | 95 | 9 | ABE13577 | Aeb13577 | Human var | 776 | 25 | 80.6 | 366 | 8 | ADT59557 | Adt59557 | Plant pol |
| 704 | 25 | 80.6 | 95 | 9 | ABE13578 | Aeb13578 | Human var | 777 | 25 | 80.6 | 366 | 9 | ADV50400 | Adv50400 | Human KIF |
| 705 | 25 | 80.6 | 95 | 9 | ABE13630 | Aeb13630 | Human var | 778 | 25 | 80.6 | 376 | 9 | ADV50399 | Adv50399 | Human KIF |
| 706 | 25 | 80.6 | 95 | 9 | ABE13631 | Aeb13631 | Human var | 779 | 25 | 80.6 | 377 | 9 | ADX55315 | Adx55315 | E. coli m |
| 707 | 25 | 80.6 | 99 | 4 | ABG21731 | Abg21731 | Novel hum | 780 | 25 | 80.6 | 377 | 9 | ADX55294 | Adx55294 | E. coli m |
| 708 | 25 | 80.6 | 100 | 7 | ADD69216 | Add69216 | Human ant | 781 | 25 | 80.6 | 377 | 9 | ADX55311 | Adx55311 | E. coli m |
| 709 | 25 | 80.6 | 100 | 7 | ADD69215 | Add69215 | Human ant | 782 | 25 | 80.6 | 377 | 9 | ADX55344 | Adx55344 | E. coli m |
| 710 | 25 | 80.6 | 103 | 7 | ADD69249 | Add69249 | Human lig | 783 | 25 | 80.6 | 377 | 9 | ADX55295 | Adx55295 | E. coli m |
| 711 | 25 | 80.6 | 105 | 2 | AAW52217 | Aaw52217 | Antibody | 784 | 25 | 80.6 | 377 | 9 | ADX55341 | Adx55341 | E. coli m |
| 712 | 25 | 80.6 | 105 | 4 | AAW18930 | Aam18930 | Peptide # | 785 | 25 | 80.6 | 377 | 9 | ADX55342 | Adx55342 | E. coli m |
| 713 | 25 | 80.6 | 105 | 4 | AB838076 | Ab838076 | Peptide # | 786 | 25 | 80.6 | 377 | 9 | ADX55351 | Adx55351 | E. coli m |
| 714 | 25 | 80.6 | 105 | 4 | AAW31498 | Aam31498 | Peptide # | 787 | 25 | 80.6 | 377 | 9 | ADX55352 | Adx55352 | E. coli m |
| 715 | 25 | 80.6 | 105 | 4 | AB823296 | Ab823296 | Protein # | 788 | 25 | 80.6 | 377 | 9 | ADX55270 | Adx55270 | E. coli m |
| 716 | 25 | 80.6 | 105 | 4 | AAW71217 | Aam71217 | Human bra | 789 | 25 | 80.6 | 377 | 9 | ADX55320 | Adx55320 | E. coli m |
| 717 | 25 | 80.6 | 105 | 4 | AAW58711 | Aam58711 | Human pep | 790 | 25 | 80.6 | 377 | 9 | ADX55345 | Adx55345 | E. coli m |
| 718 | 25 | 80.6 | 105 | 5 | ABG41014 | Abg41014 | Human lge | 791 | 25 | 80.6 | 377 | 9 | ADX55273 | Adx55273 | E. coli m |
| 719 | 25 | 80.6 | 106 | 5 | ABG30449 | Abg30449 | Human lge | 792 | 25 | 80.6 | 377 | 9 | ADX55272 | Adx55272 | E. coli m |
| 720 | 25 | 80.6 | 107 | 9 | AEA40458 | Aea40458 | Anti-VEGF | 793 | 25 | 80.6 | 377 | 9 | ADX55300 | Adx55300 | E. coli m |
| 721 | 25 | 80.6 | 107 | 9 | AEA40473 | Aea40473 | Anti-VEGF | 794 | 25 | 80.6 | 378 | 9 | ADV50398 | Adv50398 | Human KIF |
| 722 | 25 | 80.6 | 108 | 2 | AAW21286 | Aar21286 | Murine VL | 795 | 25 | 80.6 | 382 | 7 | ABO63695 | AbO63695 | Klebsiell |
| 723 | 25 | 80.6 | 109 | 9 | ADY96994 | Ady96994 | Human imm | 796 | 25 | 80.6 | 388 | 7 | ADP74135 | Adp74135 | Human nov |
| 724 | 25 | 80.6 | 126 | 3 | ABG60073 | Abg60073 | Arabidops | 797 | 25 | 80.6 | 388 | 9 | ADV50397 | Adv50397 | Human KIF |
| 725 | 25 | 80.6 | 131 | 5 | ABP51941 | Abp51941 | Silenced | 798 | 25 | 80.6 | 411 | 8 | ADT28263 | Adt28263 | Bacterial |
| 726 | 25 | 80.6 | 131 | 5 | ABP51938 | Abp51938 | Silenced | 799 | 25 | 80.6 | 420 | 7 | ADC37552 | Adc37552 | Bacterial |
| 727 | 25 | 80.6 | 133 | 5 | ABP51939 | Abp51939 | Silenced | 800 | 25 | 80.6 | 426 | 8 | ADN18465 | Adn18465 | Bacterial |
| 728 | 25 | 80.6 | 134 | 3 | AAW13014 | Aag13014 | Arabidops | 801 | 25 | 80.6 | 427 | 2 | AAW26435 | Aar26435 | P.falciPa |
| 729 | 25 | 80.6 | 145 | 8 | ADX94677 | Adx94677 | Plant ful | 802 | 25 | 80.6 | 429 | 6 | ABU43031 | Abu43031 | Protein e |
| 730 | 25 | 80.6 | 155 | 8 | ADP15892 | Adp15892 | Extended | 803 | 25 | 80.6 | 429 | 6 | ADU20640 | Adu20640 | S. epider |
| 731 | 25 | 80.6 | 164 | 3 | ABG60072 | Abg60072 | Arabidops | 804 | 25 | 80.6 | 431 | 4 | AAW85042 | Aag85042 | Shrimp wh |
| 732 | 25 | 80.6 | 164 | 3 | ABG60072 | Abg60072 | Arabidops | 805 | 25 | 80.6 | 434 | 7 | ADT08569 | Adt08569 | Novel pro |
| 733 | 25 | 80.6 | 167 | 5 | ABU05392 | Abu05392 | M. tuberc | 806 | 25 | 80.6 | 435 | 4 | AAW95024 | Aab95024 | Human pro |
| 734 | 25 | 80.6 | 181 | 4 | ADW19996 | Adw19996 | Protein e | 807 | 25 | 80.6 | 435 | 4 | AAE04773 | Aae04773 | Human ves |
| 735 | 25 | 80.6 | 184 | 3 | AAW13012 | Aag13012 | Arabidops | 808 | 25 | 80.6 | 435 | 6 | ABU56561 | Abu56561 | Lung canc |
| 736 | 25 | 80.6 | 209 | 2 | AAW63117 | Aar63117 | Light cha | 809 | 25 | 80.6 | 435 | 7 | ADJ68841 | Adj68841 | Human bea |
| 737 | 25 | 80.6 | 213 | 9 | AAW95495 | Abm95495 | M. xanthu | 810 | 25 | 80.6 | 444 | 6 | ABU34078 | Abu34078 | Protein e |
| 738 | 25 | 80.6 | 214 | 9 | ADW18564 | Adw18564 | VEGF-spec | 811 | 25 | 80.6 | 445 | 5 | ABP40103 | Abp40103 | Staphyloc |
| 739 | 25 | 80.6 | 214 | 9 | ADW18565 | Adw18565 | VEGF-spec | 812 | 25 | 80.6 | 445 | 8 | ADY12725 | Ady12725 | Plant ful |
| 740 | 25 | 80.6 | 214 | 9 | AEA13947 | Aea13947 | VEGF rela | 813 | 25 | 80.6 | 445 | 8 | ADY12725 | Ady12725 | Plant ful |
| 741 | 25 | 80.6 | 214 | 9 | AEA13949 | Aea13949 | VEGF rela | 814 | 25 | 80.6 | 447 | 8 | ADR86233 | Adr86233 | Aspergill |
| 742 | 25 | 80.6 | 221 | 4 | ABW86191 | Abw86191 | Human Ki- | 815 | 25 | 80.6 | 449 | 8 | ADT78289 | Adt78289 | Amiotran |
| 743 | 25 | 80.6 | 231 | 8 | ADQ95930 | Adq95930 | T cell ac | 816 | 25 | 80.6 | 463 | 9 | ABM91955 | Abm91955 | M. xanthu |
| 744 | 25 | 80.6 | 236 | 7 | ADD93785 | Ad93785 | Monoclonal | 817 | 25 | 80.6 | 511 | 4 | ABG19568 | Abg19568 | Novel hum |
| 745 | 25 | 80.6 | 240 | 4 | AAW46040 | Aab46040 | Human TF | 818 | 25 | 80.6 | 518 | 4 | AAW83276 | Aag83276 | Chlamydia |
| 746 | 25 | 80.6 | 248 | 3 | AAW06148 | Aag06148 | Arabidops | 819 | 25 | 80.6 | 518 | 5 | ABW94247 | Abw94247 | Chlamydia |
| 747 | 25 | 80.6 | 248 | 3 | AAW060071 | Aag60071 | Arabidops | 820 | 25 | 80.6 | 528 | 6 | ADA48594 | Ada48594 | Rice prot |
| 748 | 25 | 80.6 | 250 | 8 | ADL05914 | Adl05914 | M. catarr | 821 | 25 | 80.6 | 528 | 7 | ABW90080 | Abw90080 | Rice abio |
| 749 | 25 | 80.6 | 281 | 4 | AAW42239 | Aam42239 | Soybean r | 822 | 25 | 80.6 | 554 | 4 | AAW17983 | Aam17983 | Peptide # |
| 750 | 25 | 80.6 | 313 | 8 | ADQ89848 | Adq89848 | Antagonis | 823 | 25 | 80.6 | 554 | 4 | ABB37013 | Abb37013 | Peptide # |
| 751 | 25 | 80.6 | 314 | 8 | ADQ66606 | Adq66606 | Novel hum | 824 | 25 | 80.6 | 554 | 4 | AAW30491 | Aam30491 | Peptide # |
| 752 | 25 | 80.6 | 318 | 8 | ADQ66627 | Adq66627 | Plant ful | 825 | 25 | 80.6 | 554 | 4 | ABB31784 | Abb31784 | Peptide # |
| 753 | 25 | 80.6 | 326 | 8 | ADY13535 | Ady13535 | Plant ful | 826 | 25 | 80.6 | 554 | 4 | ABB22327 | Abb22327 | Protein # |
| 754 | 25 | 80.6 | 331 | 7 | ADC31639 | Adc31639 | Human nov | 827 | 25 | 80.6 | 554 | 4 | AAW70153 | Aam70153 | Human bon |

974 24 77.4 95 7 ADF09968
 975 24 77.4 95 7 ADF10176
 976 24 77.4 95 7 ADF10074
 977 24 77.4 95 7 ADF09969
 978 24 77.4 95 7 ADF10175
 979 24 77.4 95 7 ADF09872
 980 24 77.4 95 7 ADJ80244
 981 24 77.4 95 7 ADJ80243
 982 24 77.4 95 8 ADJ07313
 983 24 77.4 95 8 ADJ07312
 984 24 77.4 95 8 ADJ06533
 985 24 77.4 95 8 ADJ06534
 986 24 77.4 95 9 ADJ75418
 987 24 77.4 95 9 ADJ75417
 988 24 77.4 95 9 ADZ47744
 989 24 77.4 95 9 AEB13628
 990 24 77.4 95 9 AEB13576
 991 24 77.4 95 9 AEB13575
 992 24 77.4 95 9 AEB13629
 993 24 77.4 95 9 AEB70426
 994 24 77.4 96 5 ABB55546
 995 24 77.4 98 9 ADY31694
 996 24 77.4 103 2 AAW04603
 997 24 77.4 104 2 AAW62819
 998 24 77.4 104 2 AAW62821
 999 24 77.4 105 2 AAW80978
 1000 24 77.4 105 2 AAW80964

ALIGNMENTS

RESULT 1

AAW70196

ID AAR70196 standard; protein; 7 AA.

XX

AC AAR70196;

DT 25-MAR-2003 (revised)

DT 20-SEP-1995 (first entry)

XX

DE MAB 3B9 light chain CDR.

XX

XX Chimeric antibody; humanized antibody; antibody engineering;

KW monoclonal antibody; MAB; interleukin-4; IL-4; allergy; CDR;

KW complementarity determining region.

XX

OS Mus sp.

XX

XX WO9507301-A1.

XX

PD 16-MAR-1995.

XX

PF 07-SEP-1994; 94WU-05010308.

XX

XX 07-SEP-1993; 93US-00117366.

PR 14-OCT-1993; 93US-00136783.

XX

XX (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX

PI Holmes S, Gross MS, Sylvester DR;

XX

XX WPI; 1995-123387/16.

XX

XX Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from

PT high affinity mAbs - useful in treatment of IL-4-mediated and IgE-

PT mediated allergic conditions.

XX

XX Disclosure; Page 55; 97pp; English.

XX

XX Spleen cells from mice immunized with human IL-4 were used to prepare

CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only clone

CC

CC 3B9 was positive. cDNA clones of the 3B9 light and heavy chains were
 CC cloned into pGEMTf+ and transformed into E. coli DH5-alpha. A light chain
 CC cDNA clone was sequenced (AAQ83490) that encoded the protein given in
 CC AAR70189. 3 CDRs (AAR70195-97) were identified. (Updated on 25-MAR-2003
 CC to correct PN field.)

XX
 SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

DB 1 AASNLES 7

RESULT 2

AAW83028

ID AAW83028 standard; peptide; 7 AA.

XX

AC AAW83028;

XX

DT 25-MAR-2003 (revised)

DT 15-MAR-1999 (first entry)

XX

DE Anti-Fas MAB HFE7A light chain CDR-L2.

XX

KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis;

KW autoimmune disease; Hashimoto's disease; systemic lupus erythematosus;

KW graft versus host disease; Sjogren syndrome; pernicious anaemia;

KW Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease;

KW sterility; rheumatoid arthritis; autoimmune haemolytic anaemia;

KW myasthenia gravis; multiple sclerosis; Basedow's disease;

KW thrombopenia purpura; insulin-dependent diabetes; allergy; atopy;

KW arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis;

KW hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy;

KW complementarity determining region; CDR.

XX

OS Mus musculus.

XX

XX AU9859701-A.

PN

XX

PD 08-OCT-1998.

XX

XX 30-MAR-1998; 98AU-00059701.

PF

PR 01-APR-1997; 97JP-00082953.

PR 25-JUN-1997; 97JP-00169088.

PR 08-OCT-1997; 97JP-00276084.

XX

XX (SANY) SANKYO CO LTD.

PA

XX

XX Nobufusa S, Kimihisa I, Jun O, Masahiko O, Hideyuki H, Tohru T;

PI Hiroko Y, Akio S, Shin Y;

XX

XX WPI; 1998-543440/01.

XX

XX New antibodies and proteins bind conserved epitope of Fas antigen - used

PT to evaluate drugs in animal models and to treat Fas-associated diseases

PT e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis,

PT hepatitis and AIDS.

XX

PS Claim 9; Page 185; 292pp; English.

XX

XX This is the amino acid of complementarity determining region 2 (CDR-L2)

CC of the light chain (see AAW83042) of murine anti-human Fas monoclonal

CC antibody HFE7A. The invention relates to antibodies, especially humanised

CC antibodies (see AAW83031-37), recognising the Fas antigen. Such

CC antibodies preferably comprise a heavy chain and a light chain including

CC CDRs (see AAW83024-29) from the heavy and light chains of HFE7A.

CC Humanised antibodies are produced by CDR grafting. The antibodies are

CC capable of inducing apoptosis in abnormal cells expressing Fas, and of

CC inhibiting Fas-induced apoptosis in normal cells. They are used to
 CC evaluate, in animal models, treatments of diseases that involve Fas/Fas
 CC ligand interactions, and also to treat such diseases, including
 CC autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's
 CC disease, graft versus host disease, Sjogren syndrome, pernicious anaemia,
 CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease,
 CC rheumatoid arthritis, autoimmune haemolytic anaemia, sterility,
 CC myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia
 CC purpura and insulin-dependent diabetes), allergies, atopy,
 CC arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis,
 CC hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all
 CC claimed). (Updated on 25-MAR-2003 to correct DR field.)
 CC
 XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 |||||
 Db 1 AASNLES 7

RESULT 3

AAV23773
 ID AAV23773 standard; peptide; 7 AA.

AC AAV23773;

XX 13-SEP-1999 (first entry)

DT 13-SEP-1999 (first entry)

DE CDR of the light chain variable region of antibody 3B9.

XX Light chain variable region; interleukin-4; IL-4; antibody 3B9;

XX Chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;

KW Immunoglobulin E-mediated allergic reaction; allergic rhinitis;

KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;

KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy;

KW complementarity determining region.

XX Mus sp.

OS US528904-A.

PN 27-JUL-1999.

PD 07-JUN-1995; 95US-00483632.

PF 07-SEP-1993; 93US-00117366.

PR 14-OCT-1993; 93US-00136783.

PR 07-SEP-1994; 94WO-US010308.

XX (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX Holmes SD, Sylvester DR, Gross MS;

PI WPI; 1999-429500/36.

DR N-PSDB; AAX85890.

XX New DNA molecules encoding recombinant antibodies useful for treating IL4

PT mediated conditions.

XX Example 3; Col 43-44; 50pp; English.

PS The present sequence represents a complementarity determining region

XX (CDR) of the light chain variable region of murine interleukin-4 (IL-4)

CC antibody 3B9. The specification describes chimeric and humanised IL-4

CC monoclonal antibodies. The antibodies of the invention are used in

CC therapeutic and pharmaceutical compositions for treating IL-4 mediated

CC and immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis,

CC conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock,

CC rheumatoid arthritis, host-versus-graft disease and renal disease. They
 CC are also useful in the diagnosis of an allergy or condition associated
 CC with excess IL-4 production through the measurement e.g. by ELISA of
 CC circulating endogenous IL-4 levels in humans
 XX
 SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

|||||

Db 1 AASNLES 7

RESULT 4

AAV18115
 ID AAV18115 standard; peptide; 7 AA.

AC AAV18115;

XX 11-AUG-1999 (first entry)

DT 11-AUG-1999 (first entry)

DE Light chain CDR for hIL-4 specific antibody.

XX Antibody; interleukin-4; IL4; immunoglobulin E; IGE mediated disease;

KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;

KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;

KW autoimmune disease; graft versus host disease;

KW complementarity determining region; CDR.

XX Synthetic.

XX US5914110-A.

XX 22-JUN-1999.

PF 07-JUN-1995; 95US-00483636.

PR 07-SEP-1993; 93US-00117366.

PR 14-OCT-1993; 93US-00136783.

PR 07-SEP-1994; 94WO-US010308.

XX (SMIK) SMITHKLINE BEECHAM PLC.

PA (SMIK) SMITHKLINE BEECHAM CORP.

XX Sylvester DR, Holmes SD, Gross MS;

PI WPI; 1999-370482/31.

DR N-PSDB; AAX79514.

XX Recombinant IL4 antibodies useful for treatment of allergic rhinitis,

PT atopic asthma and anaphylactic shock.

XX Claim 7; Col 43; 50pp; English.

PS This sequence represents a light chain complementarity determining region

XX (CDR) from an antibody of the invention. The antibody is a chimeric or

CC humanised interleukin-4 (IL4) monoclonal antibody for the treatment of

CC immunoglobulin E (IGE) mediated diseases. The antibodies are useful for

CC the treatment of allergic disorders such as allergic rhinitis,

CC conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.

CC The antibodies are also useful for regulating B and T cell proliferation

CC and as such are useful in the treatment of autoimmune diseases and graft

CC versus host disease
 XX
 SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 AASNLES 7
Db      1 AASNLES 7

RESULT 5
AAB14745
ID  AAB14745 standard; peptide; 7 AA.
XX
AC  AAB14745;
XX
DT  24-NOV-2000 (first entry)
XX
DE  Mouse anti-Fas antibody HFE7A light chain CDR2.
XX
KW  Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine;
KW  complementarity determining region; CDR; human Fas; Fas ligand;
KW  apoptosis modulator; programmed cell death; autoimmune disease; allergy;
KW  atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis;
KW  aplastic anaemia; pancytopenia; hepatitis; AIDS; graft rejection;
KW  light chain.
XX
OS  Mus musculus.
XX
FN  JP2000169393-A.
XX
PD  20-JUN-2000.
XX
PF  30-SEP-1999; 99JP-00278301.
XX
PR  30-SEP-1998; 98JP-00276883.
XX
PA  (SANY ) SANKYO CO LTD.
XX
DR  WPI; 2000-485645/43.
XX
PT  Preventive or treating agent for the diseases caused by an abnormality in
PT  the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas
PT  antibody.
XX
PS  Claim 10; Page 65; 139pp; Japanese.
XX
CC  The invention relates to compositions for the prevention or treatment or
CC  diseases caused by an abnormality in the Fas/Fas ligand system containing
CC  an anti-Fas antibody as the active component. The anti-Fas antibody is
CC  either the murine anti-human Fas monoclonal antibody HFE7A, or a
CC  humanised version of HFE7A containing identical CDRs (complementarity
CC  determining regions) to antibody HFE7A. Via its interaction with Fas, the
CC  antibody of the invention acts as a modulator of apoptosis. The
CC  compositions of the invention may therefore be used in the treatment or
CC  prevention of conditions such as autoimmune diseases, allergy, atopy,
CC  arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis,
CC  aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft
CC  rejection. Sequences AAB14744-B14746 represent CDRs 1-3 of the light
CC  chain of the murine anti-human Fas monoclonal antibody HFE7A, which is
CC  produced by hybridoma HFE7A (FERM-BP-5828)
XX
SQ  Sequence 7 AA;

Query Match      100.0%; Score 31; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AASNLES 7
Db      1 AASNLES 7

RESULT 6
AAY51137
ID  AAY51137 standard; protein; 7 AA.
XX
AC  AAY51137;
XX

31-MAR-2000 (first entry)
Murine CD4/CD34 recognizing antibody light chain CDR-2 region #1.
Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
HIV infection; autoimmune disease; complementarity determining region;
CDR-2; light chain; murine.
Mus sp.
WO9961629-A1.
02-DEC-1999.
24-MAY-1999; 99WO-JP002711.
25-MAY-1998; 98JP-00159957.
26-MAY-1998; 98JP-00163023.
(ASAH ) ASAH KASEI KOGYO KK.
(ASAH ) ASAH MEDICAL CO LTD.
Ono M, Soka T, Morimoto I, Miyamura K;
WPI; 2000-086720/07.
Devices containing antibodies recognising CD4 or CD34 and their use for
the separation of CD4 or CD34 positive cells.
Claim 3; Page 77; 111pp; Japanese.
This invention describes a novel device (I) for separating cluster
differentiation (CD)-positive cells using a recombinant (chimeric or
single-chain) antibody recognising CD4 or CD34. The devices are useful
for the separation of CD4 or CD34 positive cells, which is useful for the
collection of hematopoietic undifferentiated cells, elimination of
lymphocytes from cells to be used in bone marrow transplantation, the
detection of leukemic cells and the production of medicinal compositions
for the treatment of HIV infection and autoimmune diseases. This sequence
represents a murine derived complementarity determining region CDR-2
protein fragment which is used to illustrate the method of the invention
Sequence 7 AA;

Query Match      100.0%; Score 31; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AASNLES 7
Db      1 AASNLES 7

RESULT 7
AAW90895
ID  AAW90895 standard; peptide; 7 AA.
XX
AC  AAW90895;
XX
DT  08-AUG-2000 (first entry)
XX
DE  Murine anti-Fas antibody peptide fragment #5.
XX
KW  Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic;
KW  anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
KW  dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW  nephrotropic; antifertility; neuroprotective; antiarteriosclerotic;
KW  hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW  Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW  Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW  Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;

```

KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 OS Mus musculus.
 XX EP990663-A2.
 XX 05-APR-2000.
 XX 29-SEP-1999; 99EP-00307711.
 XX 30-SEP-1998; 98JP-00276881.
 PR 30-SEP-1998; 98JP-00276882.
 XX (SANY) SANKYO CO LTD.
 PA Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 PI WPI; 2000-258930/23.
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems.
 XX Disclosure; Page 98; 263pp; English.
 PS This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antineumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatotropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a murine anti-Fas antibody peptide fragment described in the method of
 CC the invention
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 31; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AASNLES 7
 Db |||||
 1 AASNLES 7
 RESULT 8
 ID AAY59260
 AC AAY59260 standard; peptide; 7 AA.
 XX
 AC AAY59260;
 XX 17-APR-2000 (first entry)

XX Antibody 4H5 L chain variable region CDR2 fragment.
 DE CD4 antigen; anti-human; antibody; 4H5; drug; CDR;
 KW complementarity determining region.
 XX Mus sp.
 XX JP11332563-A.
 XX 07-DEC-1999.
 XX 26-MAY-1998; 98JP-00163034.
 XX 26-MAY-1998; 98JP-00163034.
 XX (ASAH) ASahi KASEI KOGYO KK.
 PA WPI; 2000-091351/08.
 DR An antibody and the nucleic acid coding the antibody.
 XX Claim 2; Page 14; 25pp; Japanese.
 XX The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. Sequences
 CC AAY59259-61 represent the complementarity determining region (CDR)-1, CDR
 CC -2 and CDR-3 fragments in the L chain variable region of the antibody 4H5
 CC respectively
 XX Sequence 7 AA;
 SQ
 Query Match 100.0%; Score 31; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AASNLES 7
 Db |||||
 1 AASNLES 7
 RESULT 9
 ID AAO18540
 AC AAO18540 standard; peptide; 7 AA.
 XX
 XX 11-OCT-2002 (first entry)
 DE Murine Mab 1F7 light chain CDR2 region.
 XX Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR;
 KW complementarity determining region; framework-determining region; FR;
 KW heavy chain; light chain; HIV infection.
 XX Mus sp.
 XX WO200255668-A2.
 XX 18-JUL-2002.
 XX 11-JAN-2002; 2002WO-US000927.
 XX 11-JAN-2001; 2001US-00759112.
 XX (IMMP-) IMMIPHERON INC.
 PI Muller S, Kohler H;
 XX WPI; 2002-590668/63.
 DR N-PSDB; AAL48665.
 XX

PT New polynucleotide encoding a complementarity- or framework-determining
PT region of an anti-idiotypic antibody that binds to human or primate anti-
PT human immunodeficiency virus (HIV) antibodies, for use in vaccines
PT against HIV.

XX Claim 4; Page 26; 27pp; English.

XX PS
XX PS
CC The present invention relates to coding sequences of the murine 1F7 anti-
CC idiotypic antibody complementarity-determining region (CDR) or framework-
CC determining region (FR). The antibody binds to human or primate anti-
CC human immunodeficiency virus (HIV) antibodies and can be used in the
CC treatment of HIV infection. The present sequence is a region of the 1F7
CC light chain

XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
DB 1 AASNLES 7

RESULT 10

ABB74910
ID ABB74910 standard; peptide; 7 AA.

XX AC ABB74910;

XX DT 30-APR-2002 (first entry)

XX DE Humanised anti-Fas antibody related peptide SEQ ID NO 27.

XX KW Human; mouse; Fas/Fas ligand system; Fas; antibody; light chain;
XX heavy chain; apoptosis; antiallergic; immunosuppressive; apoptotic;
XX autoimmunity disease; allergy; atopy.

XX OS Homo sapiens.

XX JP2001342149-A.

XX PD 11-DEC-2001.

XX PF 28-MAR-2001; 2001JP-00093243.

XX PR 29-MAR-2000; 2000JP-00091144.

XX PA (SANY) SANKYO CO LTD.

XX DR WPI; 2002-145114/19.

XX PT Drug for preventing or treating e.g. autoimmune disease or allergy,
XX comprises humanized anti-Fas antibody.

XX PS Example 6 (preparatory); Page 26; 154pp; Japanese.

XX CC The invention relates to a preventive or treating agent for diseases
XX caused by abnormality in the Fas/Fas ligand system containing, as the
XX active component, an antibody having a light chain subunit and a heavy
XX chain subunit and an activity of combining specifically with mammalian
XX Fas and an activity of inducing apoptosis in a cell expressing Fas. The
XX agent has antiallergic, immunosuppressive and apoptotic activity and is
XX used for preventing and treating autoimmune diseases, allergy, atopy and
XX others. The present sequence is that of a peptide useful to the invention

XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
DB 1 AASNLES 7

RESULT 11

AAU70353

ID AAU70353 standard; peptide; 7 AA.

XX AC AAU70353;

XX DT 14-FEB-2002 (first entry)

XX DE Mouse Kappa III light chain CDR2.

XX KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
XX complementarity determining region; framework region; IgBP;
XX transgenic plant; immunoglobulin binding protein array; IgM; IgA;
XX IgD; IgE; IgY; IgM; kappa; lambda; CHBP.

XX OS Mus musculus.

XX PN WO200183806-A1.

XX PD 08-NOV-2001.

XX PF 02-MAY-2001; 2001WO-US014349.

XX PR 02-MAY-2000; 2000US-00563222.

XX PA (EPIC-) EPICYTE PHARM INC.

XX PI Hiatt AC, Hein MB;

XX DR WPI; 2002-055482/07.

XX PT Preparing immunoglobulin binding protein array in plant cells by
XX transforming the cells with different polynucleotides encoding binding
XX protein polypeptides specific to ligand, selecting plant cells for
XX preparing array.

XX PS Disclosure; Page 14; 129pp; English.

XX CC The invention relates to transforming a population of cells (e.g. plant
XX cells), comprising using a library of two different polynucleotides
XX encoding different immunoglobulin binding protein (IgBP) polypeptides
XX that specifically bind to a ligand or form one or more disulphide bonds
XX with polypeptides in transfected cells, to generate an IgBP that binds to
XX a ligand, and transformed plant cells are selected, and preparing an IgBP
XX array in plant cells. At least one peptide sequence has at least 75%
XX sequence identity to a framework region (FR) of a native IgM, IgG, IgA,
XX IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
XX useful for preparing an immunoglobulin binding protein array, preferably
XX heavy chain binding protein (CHBP) array in eukaryotic cells especially
XX plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
XX cells (e.g. insect cells or mammalian cells). The CHBP is useful for
XX discovery of e.g. screening assays of IgBPs having desired
XX characteristics. The present sequence is a mammalian immunoglobulin
XX derived peptide that may be incorporated into an IgBP of the invention

XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
DB 1 AASNLES 7

RESULT 12

ABB74864

DR N-PSDB; AAD56795.

XX New chemokine construct comprising scFV anti-CD4 and a RANTES chemokine,
PT useful for the preparing a composition for treating HIV-infection or
PT inflammatory or autoimmune diseases.

XX Claim 11; Page 58; 109pp; English.

XX The present invention relates to a chemokine construct comprising scFV
CC anti-CD4 and a RANTES chemokine or their fragments. Sequences of the
CC invention are useful for preparing a pharmaceutical composition for
CC treating human immunodeficiency virus (HIV)-infection or acquired immune
CC deficiency syndrome (AIDS) or inflammatory and/or autoimmune diseases.
CC They are used as vaccines and in gene therapy. The present sequence is
CC mouse anti-CD4 VL CDR2 protein

XX Sequence 7 AA;
SQ

Query Match 100.0%; Score 31; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AASNLES 7
|||||
Db 1 AASNLES 7

RESULT 15
AAO29928
ID AAO29928 standard; peptide; 7 AA.
AC AAO29928;
XX
XX 03-SEP-2003 (first entry)
XX Mouse anti-CD30 antibody (AC10) light chain CDR2 (L2).

XX Immunological disorder; CD30; cytostatic; lymphocyte related disorder;
KW cytotoxic; atopic dermatitis; systemic lupus erythematosus; psoriasis;
KW atopic asthma; rhinoconjunctivitis; allergic rhinitis; Grave's disease;
KW Omenn's syndrome; tuberculosis; Sjogren's syndrome; multiple sclerosis;
KW graft-versus-host disease; primary biliary cirrhosis; viral infection;
KW rheumatoid arthritis; Hashimoto's thyroiditis; Wegener's granulomatosis;
KW human immunodeficiency virus; HIV; therapy; antibody; mouse; CDR;
KW complementarity determining region.

XX Mus musculus.
XX WO2003043583-A2.
XX 30-MAY-2003.
XX 20-NOV-2002; 2002WO-US037223.
XX 20-NOV-2001; 2001US-0331750P.
XX (SEAT-) SEATTLE GENETICS INC.
XX Law C, Klussman K, Wahl AF, Senter P, Doronina S, Toki B;
XX WPI; 2003-468727/44.
XX N-PSDB; AAL60615.

XX Treating immunological disorder that is not cancer, in a subject, by
PT administering composition comprising a first antibody that specifically
PT binds CD30 and exerts a cytostatic or cytotoxic effect on activated
PT lymphocyte.

XX Disclosure; Page 190; 194pp; English.

XX The invention relates to a method of treating an immunological disorder
CC in a subject where the immunological disorder is not cancer. The method
CC involves administering to the subject a pharmaceutical composition

CC comprising an antibody that immunospecifically binds CD30 and exerts a
CC cytostatic or cytotoxic effect on an activated lymphocyte and a carrier.
CC The method is useful for treating Th 2-lymphocyte related disorders such
CC as atopic dermatitis, systemic lupus erythematosus, atopic asthma,
CC rhinoconjunctivitis, allergic rhinitis, Omenn's syndrome, systemic
CC sclerosis or chronic graft-versus-host disease. The method is also useful
CC for treating Th 1-lymphocyte-related immunological disorders such as
CC rheumatoid arthritis, multiple sclerosis, psoriasis, Sjogren's syndrome,
CC Hashimoto's thyroiditis, Grave's disease, primary biliary cirrhosis,
CC Wegener's granulomatosis, tuberculosis or acute graft-versus host disease
CC or for treating an immunological disorder due to viral infection that
CC involves Epstein-Barr virus, human immunodeficiency virus (HIV), human T
CC leukaemia virus, hepatitis B virus or measles virus or for treating an
CC activated B lymphocyte-related disorder. The present sequence is mouse
CC anti-CD30 antibody (AC10) light chain complementarity determining region
CC (CDR)

XX Sequence 7 AA;
SQ

Query Match 100.0%; Score 31; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AASNLES 7
|||||
Db 1 AASNLES 7

RESULT 16
ADJ87916
ID ADJ87916 standard; protein; 7 AA.
AC ADJ87916;
XX
XX 06-MAY-2004 (first entry)
XX Mouse AC10 CD30 antibody light chain-CDR2, L2.

XX CD30; cytostatic; cytotoxic; Hodgkin's disease; gene therapy; mouse;
KW AC10; antibody.

XX Mus musculus.
XX US2004018194-A1.
XX 29-JAN-2004.
XX 28-MAY-2003; 2003US-00447257.
XX 28-NOV-2000; 2000US-00724406.
XX 28-NOV-2001; 2001WO-US044811.
XX 31-JUL-2002; 2002US-0400403P.
XX (FRAN/) FRANCISCO J A.
XX (RISD/) RISDON G.
XX (WAHL/) WAHL A F.
XX (SIEG/) SIEGALL C.
XX (SENT/) SENTER P D.
XX (DORO/) DORONINA S.
XX (TOKI/) TOKI B E.
XX Francisco JA, Risdon G, Wahl AF, Siegall C, Senter PD;
XX Doronina S, Toki BE;
XX WPI; 2004-121987/12.
XX N-PSDB; ADJ87915.

XX New antibodies that immunospecifically bind CD30 and exert a cytostatic
PT or cytotoxic effect on a Hodgkin's disease cell line, useful for
PT treating, inhibiting or preventing Hodgkin's Disease.
XX Disclosure; SEQ ID NO 14; 68pp; English.

CC The present invention relates to antibodies that immunospecifically bind CD30 and exert a cytostatic or cytotoxic effect on a Hodgkin's disease. CC The invention is useful for treating, inhibiting or preventing Hodgkin's disease. The invention is also useful in gene therapy. The present CC sequence is mouse AC10 CD30 antibody light chain-complementarity CC determining region (CDR) protein.

XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 AASNLES 7
| | | | |
DB 1 AASNLES 7

RESULT 17

ADY93300
ID ADY93300 standard; peptide; 7 AA.

XX AC ADY93300;

XX 02-JUN-2005 (first entry)

DT mAb CG10 light chain, CDR2.

DE epitope mapping; screening; peptide library; antibody; mAb CG10;

KW complementarity determining region; CDR.

XX Unidentified.

XX WO2005026379-A2.

XX 24-MAR-2005.

XX 08-SEP-2004; 2004WO-US029290.

XX 08-SEP-2003; 2003US-0500689P.

XX (UYRA-) UNIV RAMOT AT TEL AVIV.

XX Denisov D, Denisova G, Gershoni JM;

XX WPI; 2005-233509/24.

XX A method for improved prediction of a region on a surface of proteinaceous material representing a binding surface that associates with a predetermined binding molecule by screening a peptide library with the binding molecule.

XX Example 3; SEQ ID NO 31; 132pp; English.

XX The invention relates to a method for improved prediction of a region on a surface of a proteinaceous material representing a binding surface (epitope) that associates with a predetermined binding molecule. The method comprises screening a peptide library with a predetermined binding molecule, mapping on a three-dimensional model of the proteinaceous material the pairs of amino acids represented by tandem pairs of symbols, and determining clusters of amino acid pairs. Also described are: (i) a method of identifying a basic element of a binding surface on a proteinaceous material, which associates with a predetermined binding molecule, (ii) a method of producing a binding surface mimetic, (iii) a pharmaceutical composition including one or more of the basic elements of the binding surface of gp120 that is recognized by a broadly neutralizing antibody, comprising a carrier and one or more of the peptides consisting of amino acids 360-362, 391-396, 464-468 or 110-118 of the fully defined sequence given as SEQ ID NO:1 in the specification, and (iv) a molecule mimetic of the binding surface of gp120 that is recognized by a broadly neutralizing antibody, obtained by connecting peptides 360-362, 391-396 and 464-468 of SEQ ID NO:1, each in forward or reverse sequence, in such a manner as to form a single molecule that maintains the spatial

CC orientation that the amino acids have when they are positioned at 360-362, 391-396 and 464-468 of gp120. The method is useful for improved CC prediction of a region on a surface of proteinaceous material CC representing a binding surface that associates with a predetermined CC binding molecule. This sequence represents a complementarity determining CC region (CDR) of a monoclonal antibody (mAb) used in the examples of the CC present invention.

XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 AASNLES 7
| | | | |
DB 1 AASNLES 7

RESULT 18

AAR66144

ID AAR66144 standard; peptide; 15 AA.

XX AC AAR66144;

XX 12-JUL-1995 (first entry)

DT CD-4 antibody variable region complementary peptide.

DE CD-4 antibody variable region; complementary peptide;

KW extra-corporeal blood circulation; cell filter material.

XX Synthetic.

XX JP06269663-A.

XX 27-SEP-1994.

XX 17-MAR-1993; 93JP-00057206.

XX 17-MAR-1993; 93JP-00057206.

XX (TOYM) TOYOBO KK.

XX WPI; 1994-346316/43.

XX Material for collecting cells positive for CD-4 antibody - comprises nonwoven fabric having keto-alkyl halide functional gp.

XX Example 2; Page 7; 9pp; Japanese.

XX AAR66140-R66146 are peptides complementary to the variable region of the CD-4 antibody, these peptides are fixed onto a claimed nonwoven fabric (average fibre dia. of 1-30 microns) coated with keto-alkyl halide functional groups. This material can be used as a filter for CD-4 positive cells in a medical treatment involving the extra-corporeal circulation of blood

XX Sequence 15 AA;

Query Match 100.0%; Score 31; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.8; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 AASNLES 7
| | | | |
DB 9 AASNLES 15

RESULT 19

AAY91015

ID AAY91015 standard; protein; 41 AA.

XX

AC AAY91015;
XX
DT 05-SEP-2000 (first entry)
XX
DE 1F7 antibody variable light chain L2 amino acid sequence SEQ ID NO:6.
XX
DE 1F7 antibody; murine; monoclonal antibody; diagnosis; HIV; infection;
KW AIDS; anti-HIV; human immunodeficiency virus; detection;
KW acquired immunodeficiency syndrome.
XX
OS Mus sp.
XX
XX US6057421-A.
XX
XX 02-MAY-2000.
XX
XX 03-DEC-1997; 97US-00984277.
XX
XX 30-NOV-1994; 94US-00351193.
XX (IMMP-) IMMOPHERON INC.
XX
XX Muller S, Kohler H;
XX
XX WPI; 2000-338622/29.
XX
XX Variable heavy and light chain regions of murine monoclonal antibody 1F7,
XX useful for treating HIV infection and AIDS.
XX
XX Claim 1; Fig 8; 45pp; English.
XX
XX The present invention describes the variable heavy and light chain
XX regions (I) of murine monoclonal antibody (mAb) 1F7. AAY91014 to AAY91016
XX represent specifically claimed amino acid sequences of the variable light
XX chain, and AAY91017 to AAY91019 represent specifically claimed amino acid
XX sequence of the variable heavy chain. The antibodies are used for
XX treatment of HIV (human immunodeficiency virus) infection and AIDS
XX (acquired immunodeficiency syndrome). They are also used for detecting
XX HIV in serum and for stimulating HIV antigen related and committed B
XX cells to produce broadly reactive and neutralising antibodies by
XX clonotypic stimulation
XX
SQ Sequence 41 AA;

Query Match 100.0%; Score 31; DB 3; Length 41;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
DB 12 AASNLES 18

RESULT 20
AAY51140
ID AAY51140 standard; protein; 103 AA.
XX
XX AAY51140;
XX
XX 31-MAR-2000 (first entry)
XX
XX Murine derived protein fragment #2.
XX
XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
KW HIV infection; autoimmune disease; murine.
XX
XX Mus sp.
XX
XX WO9961629-A1.
XX
XX 02-DEC-1999.
XX

PF 24-MAY-1999; 99WO-JP002711.
XX
XX 25-MAY-1998; 98JP-00159957.
PR 26-MAY-1998; 98JP-00163023.
XX
XX (ASAH) ASAH KASEI KOGYO KK.
PA (ASAH) ASAH KASEI KOGYO KK.
PA (ASAH) ASAH MEDICAL CO LTD.
XX
XX Ono M, Soka T, Morimoto I, Miyamura K;
XX
XX WPI; 2000-086720/07.
DR N-PSDB; AAZ44204.
XX
XX Devices containing antibodies recognising CD4 or CD34 and their use for
XX the separation of CD4 or CD34 positive cells.
XX
XX Claim 22; Page 79; 11pp; Japanese.
XX
XX This invention describes a novel device (I) for separating cluster
XX differentiation (CD)-positive cells using a recombinant (chimeric or
XX single-chain) antibody recognising CD4 or CD34. The devices are useful
XX for the separation of CD4 or CD34 positive cells, which is useful for the
XX collection of hematopoietic undifferentiated cells, elimination of
XX lymphocytes from cells to be used in bone marrow transplantation, the
XX detection of leukemic cells and the production of medicinal compositions
XX for the treatment of HIV infection and autoimmune diseases. This sequence
XX represents a murine derived protein fragment which is used to illustrate
XX the method of the invention
XX
SQ Sequence 103 AA;

Query Match 100.0%; Score 31; DB 3; Length 103;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
DB 46 AASNLES 52

RESULT 21
AAY59263
ID AAY59263 standard; protein; 103 AA.
XX
XX AAY59263;
XX
XX 17-APR-2000 (first entry)
XX
XX Antibody 4H5 L chain variable region.
XX
XX CD4 antigen; anti-human; antibody; 4H5; drug.
XX
XX Mus sp.
XX
XX JP11332563-A.
XX
XX 07-DEC-1999.
XX
XX 26-MAY-1998; 98JP-00163034.
XX
XX 26-MAY-1998; 98JP-00163034.
XX
XX (ASAH) ASAH KASEI KOGYO KK.
XX
XX WPI; 2000-091351/08.
DR N-PSDB; AAZ58662.
XX
XX An antibody and the nucleic acid coding the antibody.
XX
XX Claim 5; Page 15-16; 25pp; Japanese.
XX
XX The invention provides an antibody having affinity to CD4 antigen. The
XX anti-human CD4 antibody 4H5 is used for the detection of antigen and
XX

CC application for drugs. It is highly safe in human dose. The present
 CC sequence represents the L chain variable region of the antibody 4H5
 XX
 SQ Sequence 103 AA;

Query Match 100.0%; Score 31; DB 3; Length 103;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 |||||
 Db 46 AASNLES 52

RESULT 22

AAE37732
 ID AAE37732 standard; protein; 105 AA.

XX
 AC AAE37732;

XX 06-NOV-2003 (first entry)

XX MT413 modified VL protein.

XX Chemokine; scFV; CD4 antibody; human immunodeficiency virus; HIV; RANTES;
 KW pharmaceutical; infection; acquired immune deficiency syndrome; AIDS;
 KW inflammatory; autoimmune disease; gene therapy; immunosuppressive;
 KW vaccine.

XX Unidentified.

XX WO2003054017-A2.

XX 03-JUL-2003.

XX 20-DEC-2002; 2002WO-EP014683.

XX 21-DEC-2001; 2001EP-00130746.

XX (MICK-) MICROMET AG.

XX Mack M, Schloendorff D;

XX WPI; 2003-559125/52.

XX N-PSDB; AAD56804.

XX New chemokine construct comprising scFV anti-CD4 and a RANTES chemokine,
 PT useful for the preparing a composition for treating HIV-infection or
 PT inflammatory or autoimmune diseases.

XX Disclosure; Page 19; 109pp; English.

XX The present invention relates to a chemokine construct comprising scFV
 CC anti-CD4 and a RANTES chemokine or their fragments. Sequences of the
 CC invention are useful for preparing a pharmaceutical composition for
 CC treating human immunodeficiency virus (HIV)-infection or acquired immune
 CC deficiency syndrome (AIDS) or inflammatory and/or autoimmune diseases.
 CC They are used as vaccines and in gene therapy. The present sequence is
 CC MT413 modified VL protein

XX Sequence 105 AA;

Query Match 100.0%; Score 31; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 |||||
 Db 48 AASNLES 54

RESULT 23

AAR33309

ID AAR33309 standard; protein; 106 AA.

XX AAR33309;

XX 25-MAR-2003 (revised)

DT 05-JUL-1993 (first entry)

XX MAE15 light chain.

XX Antibody; high affinity; FCEH; low affinity; FCEL; IGE receptor;
 KW histamine; mast cell; basophil; Kabat; CDR; murine; MAE11; MAE13; MAE15;
 KW MAE17.

XX Synthetic.

XX WO9304173-A1.

XX 04-MAR-1993.

XX 14-AUG-1992; 92WO-US006860.

XX 14-AUG-1991; 91US-00744768.

PR 07-MAY-1992; 92US-00879495.

XX (GETH) GENENTECH INC.

XX Jardieu PM, Presta LG;

XX WPI; 1993-094004/11.

XX Polypeptide(s) binding to specific Fc epsilon receptors - act as IGE
 PT antagonists; useful for treating and preventing IGE-mediated disorders
 PT e.g. allergies.

XX Disclosure; Fig 2; 113pp; English.

XX Antibodies capable of binding FCEL-bound IGE but which are substantially
 CC incapable of binding FCEH-bound IGE or inducing histamine release from
 CC mast cells or basophils, comprise a human Kabat CDR domain into which has
 CC been substituted a positionally analogous residue from a Kabat CDR domain
 CC of the murine anti-huIGE antibodies MAE11, MAE13, MAE15 or MAE17.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 106 AA;

Query Match 100.0%; Score 31; DB 2; Length 106;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

Db 54 AASNLES 60

RESULT 24

AAV85197

ID AAV85197 standard; protein; 106 AA.

XX AAV85197;

XX 29-JUN-2000 (first entry)

XX Light chain amino acid sequence of mouse antibody MAE15.

XX Immunoglobulin E; IGE; anti-human IGE; bispecific antibody; FCEL; FCEH;
 KW low affinity binding receptor; high affinity binding receptor; allergy;
 KW diagnosis; treatment; histamine release; prevent; light chain.

XX Mus sp.

XX US6037453-A.

XX 14-MAR-2000.

XX PF 06-JUN-1995; 95US-00466151.
 XX PR 14-AUG-1992; 92WO-US006860.
 PR 26-JAN-1994; 94US-00185899.
 PR 15-MAR-1995; 95US-00405617.
 XX (GETH) GENENTECH INC.
 PA Presta LG, Jardieu PM;
 XX PI WPI; 2000-269913/23.
 XX DR New bispecific antibodies, useful for treating immunoglobulin E-mediated
 PT disease, binds to IgE, but only when on the low affinity receptor, and to
 PT an antigen other than IgE.
 XX Claim 1; Fig 2; 48pp; English.
 XX CC This sequence represents the light chain amino acid sequence of a mouse
 CC anti-human immunoglobulin E (IgE) antibody. The invention relates to a
 CC bispecific antibody that binds specifically to IgE when IgE is bound to
 CC its low affinity receptor (FcεR), but does not bind to IgE, when IgE is
 CC bound to its high affinity receptor (FcεR). The bispecific antibody
 CC comprises an IgE-binding arm with human framework residues of a recipient
 CC human antibody and donor murine CDR (complementarity determining region)
 CC residues, but with at least one human CDR residue replacing the analogous
 CC murine residue. The antibody also comprises an Fv that is specific for a
 CC predetermined antigen other than IgE. The antibodies work by displacing
 CC bound IgE from its receptor, or via competitive inhibition of its
 CC binding. The bispecific antibodies are used for diagnosis, treatment and
 CC prevention of allergy and other IgE-mediated diseases, also, when
 CC immobilised, for the isolation of FcεR from cells (for research or
 CC therapy). The bispecific antibodies of the invention do not cause
 CC granulation or release of histamine from mast cells
 XX SQ Sequence 106 AA;
 Query Match 100.0%; Score 31; DB 3; Length 106;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AASNLES 7
 DB 54 AASNLES 60
 RESULT 25
 ID AAO18536 standard; protein; 110 AA.
 AC AAO18536;
 XX 11-OCT-2002 (first entry)
 DT Murine Mab 1F7 light chain.
 DE Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR;
 KW complementarity determining region; framework-determining region; FR;
 KW heavy chain; light chain; HIV infection.
 XX Mus sp.
 OS WO200255669-A2.
 PN 18-JUL-2002.
 PD 11-JAN-2002; 2002WO-US000927.
 PF 11-JAN-2001; 2001US-00759112.
 XX (IMMP-) IMMIPHERON INC.
 XX

PI Muller S, Kohler H;
 XX WPI; 2002-590668/63.
 DR N-PSDB; AAL48661.
 XX New polynucleotide encoding a complementarity- or framework-determining
 PT region of an anti-idiotypic antibody that binds to human or primate anti-
 PT human immunodeficiency virus (HIV) antibodies, for use in vaccines
 PT against HIV.
 XX Claim 9; Page 23-24; 27pp; English.
 XX CC The present invention relates to coding sequences of the murine 1F7 anti-
 CC idiotypic antibody complementarity-determining region (CDR) or framework-
 CC determining region (FR). The antibody binds to human or primate anti-
 CC human immunodeficiency virus (HIV) antibodies and can be used in the
 CC treatment of HIV infection. The present sequence is the 1F7 light chain
 XX SQ Sequence 110 AA;
 Query Match 100.0%; Score 31; DB 5; Length 110;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AASNLES 7
 DB 53 AASNLES 59
 RESULT 26
 ID AAP90541 standard; protein; 111 AA.
 XX AAP90541;
 AC 24-OCT-2003 (revised)
 DT 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 20-OCT-1989 (first entry)
 XX Immunoglobulin L chain variable region.
 DE Immunoglobulin; L chain variable region; HIV.
 KW Mus musculus.
 XX EP327000-A.
 PN 09-AUG-1989.
 PD 30-JAN-1989; 89EP-00101583.
 XX 30-JAN-1988; 88JP-00020255.
 PR 08-JUL-1988; 88JP-00171385.
 XX (KAGA) CEMO SERO THERAPEUTIC RES INS.
 PA Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Matsushita S, Hattori T;
 PI Takatsuki K;
 XX WPI; 1989-229050/32.
 DR N-PSDB; AAN90491, AAN90492, AAN90493.
 XX Chimeric anti-human immune virus antibodies - contg. mouse variable
 PT regions and human constant regions for diagnosis, treatment and
 PT prevention of AIDS.
 XX Claim 5; Page 15; 33pp; English.
 XX CC The sequence is an L chain variable region from an immunoglobulin with
 CC anti-HIV neutralising activity. See AAN90491-3, and AAN90495. (Updated on
 CC 25-MAR-2003 to correct PA field.) (Updated on 27-AUG-2003 to correct OS
 CC field.) (Updated on 24-OCT-2003 to standardise OS field)

XX SQ Sequence 111 AA;
 Query Match 100.0%; Score 31; DB 1; Length 111;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 DB 54 AASNLES 60
 |||||

RESULT 27
 AAR55123
 ID AAR55123 standard; protein; 111 AA.
 AC AAR55123;
 XX 27-JAN-1995 (first entry)
 DT Mouse anti-HIV mu5.5 light chain variable region.
 DE
 XX Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;
 KW human immunodeficiency virus; variable region; VH chain; murine.
 XX Mus musculus.
 XX Key Location/Qualifiers
 FH Region 1..23
 FT /label= FR1
 FT Region 24..38
 FT /label= CDR1
 FT Region 39..53
 FT /label= FR2
 FT Region 54..60
 FT /label= CDR2
 FT Region 61..92
 FT /label= FR3
 FT Region 93..101
 FT /label= CDR3
 FT Region 102..111
 FT /label= FR4
 FT /label= FR4
 XX JP06125783-A.
 PN 10-MAY-1994.
 PD 28-DEC-1991; 91JP-00359808.
 XX 28-DEC-1991; 91JP-00359808.
 XX (KAGA-) ZH KAGAKU KESSEI-RYOHO KENKYUSHO.
 PA WPI; 1994-187942/23.
 DR N-PSDB; AAQ65554.
 XX Mouse-human chimeric anti-HIV antibody heavy and light chains - and
 PT recombinant antibody consisting of the H- and L-chains, useful in AIDS
 PT therapy.
 XX Example 3; Fig 4; 22pp; Japanese.
 PS Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV. The
 CC heavy and light chain variable regions from these antibodies were
 CC sequenced (AAR55120-R55123). The murine anti-HIV CDRs were introduced
 CC into human framework regions to construct chimeric antibodies (AAR55124-
 CC R55127)
 XX Sequence 111 AA;
 Query Match 100.0%; Score 31; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 DB 54 AASNLES 60
 |||||

RESULT 28
 AAR55127
 ID AAR55127 standard; protein; 111 AA.
 XX AAR55127;
 AC AAR55127;
 XX 16-OCT-2003 (revised)
 DT 30-JAN-1995 (first entry)
 XX Mouse-human chimeric anti-HIV mu5.5-derived light chain V region.
 DE
 XX Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;
 KW human immunodeficiency virus; variable region; VL chain; murine;
 KW chimeric; humanised.
 XX Mus musculus.
 OS Homo sapiens.
 OS Chimeric.
 XX Key Location/Qualifiers
 FH Region 1..23
 FT /label= FR1
 FT /note= "human"
 FT Region 24..38
 FT /label= CDR1
 FT /note= "murine"
 FT Region 39..53
 FT /label= FR2
 FT Region 54..60
 FT /label= CDR2
 FT /note= "murine"
 FT Region 61..92
 FT /label= FR3
 FT /note= "human"
 FT Region 93..101
 FT /label= CDR3
 FT /note= "murine"
 FT Region 102..111
 FT /label= FR4
 FT /note= "human"
 FT /label= FR4
 XX JP06125783-A.
 PN 10-MAY-1994.
 PD 28-DEC-1991; 91JP-00359808.
 XX 28-DEC-1991; 91JP-00359808.
 XX (KAGA-) ZH KAGAKU KESSEI-RYOHO KENKYUSHO.
 PA WPI; 1994-187942/23.
 DR N-PSDB; AAQ65558.
 XX Mouse-human chimeric anti-HIV antibody heavy and light chains - and
 PT recombinant antibody consisting of the H- and L-chains, useful in AIDS
 PT therapy.
 XX Claim 5; Fig 12; 22pp; Japanese.
 PS Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV. The
 CC heavy and light chain variable regions from these antibodies were
 CC sequenced (AAR55120-R55123). The murine anti-HIV CDRs were introduced
 CC into human framework regions to construct chimeric antibodies (AAR55124-
 CC R55127). (Updated on 16-Oct-2003 to standardise OS field)
 XX Sequence 111 AA;
 SQ

Query Match 100.0%; Score 31; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||||
54 AASNLES 60

RESULT 29

AAR60302

ID AAR60302 standard; protein; 111 AA.

XX

AC AAR60302;

XX

DT 25-MAR-2003 (revised)

DT 09-MAR-1995 (first entry)

XX

DE Anti HIV antibody light chain variable region.

XX

KW Antibody; heavy chain; light chain; human immunodeficiency virus; HIV;

KW acquired immune deficiency syndrome; AIDS: treatment; prophylaxis;

KW Mus musculus; Homo sapiens.

XX

OS Mus musculus.

XX

FH Key Location/Qualifiers

FT Region 1..23

FT /label= Framework region 1.

FT Region

FT /label= CDR1.

FT Region

FT /label= Framework region 2.

FT Region

FT /label= CDR2.

FT Region

FT /label= Framework region 3.

FT Region

FT /label= CDR3.

FT Region

FT /label= Framework region 4.

XX

FN WO9415969-A1.

XX

PD 21-JUL-1994.

XX

PF 14-JAN-1993; 93WO-JP000039.

XX

PR 14-JAN-1993; 93WO-JP000039.

XX

PA (KAGA) CHEMO SERO THERAPEUTIC RES INST.

XX

PI Maeda H, Kimachi K, Eda Y, Shiosaki K, Osatomi K, Tokiyoshi S;

XX

DR WPI; 1994-249145/30.

DR N-PSDB; AAQ70372.

XX

PT Recombinant chimeric anti HIV antibody - useful for the treatment and

PT prevention of HIV.

XX

PS Claim 15; Fig 4; 51pp; Japanese.

XX

CC The recombinant antibody light chain has neutralising activity against

CC HIV. Chimeric antibodies comprising both mouse and human sequences are

CC useful in the treatment/prevention of AIDS caused by HIV. (Updated on 25-

CC MAR-2003 to correct PN field.)

XX

SQ Sequence 111 AA;

Query Match 100.0%; Score 31; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||||
54 AASNLES 60

RESULT 30

AAR60306

ID AAR60306 standard; protein; 111 AA.

XX

AC AAR60306;

XX

DT 16-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 13-MAR-1995 (first entry)

XX

DE Chimeric anti HIV antibody light chain variable region.

XX

KW Antibody; heavy chain; light chain; human immunodeficiency virus; HIV;

KW acquired immune deficiency syndrome; AIDS: treatment; prophylaxis;

KW Mus musculus; Homo sapiens.

XX

OS Homo sapiens.

OS Mus musculus.

OS Chimeric.

XX

FH Key Location/Qualifiers

FT Region 1..23

FT /label= Framework region 1.

FT Region

FT /label= CDR1.

FT Region

FT /note= "Mouse derived amino acid sequence."

FT Region

FT /label= Framework region 2.

FT Region

FT /label= CDR2.

FT Region

FT /note= "Mouse derived amino acid sequence."

FT Region

FT /label= Framework region 3.

FT Region

FT /label= CDR3.

FT Region

FT /note= "Mouse derived amino acid sequence."

FT Region

FT /label= Framework region 4.

XX

FN WO9415969-A1.

XX

PD 21-JUL-1994.

XX

PF 14-JAN-1993; 93WO-JP000039.

XX

PR 14-JAN-1993; 93WO-JP000039.

XX

PA (KAGA) CHEMO SERO THERAPEUTIC RES INST.

XX

PI Maeda H, Kimachi K, Eda Y, Shiosaki K, Osatomi K, Tokiyoshi S;

XX

DR WPI; 1994-249145/30.

DR N-PSDB; AAR60306.

XX

PT Recombinant chimeric anti HIV antibody - useful for the treatment and

PT prevention of HIV.

XX

PS Claim 14; Fig 12; 51pp; Japanese.

XX

CC The recombinant antibody light chain has neutralising activity against

CC HIV. Chimeric antibodies comprising both mouse and human sequences are

CC useful in the treatment/prevention of AIDS caused by HIV. (Updated on 25-

CC MAR-2003 to correct PN field.)

XX

SQ Sequence 111 AA;

Query Match 100.0%; Score 31; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 DB 54 AASNLES 60

RESULT 31

AAV23781
 ID AAY23781 standard; protein; 111 AA.

XX AAY23781;

XX 13-SEP-1999 (first entry)

DT Light chain variable region of Ig REI.

DE Light chain variable region of Ig REI.

XX Light chain variable region; interleukin-4; IL-4; antibody 3B9;

KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;

KW Immunoglobulin E-mediated allergic reaction; allergic rhinitis;

KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;

KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy;

KW Ig REI.

XX Synthetic.

XX US5928904-A.

PN 27-JUL-1999.

PD 07-JUN-1995; 95US-00483632.

XX 07-SEP-1993; 93US-00117366.

XX 14-OCT-1993; 93US-00136783.

PR 07-SEP-1994; 94WO-US010308.

XX (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX Holmes SD, Sylvester DR, Gross MS;

XX WPI; 1999-429500/36.

XX N-PSDB; AAX85937.

XX New DNA molecules encoding recombinant antibodies useful for treating IL4

PT -mediated conditions.

XX Disclosure; Col 69-70; 50pp; English.

XX The specification describes chimeric and humanised IL-4 monoclonal

CC antibodies. The antibodies of the invention are used in therapeutic and

CC pharmaceutical compositions for treating IL-4 mediated and immunoglobulin

CC E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis,

CC atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid

CC arthritis, host-versus-graft disease and renal disease. They are also

CC useful in the diagnosis of an allergy or condition associated with excess

CC IL-4 production through the measurement e.g. by ELISA of circulating

CC endogenous IL-4 levels in humans. The present sequence represents the

CC light chain variable region of Ig REI, and is used in the course of the

CC invention

XX Sequence 111 AA;

QY Query Match 100.0%; Score 31; DB 2; Length 111;

DB Best Local Similarity 100.0%; Pred. No. 49;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

DB 54 AASNLES 60

RESULT 32

AAV18123

ID AAY18123 standard; protein; 111 AA.

XX AAY18123;

XX 11-AUG-1999 (first entry)

DT Light chain sequence for humanised 3B9 antibody.

DE Light chain sequence for humanised 3B9 antibody.

XX Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;

KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;

KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;

KW autoimmune disease; graft versus host disease.

XX Synthetic.

XX US5914110-A.

PN 22-JUN-1999.

PD 07-JUN-1995; 95US-00483636.

XX 07-SEP-1993; 93US-00117366.

XX 14-OCT-1993; 93US-00136783.

PR 07-SEP-1994; 94WO-US010308.

XX (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX Sylvester DR, Holmes SD, Gross MS;

XX WPI; 1999-370482/31.

XX N-PSDB; AAX79531.

XX Recombinant IL4 antibodies useful for treatment of allergic rhinitis,

PT atopic asthma and anaphylactic shock.

XX Example 3; Col 69-70; 50pp; English.

XX This sequence represents the light chain of the humanised 3B9 antibody of

CC the invention. The antibody is a chimeric or humanised interleukin-4

CC (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE)

CC mediated diseases. The antibodies are useful for the treatment of

CC allergic disorders such as allergic rhinitis, conjunctivitis, atopic

CC dermatitis, atopic asthma and anaphylactic shock. The antibodies are also

CC useful for regulating B and T cell proliferation and as such are useful

CC in the treatment of autoimmune diseases and graft versus host disease

XX Sequence 111 AA;

QY Query Match 100.0%; Score 31; DB 2; Length 111;

DB Best Local Similarity 100.0%; Pred. No. 49;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

DB 54 AASNLES 60

DT 31-MAR-2000 (first entry)

XX Murine derived protein fragment #8.

XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;

KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;

KW HIV infection; autoimmune disease; murine.
 XX Mus sp.
 OS WO9961629-A1.
 XX PN
 XX PD 02-DEC-1999.
 XX PF 24-MAY-1999; 99WO-JP002711.
 XX PR 25-MAY-1998; 98JP-00159957.
 XX PR 26-MAY-1998; 98JP-00163023.
 XX PA (ASAH) ASahi KASEI KOGYO KK.
 XX PA (ASAH) ASahi MEDICAL CO LTD.
 XX PI Ono M, Soka T, Morimoto I, Miyamura K;
 XX WPI; 2000-086720/07.
 XX DR N-PSDB; AAZ44232.
 XX PT Devices containing antibodies recognising CD4 or CD34 and their use for
 XX the separation of CD4 or CD34 positive cells.
 XX PS Disclosure; Page 97-98; 111pp; Japanese.
 XX CC This invention describes a novel device (I) for separating cluster
 CC differentiation (CD)-positive cells using a recombinant (chimeric or
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful
 CC for the separation of CD4 or CD34 positive cells, which is useful for the
 CC collection of hematopoietic undifferentiated cells, elimination of
 CC lymphocytes from cells to be used in bone marrow transplantation, the
 CC detection of leukemic cells and the production of medicinal compositions
 CC for the treatment of HIV infection and autoimmune diseases. This sequence
 CC represents a murine derived protein fragment which is used to illustrate
 CC the method of the invention
 XX SQ Sequence 111 AA;
 XX Query Match 100.0%; Score 31; DB 3; Length 111;
 XX Best Local Similarity 100.0%; Pred. No. 49;
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AASNLES 7
 Db |||||
 54 AASNLES 60
 RESULT 34
 AAY51144
 ID AAY51144 standard; protein; 111 AA.
 XX AC AAY51144;
 XX DT 31-MAR-2000 (first entry)
 XX DE Murine derived protein fragment #6.
 XX KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
 KW HIV infection; autoimmune disease; murine.
 XX OS Mus sp.
 XX PN WO9961629-A1.
 XX PD 02-DEC-1999.
 XX PF 24-MAY-1999; 99WO-JP002711.
 XX PR 25-MAY-1998; 98JP-00159957.
 XX PR 26-MAY-1998; 98JP-00163023.
 XX

PA (ASAH) ASahi KASEI KOGYO KK.
 PA (ASAH) ASahi MEDICAL CO LTD.
 XX PI Ono M, Soka T, Morimoto I, Miyamura K;
 XX WPI; 2000-086720/07.
 XX PT Devices containing antibodies recognising CD4 or CD34 and their use for
 XX the separation of CD4 or CD34 positive cells.
 XX PS Disclosure; Page 95; 111pp; Japanese.
 XX CC This invention describes a novel device (I) for separating cluster
 CC differentiation (CD)-positive cells using a recombinant (chimeric or
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful
 CC for the separation of CD4 or CD34 positive cells, which is useful for the
 CC collection of hematopoietic undifferentiated cells, elimination of
 CC lymphocytes from cells to be used in bone marrow transplantation, the
 CC detection of leukemic cells and the production of medicinal compositions
 CC for the treatment of HIV infection and autoimmune diseases. This sequence
 CC represents a murine derived protein fragment which is used to illustrate
 CC the method of the invention
 XX SQ Sequence 111 AA;
 XX Query Match 100.0%; Score 31; DB 3; Length 111;
 XX Best Local Similarity 100.0%; Pred. No. 49;
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AASNLES 7
 Db |||||
 54 AASNLES 60
 RESULT 35
 AAY59267
 ID AAY59267 standard; protein; 111 AA.
 XX AC AAY59267;
 XX DT 17-APR-2000 (first entry)
 XX DE Antibody 4H5 L chain fragment.
 XX KW CD4 antigen; anti-human; antibody; 4H5; drug.
 XX OS Mus sp.
 XX PN JP11332563-A.
 XX PD 07-DEC-1999.
 XX PF 26-MAY-1998; 98JP-00163034.
 XX PR 26-MAY-1998; 98JP-00163034.
 XX PA (ASAH) ASahi KASEI KOGYO KK.
 XX WPI; 2000-091351/08.
 XX DR N-PSDB; AAZ58690.
 XX PT An antibody and the nucleic acid coding the antibody.
 XX PS Disclosure; Page 22-23; 25pp; Japanese.
 XX CC The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. The present
 CC sequence represents a L chain fragment of the antibody 4H5
 XX SQ Sequence 111 AA;
 XX Query Match 100.0%; Score 31; DB 3; Length 111;

Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
DB 54 AASNLES 60

RESULT 36
AAU99852
ID AAU99852 standard; protein; 111 AA.
XX AC AAU99852;
XX 07-OCT-2002 (first entry)
XX Mouse AC10 antibody light chain variable region.
XX DE
XX DE
XX XX
KW Gene therapy; vaccine; CD30 binding; cytostatic; cytotoxic;
KW Hodgkin's Disease; mouse; AC10 antibody; light chain variable region.
XX OS
XX Mus musculus.
XX PN WO200243661-A2.
XX PD 06-JUN-2002.
XX XX
XX 28-NOV-2001; 2001WO-US044811.
XX PF
XX 28-NOV-2000; 2000US-00724406.
XX PR
XX (SEAT-) SEATTLE GENETICS INC.
XX PA
XX Francisco JA, Riedon G, Wahl AF, Siegall CB;
XX PI WPI; 2002-557522/59.
XX DR N-PSDB; ABR88124.
XX

Novel antibody that immunospecifically binds to CD30, useful for treating Hodgkin's disease, exerts a cytostatic or cytotoxic effect on Hodgkin's Disease cell line, and is not monoclonal antibody AC10 or HeFi-1.

Claim 11; Page 98-99; 103pp; English.

The invention describes an antibody (I) that immunospecifically binds to CD30, exerts a cytostatic or cytotoxic effect on Hodgkin's Disease cell line, and is not monoclonal antibody AC10 or HeFi-1 and does not result from cleavage of AC10 or HeFi-1 with pepsin. (I), a protein (II) that competes for CD30 binding with the monoclonal antibodies AC10 or HeFi, or exerts a cytotoxic or cytostatic effect on a Hodgkin's Disease cell line and the nucleic acid encoding the protein (III) are useful for the treatment or prevention of Hodgkin's Disease in a subject, by administering (I) to the subject, in the absence of conjugation to a cytostatic or cytotoxic agent, respectively and a pharmaceutically acceptable carrier. This is the amino acid sequence of the mouse AC10 antibody light chain variable region, a polypeptide that competes with AC10 for CD30 binding

XX SQ Sequence 111 AA;

Query Match 100.0%; Score 31; DB 5; Length 111;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
DB 54 AASNLES 60

RESULT 37
AAO29926
ID AAO29926 standard; protein; 111 AA.
XX

AC AAO29926;
XX 03-SEP-2003 (first entry)
XX Mouse anti-CD30 antibody (AC10) light chain variable region.
XX DE
XX DE
XX KW Immunological disorder; CD30; cytostatic; lymphocyte related disorder; cytotoxic; atopic dermatitis; systemic lupus erythematosus; psoriasis; atopic asthma; rhinoconjunctivitis; allergic rhinitis; Grave's disease; Omenn's syndrome; tuberculous; Sjogren's syndrome; multiple sclerosis; graft-versus-host disease; primary biliary cirrhosis; viral infection; rheumatoid arthritis; Hashimoto's thyroiditis; Wegener's granulomatosis; human immunodeficiency virus; HIV; therapy; antibody; mouse.
XX OS
XX Mus musculus.
XX PN WO2003043583-A2.
XX PD 30-MAY-2003.
XX PF 20-NOV-2002; 2002WO-US037223.
XX PR 20-NOV-2001; 2001US-0331750P.
XX PA (SEAT-) SEATTLE GENETICS INC.
XX PI Law C, Klusman K, Wahl AF, Senter P, Doronina S, Toki B;
XX WPI; 2003-468727/44.
XX DR N-PSDB; AAL60613.
XX

Treating immunological disorder that is not cancer, in a subject, by administering composition comprising a first antibody that specifically binds CD30 and exerts a cytostatic or cytotoxic effect on activated lymphocyte.

Disclosure; Page 190; 194pp; English.

The invention relates to a method of treating an immunological disorder in a subject where the immunological disorder is not cancer. The method involves administering to the subject a pharmaceutical composition comprising an antibody that immunospecifically binds CD30 and exerts a cytostatic or cytotoxic effect on an activated lymphocyte and a carrier. The method is useful for treating Th 2-lymphocyte related disorders such as atopic dermatitis, systemic lupus erythematosus, atopic asthma, rhinoconjunctivitis, allergic rhinitis, Omenn's syndrome, systemic sclerosis or chronic graft-versus-host disease. The method is also useful for treating Th 1-lymphocyte-related immunological disorders such as rheumatoid arthritis, multiple sclerosis, psoriasis, Sjogren's syndrome, Hashimoto's thyroiditis, Grave's disease, primary biliary cirrhosis, Wegener's granulomatosis, tuberculosis or acute graft-versus host disease or for treating an immunological disorder due to viral infection that involves Epstein-Barr virus, human immunodeficiency virus (HIV), human T leukemia virus, hepatitis B virus or measles virus or for treating an activated B lymphocyte-related disorder. The present sequence is mouse anti-CD30 antibody (AC10) light chain variable region

XX SQ Sequence 111 AA;

Query Match 100.0%; Score 31; DB 7; Length 111;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
DB 54 AASNLES 60

RESULT 38
ADC27439
ID ADC27439 standard; protein; 111 AA.
XX AC ADC27439;

XX DT 18-DEC-2003 (first entry)

XX DE TMEFF2#10 light chain variable region SEQ ID NO:8.

XX KW antibody; TMEFF2#19; TMEFF2; binding inhibitor; prostate cancer;

XX KW cytostatic; vaccine; primary prostate cancer; metastatic prostate cancer;

XX KW locally advanced prostate cancer; androgen independent prostate cancer.

XX OS Synthetic.

XX PN WO2003075855-A2.

XX PD 18-SEP-2003.

XX PF 07-MAR-2003; 2003WO-US007209.

XX PR 08-MAR-2002; 2002US-0362837P.

XX PR 27-DEC-2002; 2002US-0436812P.

XX PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX PI Bhaskar V, De La Calle A, Law D, Caras I, Ramakrishnan V;

XX PI Murray R, Afar D, Powers D;

XX WPI; 2003-756783/71.

XX DR N-PSDB; ADC27438.

XX PT New antibody that competitively inhibits binding of TMEFF219 to TMEFF2,

XX PT useful for treating prostate cancer, e.g. primary, metastatic, locally

XX PT advanced, or androgen independent prostate cancer.

XX PS Example 1; SEQ ID NO 8; 51pp; English.

XX CC The present invention describes an antibody (I) that competitively

XX CC inhibits binding of TMEFF2#19 to TMEFF2. Also described: (1) a

XX CC pharmaceutical composition comprising the antibody and a carrier; (2)

XX CC detecting a prostate cancer cell in a biological sample from a patient by

XX CC contacting the biological sample with the antibody; (3) inhibiting

XX CC proliferation of a prostate cancer-associated cell by contacting the cell

XX CC with the antibody; and (4) treating prostate cancer with an antibody to

XX CC TMEFF2. (I) has cytostatic activity and can be used in vaccines. The

XX CC antibody, composition and method are useful for treating prostate cancer,

XX CC e.g. primary prostate cancer, metastatic prostate cancer, locally

XX CC advanced prostate cancer, androgen independent prostate cancer, prostate

XX CC cancer that has been treated with neoadjuvant therapy, or prostate cancer

XX CC that is refractory to treatment with neoadjuvant therapy. The present

XX CC sequence is used in the exemplification of the present invention.

XX SQ Sequence 111 AA;

Query Match 100.0%; Score 31; DB 7; Length 111;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

Db 54 AASNLES 60

RESULT 39

ADJ87912

ID ADJ87912 standard; protein; 111 AA.

XX AC ADJ87912;

XX DT 06-MAY-2004 (first entry)

XX DE Mouse AC10 CD30 antibody light chain variable region protein.

XX KW CD30; cytostatic; cytotoxic; Hodgkin's disease; gene therapy; mouse;

XX KW AC10; antibody.

OS Mus musculus.

XX US2004018194-A1.

XX PD 29-JAN-2004.

XX PF 28-MAY-2003; 2003US-00447257.

XX PR 28-NOV-2000; 2000US-00724406.

XX PR 28-NOV-2001; 2001WO-US044811.

XX PR 31-JUL-2002; 2002US-0400403P.

XX PA (FRAN/) FRANCISCO J A.

XX PA (RISD/) RISDON G.

XX PA (WAHL/) WAHL A F.

XX PA (SIEG/) SIEGALL C.

XX PA (SENT/) SENTER P D.

XX PA (DORO/) DORONINA S.

XX PA (TOKI/) TOKI B E.

XX PI Francisco JA, Risdon G, Wahl AF, Siegall C, Senter PD;

XX PI Doronina S, Toki BE;

XX DR WPI; 2004-121987/12.

XX DR N-PSDB; ADJ87911.

XX PT New antibodies that immunospecifically bind CD30 and exert a cytostatic

XX PT or cytotoxic effect on a Hodgkin's disease cell line, useful for

XX PT treating, inhibiting or preventing Hodgkin's Disease.

XX PS Disclosure; SEQ ID NO 10; 68pp; English.

XX CC The present invention relates to antibodies that immunospecifically bind

XX CC CD30 and exert a cytostatic or cytotoxic effect on a Hodgkin's disease.

XX CC The invention is useful for treating, inhibiting or preventing Hodgkin's

XX CC disease. The invention is also useful in gene therapy. The present

XX CC sequence is mouse AC10 CD30 antibody light chain variable region protein.

XX SQ Sequence 111 AA;

Query Match 100.0%; Score 31; DB 8; Length 111;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

Db 54 AASNLES 60

RESULT 40

ADY85020

ID ADY85020 standard; protein; 111 AA.

XX AC ADY85020;

XX DT 16-JUN-2005 (first entry)

XX DE Human HMGB1 A box.

XX KW High mobility group box; HMGB1; monoclonal antibody; antibody therapy;

XX KW sepsis; antibacterial immunosuppressive; graft rejection; arthritis;

XX KW antiarthritic; asthma; antiasthmatic; lupus erythematosus;

XX KW antiinflammatory; inflammation; dermatological;

XX KW respiratory distress syndrome; respiratory-gen.; psoriasis;

XX KW antipsoriatic; chronic obstructive pulmonary disease; pancreatitis;

XX KW peritonitis; burns; vulnery; ischemia; vasotropic; Behcets disease;

XX KW graft versus host disease; inflammatory bowel disease;

XX KW gastrointestinal-gen.; multiple sclerosis neuroprotective; cachexia;

XX KW anabolic; infection; musculoskeletal disease; immune disorder.

XX OS Homo sapiens.

XX OS Mus sp.

XX OS Rattus sp.

XX WO2005026209-A2.
 XX 24-MAR-2005.
 XX 10-SEP-2004; 2004WO-US029527.
 XX 11-SEP-2003; 2003US-0502568P.
 XX (CRIT-) CRITICAL THERAPEUTICS INC.
 XX Newman W, Qin S, Okeefe T, Obar R;
 XX WPI; 2005-233483/24.
 XX New antibody or its antigen-binding fragment specific to a vertebrate
 PT high mobility group box (HMGB) A box that inhibits release of a
 PT proinflammatory cytokine from a cell treated with HMGB protein, useful
 PT for treating, e.g. sepsis.
 XX
 XX Disclosure; SEQ ID NO 2; 123pp; English.
 XX
 XX The invention provides antibodies, or their antigen-binding fragments, to
 CC that bind to a vertebrate high mobility group box (HMGB) polypeptide, to
 CC methods of detecting and/or identifying an agent that binds to an HMGB
 CC polypeptide, methods of treating a condition in a subject characterized
 CC by activation of an inflammatory cytokine cascade, and methods of
 CC detecting an HMGB polypeptide in a sample. The antibody (or antigen-
 CC binding fragment) binds to a vertebrate HMGB A box but does not
 CC specifically bind to non-A box epitopes of HMGB, and inhibits release of
 CC a proinflammatory cytokine from a vertebrate cell treated with an HMGB
 CC protein. A method of treating a condition characterized by activation of
 CC an inflammatory cytokine cascade comprises administering an antibody of
 CC the invention, or its antigen-binding fragment. The condition is selected
 CC from sepsis, allograft rejection, arthritis, asthma, lupus, adult
 CC respiratory distress syndrome, chronic obstructive pulmonary disease,
 CC psoriasis, pancreatitis, peritonitis, burns, ischemia, Behcet's disease,
 CC graft versus host disease, inflammatory bowel disease, multiple sclerosis
 CC and cachexia, especially sepsis, arthritis, or lupus. The present
 CC sequence is that of the A box of human HMGB1 ADY85012. An identical
 CC sequence is also found in rat and mouse HMGB1.
 XX
 XX Sequence 111 AA;
 SQ
 Query Match 100.0%; Score 31; DB 9; Length 111;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AASNLES 7
 Db 54 AASNLES 60
 |||||
 RESULT 41
 AEB13680
 ID AEB13680 standard; protein; 111 AA.
 AC AEB13680;
 XX 25-AUG-2005 (first entry)
 DT
 DE Human v1k_4-1 germline protein with grafted CDR of AC10 VL.
 XX
 XX protein engineering; immunogenicity; germ cell; light chain; antibody;
 KW muteln.
 KW
 XX Homo sapiens.
 OS
 XX WO2005056759-A2.
 PN
 XX 23-JUN-2005.
 PD
 XX 03-DEC-2004; 2004WO-US040694.
 PF

XX 04-DEC-2003; 2003US-0527167P.
 PR 21-JUN-2004; 2004US-0581613P.
 PR 13-AUG-2004; 2004US-0601665P.
 PR 16-OCT-2004; 2004US-0619483P.
 XX (XENC-) XENCOR INC.
 XX Lazar GA, Desjarlais JR, Hammond PW;
 XX WPI; 2005-458579/46.
 XX
 XX Generating variant protein for host, by comparing parent protein sequence
 PT with natural protein sequences from host, analyzing and substituting
 PT amino acids of parent sequences with corresponding amino acid string of
 PT natural sequence.
 XX
 XX Disclosure; Fig 5a; 137pp; English.
 XX
 XX The invention relates to a novel method for generating a variant protein
 CC for a host. The method involves comparing a parent protein sequence with
 CC natural protein sequences from a host, analyzing the amino acid strings
 CC of the parent sequence with corresponding amino acid strings of each of
 CC the natural protein sequences, and substituting amino acids of a natural
 CC protein sequences with corresponding amino acid strings of a natural
 CC protein sequence on an amino acid string. The method is useful for
 CC generating a variant protein, e.g. a variant antibody for a host as
 CC compared to a parent protein. The method enables the generation of
 CC variant proteins having an increased host string content and reduced of the
 CC immunogenicity. This sequence represents a human variant antibody of the
 CC invention.
 XX
 XX Sequence 111 AA;
 SQ
 Query Match 100.0%; Score 31; DB 9; Length 111;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AASNLES 7
 Db 54 AASNLES 60
 |||||
 RESULT 42
 AEB13684
 ID AEB13684 standard; protein; 111 AA.
 XX AEB13684;
 AC AEB13684;
 XX 25-AUG-2005 (first entry)
 DT
 DE Human antibody protein L3 AC10 VL.
 XX
 XX protein engineering; immunogenicity; germ cell;
 KW light chain variable region; antibody.
 XX
 XX Homo sapiens.
 OS
 XX WO2005056759-A2.
 PN
 XX 23-JUN-2005.
 PD
 XX 03-DEC-2004; 2004WO-US040694.
 PF 04-DEC-2003; 2003US-0527167P.
 PR 21-JUN-2004; 2004US-0581613P.
 PR 13-AUG-2004; 2004US-0601665P.
 PR 16-OCT-2004; 2004US-0619483P.
 XX (XENC-) XENCOR INC.
 XX Lazar GA, Desjarlais JR, Hammond PW;
 XX

CC human antibody protein used in the invention.

XX Sequence 111 AA;

Query Match 100.0%; Score 31; DB 9; Length 111;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

DB 54 AASNLES 60

RESULT 45

AEI13683
ID AEB13683 standard; protein; 111 AA.

XX AEB13683;

XX 25-AUG-2005 (first entry)

XX Human antibody protein L2 AC10 VL.

XX protein engineering; immunogenicity; germ cell;
KW light chain variable region; antibody.

XX Homo sapiens.

XX WO2005056759-A2.

XX 23-JUN-2005.

XX 03-DEC-2004; 2004WO-US040694.

XX 04-DEC-2003; 2003US-0527167P.

XX 21-JUN-2004; 2004US-0581613P.

XX 13-AUG-2004; 2004US-0601665P.

XX 16-OCT-2004; 2004US-0619483P.

XX (XENC-) XENCOR INC.

XX Lazar GA, Desjarlais JR, Hammond PW;

XX WPI; 2005-458579/46.

XX Generating variant protein for host, by comparing parent protein sequence

XX with natural protein sequences from host, analyzing and substituting

XX amino acids of parent sequences with corresponding amino acid string of

XX natural sequence.

XX Disclosure; Fig 9a; 137pp; English.

XX The invention relates to a novel method for generating a variant protein

XX for a host. The method involves comparing a parent protein sequence with

XX natural protein sequences from a host, analyzing the amino acid strings

XX of the parent sequence with corresponding amino acid strings of each of

XX the natural protein sequences, and substituting amino acids of parent

XX protein sequences with corresponding amino acid strings of a natural

XX protein sequence on an amino acid string. The method is useful for

XX generating a variant protein, e.g. a variant antibody for a host as

XX compared to a parent protein. The method enables the generation of

XX variant proteins having an increased host string content and reduced

XX immunogenicity. This sequence represents the variable light chain of a

DB 54 AASNLES 60

RESULT 46

AAR24575
ID AAR24575 standard; protein; 112 AA.

XX AAR24575;

XX 08-DEC-1992 (first entry)

XX Human x mouse modified anti-HIV antibody Light chain RL0.5beta.

XX Heavy; light; CDR; HIV; AIDS; REI; 0.5beta.

XX Synthetic.

XX Key

XX Location/Qualifiers

XX 1..23

XX /label= FR1

XX 24..38

XX /label= CDR1

XX 39..53

XX /label= FR2

XX 54..60

XX /label= CDR2

XX 61..92

XX /label= FR3

XX 93..101

XX /label= CDR3

XX 102..112

XX /label= FR4

XX JP04141095-A.

XX 14-MAY-1992.

XX 02-OCT-1990; 90JP-00266091.

XX 02-OCT-1990; 90JP-00266091.

XX (KAGA) KAGAKU OYOBI KESSEI RYOH.

XX WPI; 1992-212765/26.

XX New recombinant modified anti-HIV antibodies - comprise human x mouse

XX modified antibody H and L chains.

XX Disclosure; Fig 2; 15pp; Japanese.

XX The framework regions (FR) are derived from the human antibody REI. The

XX CDRs are mouse monoclonal antibody 0.5beta derived sequences. The anti-

XX HIV modified antibody can be used for the prophylaxis and treatment of

XX AIDS. Specific examples of the H chain are given in AAR24556-58 and

XX AAR24560-62. A specific example of the L chain is given in AAR24575

XX Sequence 112 AA;

XX Query Match 100.0%; Score 31; DB 2; Length 112;

XX Best Local Similarity 100.0%; Pred. No. 49;

XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

DB 54 AASNLES 60

RESULT 47

ABO10750

ID ABO10750 standard; protein; 112 AA.

XX ABO10750;

XX ABO10750;

```

DT 20-AUG-2003 (first entry)
XX
DE Variable region of murine antibody MuVL-3.
XX
KW Modified antibody; deimmunised antibody; anti-PMSEA antibody;
KW prostate specific membrane antigen; immunogenic; CDR; murine;
KW complementarity determining region; J593; J415; J533; E93; mouse;
KW prostatic disorder; cancerous disorder; genitourinary inflammation;
KW prostatitis; benign enlargement; prostatic cancer; testicular cancer;
KW solid tumour; soft tissue tumour; metastatic lesion; pain; analgesic;
KW antiinflammatory; cytostatic; framework region; variable heavy chain;
KW variable light chain; VH; VL; variable region.
XX
OS Mus musculus.
XX
PN WO200298897-A2.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-US017068.
XX
PR 01-JUN-2001; 2001US-0295214P.
PR 20-SEP-2001; 2001US-0323585P.
PR 08-MAR-2002; 2002US-0362810P.
XX
PA (CORR ) CORNELL RES FOUND INC.
XX
PI Bander N, Carr FJ, Hamilton A;
XX
DR WPI; 2003-156639/15.
XX
PT New modified anti-prostate specific membrane antigen (PSMA)
PT immunoglobulins, useful for treating or preventing a prostatic or
PT cancerous disorder, e.g. genitourinary inflammation, prostatitis, or
PT prostatic or testicular cancer.
XX
PS Disclosure; Fig 10B; 254pp; English.
XX
CC The present invention relates to modified (e.g. deimmunised) antibodies
CC to prostate specific membrane antigen (PSMA). The modified anti-PSMA
CC antibodies are less immunogenic compared to the unmodified anti-PSMA
CC antibodies. The modified antibodies comprise complementarity determining
CC regions (CDRs) from a non-human antibody (e.g. murine antibody J591,J415,
CC J533 or E93), and framework sequences that are less immunogenic in humans
CC (e.g. less antigenic than the murine frameworks in which a murine CDR
CC naturally occurs). The modified antibodies bind with PMSEA, preferably
CC human PMSEA, with high affinity and specificity. The anti-PMSEA antibodies
CC are useful for treating or preventing a prostatic or cancerous disorder,
CC e.g. genitourinary inflammation, prostatitis, benign enlargement,
CC prostatic cancer or testicular cancer, or solid tumours, soft tissue
CC tumours or metastatic lesions, and its associated pain. The present
CC sequence represents a variable region from a murine antibody
XX
SQ Sequence 112 AA;
Query Match 100.0%; Score 31; DB 6; Length 112;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AASNLES 7
DB 54 AASNLES 60
RESULT 48
ABR44694
ID ABR44694 standard; protein; 112 AA.
XX
AC ABR44694;
XX
DT 25-JUL-2003 (first entry)
XX
DE Murine MuVL-3 antibody amino acid sequence SEQ ID NO:81.

```

```

XX Mouse; murine; antibody; skin disorder; binding agent; PSMA; cytostatic;
KW prostate specific membrane antigen; antipsoriatic; antiarthritis;
KW dermatological; antiinflammatory; antiallergic; vaccine; dermal disorder;
KW epidermal disorder; psoriasis; inflammatory disorder; epidermis; dermis;
KW neoplastic disorder.
XX
OS Mus musculus.
XX
PN WO2003024388-A2.
XX
PD 27-MAR-2003.
XX
PF 30-MAY-2002; 2002WO-US017204.
XX
PR 20-SEP-2001; 2001US-0324100P.
PR 08-MAR-2002; 2002US-0362612P.
XX
PA (CORR ) CORNELL RES FOUND INC.
XX
PI Bander N;
XX
DR WPI; 2003-313319/30.
XX
PT Ablating/killing aberrant prostate specific membrane antigen-expressing
PT cells for treating skin disorders, by contacting the cell with an
PT antibody that binds to the extracellular domain of prostate specific
PT membrane antigen.
XX
PS Disclosure; Page 38; 225pp; English.
XX
CC The present invention describes a method (M1) for ablating or killing an
CC aberrant prostate specific membrane antigen (PSMA)-expressing cell (e.g.
CC an epidermal and a dermal cell). M1 comprises contacting the cell, or a
CC vascular endothelial cell proximate to the cell, with an antibody (or its
CC antigen-binding fragment), which binds specifically to the extracellular
CC domain of PSMA in an amount sufficient to ablate or kill the cell. The
CC antibodies have antipsoriatic, antiarthritis, dermatological, cytostatic,
CC antiinflammatory and antiallergic activities, and can be used in
CC vaccines. M1 is useful for treating a skin disorder in a subject, by
CC administering to the subject, an amount of an antibody which binds
CC specifically to the extracellular domain of PSMA (the subject is a
CC mammal, preferably human and is having, or at risk of, a skin disorder).
CC The skin disorder is a dermal or an epidermal disorder, and is selected
CC from psoriasis (preferably chronic stationary psoriasis, psoriasis
CC vulgaris, eruptive (gluttate) psoriasis, psoriatic erythroderma,
CC generalised pustular psoriasis (Von Zumbusch), annular pustular
CC psoriasis, and localised pustular psoriasis), psoriatic arthritis,
CC exfoliative dermatitis, pityriasis rubra pilaris, pityriasis roseacea,
CC parapsoriasis, pityriasis lichenoides, lichen planus, lichen nitidus,
CC ichthyosiform dermatosis, keratodermas, dermatosis, and prokeratosis,
CC preferably psoriasis. M1 is useful for treating a skin disorder such as
CC an inflammatory or neoplastic disorder of the epidermis or dermis,
CC preferably an epidermal precancerous or cancerous lesion. M1 is also
CC useful to treat or prevent disorders involving aberrant activity of PSMA-
CC expressing cell, e.g. kidney, liver or brain cell. ACC69816 to ACC69837
CC and ABR44613 to ABR44733 represent sequences used in the exemplification
XX of the present invention
SQ Sequence 112 AA;
Query Match 100.0%; Score 31; DB 6; Length 112;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AASNLES 7
DB 54 AASNLES 60
RESULT 49
ADU67960
ID ADU67960 standard; protein; 112 AA.

```


XX AC ADU67960;
 XX DT 10-FEB-2005 (first entry)
 XX DE Mouse Kabat subgroup VKIII light chain variable region.
 XX XX antibody; antibody engineering; antibody therapy; prostate tumor;
 KW cytostatic; prostate specific membrane antigen; PSMA;
 KW heavy chain variable region; light chain variable region.
 XX XX
 OS Mus musculus.
 XX XX WO2004098535-A2.
 XX XX 18-NOV-2004.
 XX XX 03-MAR-2004; 2004WO-US006586.
 XX XX 03-MAR-2003; 2003US-00379838.
 PR XX 30-MAY-2003; 2003US-00449379.
 XX XX (MILL-) MILLENNIUM PHARM INC.
 PA Horvath CJ, Webb IJ;
 PI WPI; 2004-805058/79.
 XX XX
 XX XX Use of an anti-prostate specific membrane antigen (anti-PSMA) antibody or
 PT antigen-binding fragment for treating prostate cancer or monitoring a
 PT patient receiving an anti-PSMA antibody to treat prostate cancer.
 XX XX Disclosure; SEQ ID NO 81; 284pp; English.
 XX XX The invention relates to the use of an anti-prostate specific membrane
 CC antigen (anti-PSMA) antibody or antigen-binding fragment for treating
 CC prostate cancer, monitoring a patient receiving an anti-PSMA antibody to
 CC treat prostate cancer, or selecting a patient for treatment with an anti-
 CC PSMA antibody. Also included are a method of treating prostate cancer in
 CC a subject, a method of monitoring a patient receiving an anti-PSMA
 CC antibody to treat prostate cancer and a method of selecting a patient for
 CC treatment with an anti-PSMA antibody. Also disclosed are anti-PSMA
 CC antibodies. The antibody or antigen-binding fragment is a human antibody
 CC (or antigen-binding fragment), a modified antibody (or an antigen-binding
 CC fragment). The modified antibody is selected from CDR-grafted antibody,
 CC humanized antibody, deimmunized antibody, or antigen binding fragments.
 CC The modified antibody or antigen-binding fragment has one or more CDRs
 CC (complementarity determining region) from a mouse monoclonal antibody
 CC selected from J591, J415, J533, or E99. The anti-PSMA antibody or antigen
 CC -binding fragment is useful for treating prostate cancer, monitoring a
 CC patient receiving an anti-PSMA antibody to treat prostate cancer, or
 CC selecting a patient for treatment with an anti-PSMA antibody. The present
 CC sequence is a mouse kabat subgroup consensus sequence for a light or
 CC heavy chain variable region used to compare to a sequence from one of the
 CC mouse monoclonal antibodies listed above.
 XX XX
 SQ Sequence 112 AA;

Query Match 100.0%; Score 31; DB 8; Length 112;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
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 Db 54 AASNLES 60

RESULT 50
 AAB71895
 ID AAB71895 standard; protein; 113 AA.
 XX
 AC AAB71895;
 XX

DT 09-MAY-2001 (first entry)
 XX Monoclonal antibody ST40 light chain.
 DE
 XX Antibody; ST40; molecular mimetic; CD4; human immunodeficiency virus;
 KW HIV; infection.
 KW
 XX Unidentified.
 OS
 XX WO200109191-A1.
 PN
 XX 08-FEB-2001.
 PD
 XX 02-AUG-2000; 2000WO-GB002972.
 PF
 XX 02-AUG-1999; 99EP-00401968.
 PR
 XX (SYNT-) SYNT:EM SA.
 PA Casset F, Granier C, Kaczorek M, Lahana R, Rees A, Roux F;
 PI WPI; 2001-168699/17.
 XX
 XX Designing molecular mimetics to mimic a parent molecule activity, useful
 PT e.g. therapeutically and diagnostically, uses computational screening to
 PT identify active chemical groups by accessibility within the parent
 PT molecule.
 PT
 XX Example 1; Fig 1; 85pp; English.
 PS
 XX The present sequence was used in a method for designing a mimetic which
 CC exhibits an activity associated with a parent molecule. Such mimetics may
 CC be smaller than the parent molecule and correspondingly easier and
 CC cheaper to make, since the active region of the parent molecule is
 CC normally relatively small. The method is useful where the parent molecule
 CC is a binding domain or the hypervariable region of an antibody or other
 CC member of the immunoglobulin superfamily. It is useful when the parent
 CC molecule is an antibody and the mimetic a peptide, especially an antibody
 CC which binds CD4 and a peptide which binds CD4. The mimetics designed and
 CC produced are useful diagnostically to detect cells bearing CD4 on their
 CC surfaces or may be included in pharmaceuticals e.g. to treat conditions
 CC in which CD4 is implicated (e.g. HIV)
 XX
 SQ Sequence 113 AA;
 Query Match 100.0%; Score 31; DB 4; Length 113;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AASNLES 7
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 Db 54 AASNLES 60

Search completed: February 23, 2006, 09:39:53
 Job time : 83.3077 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 09:41:24 ; Search time 9.90769 Seconds
(without alignments)
67.979 Million cell updates/sec

Title: US-10-723-872-18
Perfect score: 31
Sequence: 1 AASNLES 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 31 | 100.0 | 65 | 2 C38601 | Ig kappa chain V r |
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| 4 | 31 | 100.0 | 110 | 1 KVM510 | Ig kappa chain V r |
| 5 | 31 | 100.0 | 111 | 1 KVM543 | Ig kappa chain V r |
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| 7 | 31 | 100.0 | 111 | 1 KVM583 | Ig kappa chain V r |
| 8 | 31 | 100.0 | 111 | 1 KVM5C1 | Ig kappa chain V r |
| 9 | 31 | 100.0 | 112 | 2 S19976 | Ig kappa chain V r |
| 10 | 31 | 100.0 | 112 | 2 S19972 | Ig kappa chain V r |
| 11 | 31 | 100.0 | 131 | 2 PH1226 | Ig kappa chain pre |
| 12 | 31 | 100.0 | 463 | 2 B64160 | hypothetical prote |
| 13 | 31 | 100.0 | 942 | 2 T39624 | 6-phosphofructokin |
| 14 | 31 | 100.0 | 1208 | 2 T00362 | hypothetical prote |
| 15 | 28 | 90.3 | 69 | 2 AH3440 | cold shock protein |
| 16 | 28 | 90.3 | 108 | 1 KIHUGL | Ig kappa chain V-I |
| 17 | 28 | 90.3 | 112 | 2 S19972 | Ig kappa chain V r |
| 18 | 28 | 90.3 | 120 | 2 S06731 | Ig kappa chain pre |
| 19 | 28 | 90.3 | 122 | 2 S40370 | Ig kappa chain - h |
| 20 | 28 | 90.3 | 209 | 2 C87521 | hypothetical prote |
| 21 | 28 | 90.3 | 228 | 2 A98166 | hypothetical prote |
| 22 | 28 | 90.3 | 228 | 2 AF3121 | hypothetical prote |
| 23 | 28 | 90.3 | 313 | 1 QMXRWN | nonstructural prot |
| 24 | 28 | 90.3 | 313 | 1 QMXRWT | capsomere protein |
| 25 | 28 | 90.3 | 579 | 2 AB2177 | hypothetical prote |
| 26 | 28 | 90.3 | 632 | 2 D71941 | ATP-dependent zinc |
| 27 | 28 | 90.3 | 784 | 1 A55236 | kinesin-related pr |
| 28 | 27 | 87.1 | 81 | 2 S42193 | Ig kappa chain V r |
| 29 | 27 | 87.1 | 91 | 2 S25462 | Ig kappa chain V r |

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|-----|----|------|-------|----------|---------------------|
| 30 | 27 | 87.1 | 95 | 2 S25177 | Ig kappa chain V r |
| 31 | 27 | 87.1 | 101 | 2 S59640 | Ig light chain V r |
| 32 | 27 | 87.1 | 102 | 2 PH1077 | Ig light chain V r |
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| 34 | 27 | 87.1 | 107 | 2 S26343 | Ig kappa chain V r |
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| 41 | 27 | 87.1 | 111 | 1 KVM575 | Ig kappa chain V r |
| 42 | 27 | 87.1 | 111 | 1 KVM584 | Ig kappa chain V r |
| 43 | 27 | 87.1 | 111 | 2 S09965 | Ig kappa chain V-J |
| 44 | 27 | 87.1 | 111 | 2 D45722 | anti-glycoprotein |
| 45 | 27 | 87.1 | 111 | 2 S09966 | Ig kappa chain V-J |
| 46 | 27 | 87.1 | 111 | 2 S09963 | Ig kappa chain V-J |
| 47 | 27 | 87.1 | 112 | 2 S45715 | Ig kappa chain V r |
| 48 | 27 | 87.1 | 115 | 2 S63596 | Ig kappa chain V r |
| 49 | 27 | 87.1 | 120 | 2 S46374 | Ig kappa chain V-J |
| 50 | 27 | 87.1 | 131 | 1 KVM5M6 | Ig kappa chain pre |
| 51 | 27 | 87.1 | 177 | 1 A55537 | CDPdiacylglycerol- |
| 52 | 27 | 87.1 | 210 | 2 A56169 | Ig kappa chain V r |
| 53 | 27 | 87.1 | 218 | 2 JC5810 | monoclonal antibod |
| 54 | 27 | 87.1 | 230 | 1 UVFUS | cutinase (EC 3.1.1- |
| 55 | 27 | 87.1 | 260 | 2 A69881 | conserved hypothet |
| 56 | 27 | 87.1 | 310 | 2 A70620 | probable PE protei |
| 57 | 27 | 87.1 | 326 | 2 AC3492 | acetoacetate-CoA l |
| 58 | 27 | 87.1 | 389 | 2 H86266 | hypothetical prote |
| 59 | 27 | 87.1 | 396 | 2 AB1382 | phosphoglycerate k |
| 60 | 27 | 87.1 | 396 | 2 AC1751 | phosphoglycerate k |
| 61 | 27 | 87.1 | 486 | 2 S63384 | hypothetical prote |
| 62 | 27 | 87.1 | 497 | 2 T41467 | hypothetical prote |
| 63 | 27 | 87.1 | 510 | 2 C87415 | ammonium transport |
| 64 | 27 | 87.1 | 517 | 2 JC7623 | protein disulfide- |
| 65 | 27 | 87.1 | 661 | 2 B97733 | exonuclease ABC s |
| 66 | 27 | 87.1 | 662 | 2 E71731 | exonuclease ABC c |
| 67 | 27 | 87.1 | 689 | 2 F84389 | excision nuclease |
| 68 | 27 | 87.1 | 746 | 2 S67203 | probable membrane |
| 69 | 27 | 87.1 | 829 | 2 AH2282 | hypothetical prote |
| 70 | 27 | 87.1 | 832 | 2 T31792 | hypothetical prote |
| 71 | 27 | 87.1 | 927 | 2 F82818 | conserved hypothet |
| 72 | 27 | 87.1 | 1425 | 2 T31153 | hypothetical prote |
| 73 | 26 | 83.9 | 114 | 2 S46377 | Ig kappa chain V-J |
| 74 | 26 | 83.9 | 132 | 1 KVM532 | Ig kappa chain pre |
| 75 | 26 | 83.9 | 173 | 2 AC2151 | hypothetical prote |
| 76 | 26 | 83.9 | 297 | 2 C70251 | hypothetical prote |
| 77 | 26 | 83.9 | 456 | 2 S23104 | choline kinase - h |
| 78 | 26 | 83.9 | 664 | 2 C84869 | probable receptor |
| 79 | 26 | 83.9 | 1407 | 2 B42239 | adenylate cyclase |
| 80 | 26 | 83.9 | 2017 | 1 A36014 | myosin II heavy ch |
| 81 | 26 | 83.9 | 2057 | 2 S61477 | myosin II heavy ch |
| 82 | 26 | 83.9 | 15281 | 2 S41309 | cyclosporin synthe |
| 83 | 25 | 80.6 | 91 | 2 S17622 | Ig kappa chain V r |
| 84 | 25 | 80.6 | 94 | 2 PL0081 | Ig kappa chain V r |
| 85 | 25 | 80.6 | 111 | 2 S0349 | Ig kappa chain V r |
| 86 | 25 | 80.6 | 117 | 2 S24207 | Ig kappa chain V r |
| 87 | 25 | 80.6 | 167 | 2 A86941 | conserved hypothet |
| 88 | 25 | 80.6 | 207 | 2 G87507 | glutathione S-tran |
| 89 | 25 | 80.6 | 219 | 2 B90810 | hypothetical prote |
| 90 | 25 | 80.6 | 219 | 2 F85669 | hypothetical prote |
| 91 | 25 | 80.6 | 241 | 2 H87684 | hypothetical prote |
| 92 | 25 | 80.6 | 288 | 2 G97087 | fructokinase limpo |
| 93 | 25 | 80.6 | 295 | 2 E81313 | aspartate carbamoy |
| 94 | 25 | 80.6 | 313 | 2 A46233 | FLAR element-bindl |
| 95 | 25 | 80.6 | 341 | 2 H71716 | 190 kd antigen pre |
| 96 | 25 | 80.6 | 351 | 2 D96761 | unknown protein [i |
| 97 | 25 | 80.6 | 361 | 1 KHBH | aleurain (EC 3.4.2 |
| 98 | 25 | 80.6 | 391 | 2 C72220 | conserved hypothet |
| 99 | 25 | 80.6 | 397 | 2 T11786 | aspartate transami |
| 100 | 25 | 80.6 | 411 | 2 E83925 | dihydrolipoamide s |
| 101 | 25 | 80.6 | 426 | 2 H69127 | histidinol dehydro |
| 102 | 25 | 80.6 | 427 | 2 A45636 | glycophorin-bindin |

| | | | | | | | | | | | | | |
|-----|----|------|------|---|--------|--------------------|-----|----|------|-----|---|--------|---------------------|
| 103 | 25 | 80.6 | 444 | 2 | B97801 | DNA repair protein | 176 | 24 | 77.4 | 263 | 2 | A64807 | endonuclease VIII |
| 104 | 25 | 80.6 | 548 | 2 | C87242 | acyl-CoA synthase | 177 | 24 | 77.4 | 265 | 2 | AF2007 | hypothetical prote |
| 105 | 25 | 80.6 | 574 | 1 | S76132 | protein kinase pkn | 178 | 24 | 77.4 | 268 | 2 | B84693 | probable tropinone |
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| 107 | 25 | 80.6 | 613 | 2 | T16885 | hypothetical prote | 180 | 24 | 77.4 | 268 | 2 | C87295 | conserved tropinone |
| 108 | 25 | 80.6 | 613 | 2 | S70520 | melatonin receptor | 181 | 24 | 77.4 | 269 | 2 | C84695 | probable tropinone |
| 109 | 25 | 80.6 | 616 | 2 | B33586 | C4-dicarboxylate t | 182 | 24 | 77.4 | 271 | 2 | D84695 | probable tropinone |
| 110 | 25 | 80.6 | 621 | 2 | D96032 | C4-dicarboxylate t | 183 | 24 | 77.4 | 275 | 2 | T51437 | hypothetical prote |
| 111 | 25 | 80.6 | 664 | 2 | B66714 | hypothetical prote | 184 | 24 | 77.4 | 277 | 2 | A43783 | hypothetical prote |
| 112 | 25 | 80.6 | 701 | 2 | AF2336 | potassium-dependen | 185 | 24 | 77.4 | 279 | 2 | G70479 | homeotic protein N |
| 113 | 25 | 80.6 | 709 | 2 | A70624 | H+/K+-exchanging A | 186 | 24 | 77.4 | 284 | 2 | T46897 | excinuclease ABC c |
| 114 | 25 | 80.6 | 714 | 2 | S56208 | hypothetical prote | 187 | 24 | 77.4 | 301 | 2 | B86287 | protein F9L1.26 [i |
| 115 | 25 | 80.6 | 731 | 2 | S76028 | hypothetical prote | 188 | 24 | 77.4 | 311 | 2 | UC5943 | catechol 1,2-dioxy |
| 116 | 25 | 80.6 | 741 | 2 | S39082 | myosin heavy chain | 189 | 24 | 77.4 | 312 | 2 | T23521 | hypothetical prote |
| 117 | 25 | 80.6 | 848 | 2 | B84107 | myosin heavy chain | 190 | 24 | 77.4 | 344 | 2 | C97131 | hypothetical prote |
| 118 | 25 | 80.6 | 936 | 2 | S39083 | myosin heavy chain | 191 | 24 | 77.4 | 348 | 2 | S09273 | ig alpha chain C r |
| 119 | 25 | 80.6 | 955 | 2 | S24348 | myosin heavy chain | 192 | 24 | 77.4 | 349 | 2 | B97720 | hypothetical prote |
| 120 | 25 | 80.6 | 1018 | 2 | T40253 | hypothetical prote | 193 | 24 | 77.4 | 348 | 2 | B82256 | probable porin VCO |
| 121 | 25 | 80.6 | 1152 | 2 | F86363 | hypothetical prote | 194 | 24 | 77.4 | 352 | 2 | T36719 | probable integral |
| 122 | 25 | 80.6 | 1392 | 2 | T51947 | probable transcrip | 195 | 24 | 77.4 | 357 | 2 | S39509 | cinnamyl-alcohol d |
| 123 | 25 | 80.6 | 1500 | 2 | T03824 | probable immediate | 196 | 24 | 77.4 | 367 | 2 | T28892 | hypothetical prote |
| 124 | 25 | 80.6 | 1661 | 2 | T43260 | RNA polymerase (BC | 197 | 24 | 77.4 | 376 | 2 | T19266 | hypothetical prote |
| 125 | 25 | 80.6 | 1751 | 2 | G71518 | hypothetical prote | 198 | 24 | 77.4 | 377 | 2 | B69828 | hypothetical prote |
| 126 | 25 | 80.6 | 1938 | 1 | JX0178 | myosin heavy chain | 199 | 24 | 77.4 | 378 | 2 | T02895 | hypothetical prote |
| 127 | 25 | 80.6 | 1940 | 2 | A23320 | myosin heavy chain | 200 | 24 | 77.4 | 386 | 2 | A34843 | telomere-binding p |
| 128 | 25 | 80.6 | 2137 | 2 | T05244 | hypothetical prote | 201 | 24 | 77.4 | 392 | 2 | T04150 | RAD23 protein homo |
| 129 | 25 | 80.6 | 2897 | 2 | B48666 | cell proliferation | 202 | 24 | 77.4 | 394 | 2 | T02190 | hypothetical prote |
| 130 | 25 | 80.6 | 3256 | 2 | A48666 | cell proliferation | 203 | 24 | 77.4 | 396 | 2 | S68174 | rod arrestin - bul |
| 131 | 24 | 77.4 | 62 | 2 | S42265 | ig kappa chain v r | 204 | 24 | 77.4 | 396 | 2 | S68173 | rod arrestin - nor |
| 132 | 24 | 77.4 | 87 | 2 | I52592 | ig kappa chain v r | 205 | 24 | 77.4 | 402 | 2 | D86575 | phosphoglycerate k |
| 133 | 24 | 77.4 | 88 | 2 | S34087 | ig kappa chain v r | 206 | 24 | 77.4 | 402 | 2 | C72049 | phosphoglycerate k |
| 134 | 24 | 77.4 | 88 | 2 | S34088 | ig kappa chain v r | 207 | 24 | 77.4 | 410 | 2 | T20397 | hypothetical prote |
| 135 | 24 | 77.4 | 95 | 2 | PH0862 | ig kappa chain v r | 208 | 24 | 77.4 | 425 | 2 | S78258 | probable transloca |
| 136 | 24 | 77.4 | 97 | 2 | G86898 | 30S ribosomal prot | 209 | 24 | 77.4 | 426 | 2 | E83981 | pyruvate dehydroge |
| 137 | 24 | 77.4 | 108 | 1 | KIHUAG | ig kappa chain v-I | 210 | 24 | 77.4 | 428 | 1 | B32804 | GTP-binding protei |
| 138 | 24 | 77.4 | 110 | 2 | S44118 | ig kappa chain v-J | 211 | 24 | 77.4 | 444 | 2 | T19855 | hypothetical prote |
| 139 | 24 | 77.4 | 111 | 2 | S37202 | ig kappa chain v r | 212 | 24 | 77.4 | 448 | 1 | A16559 | DNA repair protein |
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| 141 | 24 | 77.4 | 117 | 2 | S42263 | ig kappa chain v r | 214 | 24 | 77.4 | 449 | 2 | AE2915 | ammonium transport |
| 142 | 24 | 77.4 | 117 | 2 | S43528 | ig kappa chain v r | 215 | 24 | 77.4 | 468 | 2 | AE0152 | probable bacteriop |
| 143 | 24 | 77.4 | 122 | 2 | H85695 | hypothetical prote | 216 | 24 | 77.4 | 471 | 2 | B83127 | probable secretion |
| 144 | 24 | 77.4 | 122 | 2 | G90837 | hypothetical prote | 217 | 24 | 77.4 | 474 | 1 | OMHUIB | alpha-1-B-glycopro |
| 145 | 24 | 77.4 | 122 | 2 | F64863 | yegJ protein precu | 218 | 24 | 77.4 | 485 | 2 | T03426 | sucrose phosphoryl |
| 146 | 24 | 77.4 | 128 | 2 | S00852 | hypothetical prote | 219 | 24 | 77.4 | 485 | 2 | AE3244 | sucrose phosphoryl |
| 147 | 24 | 77.4 | 136 | 1 | S71028 | flagellar protein | 220 | 24 | 77.4 | 488 | 2 | S37466 | sucrose phosphoryl |
| 148 | 24 | 77.4 | 139 | 2 | S40365 | ig kappa chain - h | 221 | 24 | 77.4 | 494 | 2 | I52658 | neurofilament-66 - |
| 149 | 24 | 77.4 | 141 | 2 | H72599 | hypothetical prote | 222 | 24 | 77.4 | 496 | 2 | T50272 | probable aldehyde |
| 150 | 24 | 77.4 | 151 | 2 | AD0369 | cytochrome C-type | 223 | 24 | 77.4 | 501 | 2 | AH1852 | hypothetical prote |
| 151 | 24 | 77.4 | 176 | 2 | C87383 | hypothetical prote | 224 | 24 | 77.4 | 504 | 2 | I53868 | alpha-internexin - |
| 152 | 24 | 77.4 | 186 | 2 | H75004 | hypothetical prote | 225 | 24 | 77.4 | 504 | 2 | H70520 | hypothetical glyci |
| 153 | 24 | 77.4 | 186 | 2 | A71158 | hypothetical prote | 226 | 24 | 77.4 | 505 | 2 | A41023 | alpha-internexin - |
| 154 | 24 | 77.4 | 192 | 2 | A11877 | hypothetical prote | 227 | 24 | 77.4 | 508 | 2 | A83885 | hypothetical prote |
| 155 | 24 | 77.4 | 193 | 1 | HIBPA4 | thioredoxin-like p | 228 | 24 | 77.4 | 510 | 2 | C86209 | protein F22G5.20 [|
| 156 | 24 | 77.4 | 194 | 2 | T09255 | internal protein I | 229 | 24 | 77.4 | 512 | 2 | H84707 | probable ferrochel |
| 157 | 24 | 77.4 | 206 | 2 | AE2222 | granulocyte colony | 230 | 24 | 77.4 | 536 | 2 | B84549 | probable ubiquitin |
| 158 | 24 | 77.4 | 212 | 2 | S73466 | hypothetical prote | 231 | 24 | 77.4 | 543 | 2 | T07739 | probable ferrochel |
| 159 | 24 | 77.4 | 218 | 2 | S68241 | probable DNA prima | 232 | 24 | 77.4 | 546 | 2 | T31255 | pHR protein homol |
| 160 | 24 | 77.4 | 218 | 2 | C70807 | ig kappa chain v r | 233 | 24 | 77.4 | 551 | 2 | C84549 | probable ubiquitin |
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| 162 | 24 | 77.4 | 220 | 1 | B6AG55 | virB5 protein prec | 235 | 24 | 77.4 | 565 | 1 | VHIVC8 | nucleoprotein - in |
| 163 | 24 | 77.4 | 220 | 2 | A13248 | component of type | 236 | 24 | 77.4 | 571 | 2 | B96734 | hypothetical prote |
| 164 | 24 | 77.4 | 227 | 2 | S77253 | precorrin decarbox | 237 | 24 | 77.4 | 574 | 2 | T29137 | hypothetical prote |
| 165 | 24 | 77.4 | 231 | 2 | AE2290 | precorrin decarbox | 238 | 24 | 77.4 | 575 | 2 | A97635 | adenine deaminase |
| 166 | 24 | 77.4 | 244 | 2 | T41861 | AcMNPV orf124 - Bo | 239 | 24 | 77.4 | 575 | 2 | AC2858 | adenine deaminase |
| 167 | 24 | 77.4 | 257 | 1 | S22363 | guFA protein homol | 240 | 24 | 77.4 | 592 | 2 | T52139 | LRR-containing F-b |
| 168 | 24 | 77.4 | 257 | 2 | AF0890 | probable membrane | 241 | 24 | 77.4 | 604 | 2 | T15514 | hypothetical prote |
| 169 | 24 | 77.4 | 257 | 2 | H91119 | guFA protein homol | 242 | 24 | 77.4 | 632 | 2 | E84653 | cell division prot |
| 170 | 24 | 77.4 | 257 | 2 | G85964 | guFA protein homol | 243 | 24 | 77.4 | 644 | 2 | B97885 | transporter, trunc |
| 171 | 24 | 77.4 | 258 | 2 | S77261 | hypothetical prote | 244 | 24 | 77.4 | 648 | 2 | AF3181 | hypothetical prote |
| 172 | 24 | 77.4 | 258 | 2 | PQ0770 | floral homeotic pr | 245 | 24 | 77.4 | 656 | 2 | G86434 | protein F17F8.23 [|
| 173 | 24 | 77.4 | 263 | 2 | AD0590 | floral homeotic pr | 246 | 24 | 77.4 | 656 | 2 | A72428 | methyl-accepting c |
| 174 | 24 | 77.4 | 263 | 2 | A85572 | hypothetical prote | 247 | 24 | 77.4 | 659 | 1 | JC4365 | arginine-tRNA liga |
| 175 | 24 | 77.4 | 263 | 2 | C90721 | hypothetical prote | 248 | 24 | 77.4 | 682 | 2 | F70421 | conserved hypothet |

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|-----|----|------|------|---|--------|--------------------|-----|----|------|-----|---|--------|------------------------|
| 249 | 24 | 77.4 | 706 | 2 | S62501 | hypothetical prote | 322 | 23 | 74.2 | 108 | 2 | S31944 | penicillin-binding |
| 250 | 24 | 77.4 | 732 | 2 | A84107 | glycosyltransferas | 323 | 23 | 74.2 | 108 | 2 | S31953 | penicillin-binding |
| 251 | 24 | 77.4 | 733 | 2 | T40293 | hypothetical prote | 324 | 23 | 74.2 | 108 | 2 | S31946 | penicillin-binding |
| 252 | 24 | 77.4 | 749 | 2 | C87618 | excinuclease ABC | 325 | 23 | 74.2 | 108 | 2 | S31954 | penicillin-binding |
| 253 | 24 | 77.4 | 759 | 2 | T39090 | probable integral | 326 | 23 | 74.2 | 108 | 2 | T06513 | emylc protein - ga |
| 254 | 24 | 77.4 | 760 | 2 | B81808 | hypothetical prote | 327 | 23 | 74.2 | 110 | 2 | S24288 | hypothetical nucle |
| 255 | 24 | 77.4 | 761 | 2 | T34038 | hypothetical prote | 328 | 23 | 74.2 | 110 | 2 | B48562 | hypothetical chain v |
| 256 | 24 | 77.4 | 817 | 2 | S53921 | hypothetical prote | 329 | 23 | 74.2 | 111 | 2 | E53285 | hypothetical chain v |
| 257 | 24 | 77.4 | 910 | 2 | S68983 | auxilin - bovine | 330 | 23 | 74.2 | 111 | 2 | A33936 | hypothetical chain v |
| 258 | 24 | 77.4 | 918 | 2 | C72120 | s/t protein kinase | 331 | 23 | 74.2 | 115 | 2 | S67572 | probable membrane |
| 259 | 24 | 77.4 | 918 | 2 | G85502 | S/T protein kinase | 332 | 23 | 74.2 | 116 | 2 | A27594 | hypothetical chain pre |
| 260 | 24 | 77.4 | 923 | 2 | H64081 | ATP-dependent heli | 333 | 23 | 74.2 | 117 | 1 | K1H011 | hypothetical chain pre |
| 261 | 24 | 77.4 | 925 | 2 | T01384 | hypothetical prote | 334 | 23 | 74.2 | 117 | 2 | S21056 | hypothetical chain pre |
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| 263 | 24 | 77.4 | 979 | 2 | E72236 | clostripain-relate | 336 | 23 | 74.2 | 117 | 2 | S21668 | hypothetical chain v |
| 264 | 24 | 77.4 | 986 | 2 | T16087 | hypothetical prote | 337 | 23 | 74.2 | 117 | 2 | S42264 | hypothetical chain v |
| 265 | 24 | 77.4 | 1011 | 2 | S45573 | myosin IA - fruit | 338 | 23 | 74.2 | 117 | 2 | S10227 | hypothetical chain pre |
| 266 | 24 | 77.4 | 1023 | 2 | AE1280 | ATP-dependent dsDN | 339 | 23 | 74.2 | 117 | 2 | S41809 | hypothetical chain v |
| 267 | 24 | 77.4 | 1028 | 2 | T50230 | hypothetical prote | 340 | 23 | 74.2 | 117 | 2 | B21056 | hypothetical chain pre |
| 268 | 24 | 77.4 | 1042 | 2 | S43904 | hyaluronidase - Cl | 341 | 23 | 74.2 | 117 | 2 | S21527 | hypothetical chain pre |
| 269 | 24 | 77.4 | 1058 | 2 | D82654 | ankyrin-like prote | 342 | 23 | 74.2 | 117 | 2 | S46376 | hypothetical chain V-J |
| 270 | 24 | 77.4 | 1066 | 2 | T15864 | hypothetical prote | 343 | 23 | 74.2 | 117 | 2 | S41810 | hypothetical chain v |
| 271 | 24 | 77.4 | 1098 | 2 | JQ2209 | helicase homolog 9 | 344 | 23 | 74.2 | 120 | 2 | S21667 | hypothetical chain v |
| 272 | 24 | 77.4 | 1116 | 2 | S63397 | probable membrane | 345 | 23 | 74.2 | 120 | 2 | S21666 | hypothetical chain v |
| 273 | 24 | 77.4 | 1133 | 2 | JT0665 | helicase II-like p | 346 | 23 | 74.2 | 120 | 2 | H83761 | hypothetical prote |
| 274 | 24 | 77.4 | 1151 | 2 | T33777 | hypothetical prote | 347 | 23 | 74.2 | 122 | 2 | S40314 | hypothetical chain - h |
| 275 | 24 | 77.4 | 1198 | 2 | E86402 | hypothetical prote | 348 | 23 | 74.2 | 123 | 2 | S40331 | hypothetical chain - h |
| 276 | 24 | 77.4 | 1224 | 1 | ERHUAH | coatomer complex a | 349 | 23 | 74.2 | 123 | 2 | P75293 | conserved hypothet |
| 277 | 24 | 77.4 | 1225 | 1 | B64234 | hypothetical prote | 350 | 23 | 74.2 | 127 | 2 | S40367 | hypothetical chain V-J |
| 278 | 24 | 77.4 | 1289 | 2 | F72308 | hypothetical prote | 351 | 23 | 74.2 | 128 | 2 | S52448 | hypothetical chain v |
| 279 | 24 | 77.4 | 1449 | 2 | T20181 | hypothetical prote | 352 | 23 | 74.2 | 128 | 2 | JL0073 | aberrant kappa tra |
| 280 | 24 | 77.4 | 1549 | 2 | S50705 | hypothetical prote | 353 | 23 | 74.2 | 129 | 1 | K1HUKK | hypothetical chain pre |
| 281 | 24 | 77.4 | 1584 | 2 | T20180 | hypothetical prote | 354 | 23 | 74.2 | 129 | 2 | S52789 | hypothetical chain v |
| 282 | 24 | 77.4 | 1586 | 2 | T20179 | hypothetical prote | 355 | 23 | 74.2 | 129 | 2 | S52793 | hypothetical chain v |
| 283 | 24 | 77.4 | 1794 | 2 | T38459 | hypothetical prote | 356 | 23 | 74.2 | 129 | 2 | S40369 | hypothetical chain - h |
| 284 | 24 | 77.4 | 1808 | 2 | T15099 | hypothetical diver | 357 | 23 | 74.2 | 130 | 2 | S40368 | hypothetical chain - h |
| 285 | 24 | 77.4 | 2108 | 2 | S28417 | hypothetical prote | 358 | 23 | 74.2 | 133 | 2 | S04343 | cytochrome c554 - |
| 286 | 24 | 77.4 | 3328 | 2 | T30835 | breast cancer tumo | 359 | 23 | 74.2 | 136 | 2 | E90559 | hypothetical prote |
| 287 | 24 | 77.4 | 3329 | 2 | T42205 | breast cancer succ | 360 | 23 | 74.2 | 138 | 2 | S32943 | hypG protein - Rho |
| 288 | 24 | 77.4 | 3329 | 2 | T30904 | breast cancer succ | 361 | 23 | 74.2 | 140 | 2 | PN0446 | hypG protein - Rho |
| 289 | 24 | 77.4 | 3343 | 2 | T42207 | breast cancer succ | 362 | 23 | 74.2 | 141 | 2 | C82466 | hypothetical chain pre |
| 290 | 24 | 77.4 | 3418 | 1 | G02334 | hypothetical prote | 363 | 23 | 74.2 | 149 | 2 | T26485 | hypothetical prote |
| 291 | 24 | 77.4 | 4151 | 2 | T13734 | groovin gene prote | 364 | 23 | 74.2 | 152 | 2 | T15170 | hypothetical prote |
| 292 | 23 | 74.2 | 46 | 2 | I58399 | hypothetical Nf-1 | 365 | 23 | 74.2 | 152 | 2 | T28759 | hypothetical prote |
| 293 | 23 | 74.2 | 54 | 2 | JT0521 | hypothetical prote | 366 | 23 | 74.2 | 155 | 2 | A71693 | hypothetical prote |
| 294 | 23 | 74.2 | 60 | 2 | A85598 | hypothetical prote | 367 | 23 | 74.2 | 157 | 2 | G97760 | hypothetical prote |
| 295 | 23 | 74.2 | 65 | 2 | PH0880 | hypothetical prote | 368 | 23 | 74.2 | 164 | 2 | B36951 | hypothetical prote |
| 296 | 23 | 74.2 | 71 | 2 | S60673 | hypothetical prote | 369 | 23 | 74.2 | 166 | 2 | A86185 | protein T7A14.4 li |
| 297 | 23 | 74.2 | 79 | 2 | G82811 | hypothetical prote | 370 | 23 | 74.2 | 167 | 2 | I48075 | aphrodisin precurs |
| 298 | 23 | 74.2 | 86 | 2 | S34086 | hypothetical prote | 371 | 23 | 74.2 | 170 | 2 | S76067 | hypothetical prote |
| 299 | 23 | 74.2 | 86 | 2 | S16840 | hypothetical prote | 372 | 23 | 74.2 | 173 | 2 | C82921 | multiple banded an |
| 300 | 23 | 74.2 | 87 | 2 | S34084 | hypothetical prote | 373 | 23 | 74.2 | 176 | 2 | G70138 | purine-binding che |
| 301 | 23 | 74.2 | 87 | 2 | S34083 | hypothetical prote | 374 | 23 | 74.2 | 181 | 2 | D84508 | hypothetical prote |
| 302 | 23 | 74.2 | 88 | 2 | S21522 | hypothetical prote | 375 | 23 | 74.2 | 185 | 2 | D72014 | general stress pro |
| 303 | 23 | 74.2 | 88 | 2 | S21528 | hypothetical prote | 376 | 23 | 74.2 | 185 | 2 | C86609 | general stress pro |
| 304 | 23 | 74.2 | 88 | 2 | S39639 | probable dTPDgluco | 377 | 23 | 74.2 | 185 | 2 | H81523 | general stress pro |
| 305 | 23 | 74.2 | 95 | 2 | PH0864 | hypothetical prote | 378 | 23 | 74.2 | 191 | 2 | S44504 | hypothetical prote |
| 306 | 23 | 74.2 | 95 | 2 | S45324 | hypothetical prote | 379 | 23 | 74.2 | 192 | 2 | S17760 | (NADH); short-chai |
| 307 | 23 | 74.2 | 95 | 2 | PH0867 | hypothetical prote | 380 | 23 | 74.2 | 193 | 1 | S73686 | hypothetical prote |
| 308 | 23 | 74.2 | 102 | 2 | PC6027 | acetylcoline recep | 381 | 23 | 74.2 | 193 | 2 | G84942 | hypothetical prote |
| 309 | 23 | 74.2 | 103 | 2 | S18731 | hypothetical prote | 382 | 23 | 74.2 | 193 | 2 | A71098 | hypothetical prote |
| 310 | 23 | 74.2 | 106 | 2 | G72632 | hypothetical prote | 383 | 23 | 74.2 | 195 | 2 | D83237 | hypothetical prote |
| 311 | 23 | 74.2 | 107 | 2 | S36264 | hypothetical prote | 384 | 23 | 74.2 | 196 | 2 | S14725 | hypothetical prote |
| 312 | 23 | 74.2 | 107 | 2 | S36262 | hypothetical prote | 385 | 23 | 74.2 | 197 | 2 | T15923 | hypothetical prote |
| 313 | 23 | 74.2 | 107 | 2 | S40183 | hypothetical prote | 386 | 23 | 74.2 | 200 | 2 | C85096 | hypothetical prote |
| 314 | 23 | 74.2 | 107 | 2 | I69017 | anti-HIV1 envelope | 387 | 23 | 74.2 | 209 | 2 | A25828 | hypothetical prote |
| 315 | 23 | 74.2 | 107 | 2 | AH1164 | hypothetical prote | 388 | 23 | 74.2 | 212 | 2 | S44805 | hypothetical prote |
| 316 | 23 | 74.2 | 108 | 1 | K1HUKA | hypothetical prote | 389 | 23 | 74.2 | 215 | 2 | C38611 | hypothetical prote |
| 317 | 23 | 74.2 | 108 | 1 | K1HUKU | hypothetical prote | 390 | 23 | 74.2 | 215 | 2 | A39459 | hypothetical prote |
| 318 | 23 | 74.2 | 108 | 1 | KVMS06 | hypothetical prote | 391 | 23 | 74.2 | 215 | 2 | JN0556 | hypothetical prote |
| 319 | 23 | 74.2 | 108 | 2 | S47182 | hypothetical prote | 392 | 23 | 74.2 | 215 | 2 | S20405 | hypothetical prote |
| 320 | 23 | 74.2 | 108 | 2 | PH0092 | hypothetical prote | 393 | 23 | 74.2 | 215 | 2 | S14724 | hypothetical prote |
| 321 | 23 | 74.2 | 108 | 2 | B49047 | hypothetical prote | 394 | 23 | 74.2 | 217 | 2 | T31875 | hypothetical prote |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|--------|--------------------|-----|----|------|-----|---|--------|---------------------|
| 395 | 23 | 74.2 | 218 | 2 | E64704 | distal basal body | 468 | 23 | 74.2 | 360 | 2 | S59598 | cysteine proteinase |
| 396 | 23 | 74.2 | 218 | 2 | E71814 | hypothetical prote | 469 | 23 | 74.2 | 360 | 2 | S42431 | dtDPglucose 4,6-de |
| 397 | 23 | 74.2 | 229 | 2 | G83730 | hypothetical prote | 470 | 23 | 74.2 | 361 | 2 | AF0767 | dtDPglucose 4,6-d |
| 398 | 23 | 74.2 | 233 | 2 | JC5322 | p53 specific singl | 471 | 23 | 74.2 | 361 | 2 | S78542 | dtDPglucose 4,6-de |
| 399 | 23 | 74.2 | 234 | 2 | AD2228 | hypothetical prote | 472 | 23 | 74.2 | 361 | 2 | S15299 | dtDPglucose 4,6-de |
| 400 | 23 | 74.2 | 235 | 1 | ASUJG4 | vif protein - simi | 473 | 23 | 74.2 | 361 | 2 | S41534 | dtDPglucose 4,6-de |
| 401 | 23 | 74.2 | 238 | 2 | T16788 | hypothetical prote | 474 | 23 | 74.2 | 362 | 1 | KHRZOG | oryzain (EC 3.4.22 |
| 402 | 23 | 74.2 | 239 | 2 | T02551 | probable carboxyme | 475 | 23 | 74.2 | 375 | 2 | AB3165 | conserved hypothet |
| 403 | 23 | 74.2 | 239 | 2 | S66341 | ribonuclease I (EC | 476 | 23 | 74.2 | 376 | 2 | T16059 | hypothetical prote |
| 404 | 23 | 74.2 | 240 | 2 | A22831 | 19K zein precursor | 477 | 23 | 74.2 | 377 | 2 | D72317 | hypothetical prote |
| 405 | 23 | 74.2 | 240 | 2 | F69885 | processing protein | 478 | 23 | 74.2 | 379 | 2 | A70384 | glutamate N-acetyl |
| 406 | 23 | 74.2 | 241 | 2 | H97723 | hypothetical prote | 479 | 23 | 74.2 | 379 | 2 | T34100 | hypothetical prote |
| 407 | 23 | 74.2 | 244 | 2 | A75184 | ATP-binding transp | 480 | 23 | 74.2 | 379 | 2 | T14337 | hypothetical prote |
| 408 | 23 | 74.2 | 245 | 2 | G70748 | hypothetical prote | 481 | 23 | 74.2 | 382 | 2 | A44292 | RA23 protein, iso |
| 409 | 23 | 74.2 | 245 | 2 | B83108 | hypothetical prote | 482 | 23 | 74.2 | 382 | 2 | F85773 | cyclopropane fatty |
| 410 | 23 | 74.2 | 255 | 2 | B86254 | hypothetical prote | 483 | 23 | 74.2 | 382 | 2 | B90925 | cyclopropane fatty |
| 411 | 23 | 74.2 | 255 | 2 | AD1316 | heptaprenyl diphos | 484 | 23 | 74.2 | 382 | 2 | T14336 | RA23 protein, iso |
| 412 | 23 | 74.2 | 258 | 2 | JC6327 | 4-hydroxy-2-oxoval | 485 | 23 | 74.2 | 383 | 2 | G96629 | hypothetical prote |
| 413 | 23 | 74.2 | 264 | 2 | G70075 | amino acid ABC tra | 486 | 23 | 74.2 | 383 | 2 | AE0376 | O-antigen chain le |
| 414 | 23 | 74.2 | 265 | 2 | D41839 | ribosomal protein | 487 | 23 | 74.2 | 389 | 2 | G84368 | hypothetical prote |
| 415 | 23 | 74.2 | 266 | 2 | AF0145 | probable ABC trans | 488 | 23 | 74.2 | 390 | 2 | E81408 | probable periplasm |
| 416 | 23 | 74.2 | 267 | 2 | E64175 | hypothetical prote | 489 | 23 | 74.2 | 392 | 2 | A70957 | hypothetical prote |
| 417 | 23 | 74.2 | 271 | 2 | C97317 | nudix (MutT) fami | 490 | 23 | 74.2 | 395 | 2 | AB3543 | succinyl-diaminopi |
| 418 | 23 | 74.2 | 274 | 2 | B82179 | ABC transporter, p | 491 | 23 | 74.2 | 396 | 2 | AD0792 | anaerobic glycerol |
| 419 | 23 | 74.2 | 275 | 2 | E65648 | 5-Keto-4-deoxyuron | 492 | 23 | 74.2 | 400 | 1 | A39822 | leukosialin precur |
| 420 | 23 | 74.2 | 277 | 2 | A87184 | thiosulfate sulfur | 493 | 23 | 74.2 | 401 | 2 | G82210 | amino acid ABC tra |
| 421 | 23 | 74.2 | 280 | 2 | D69216 | extragenic suppres | 494 | 23 | 74.2 | 405 | 2 | AC3644 | alpha-methylacyl-C |
| 422 | 23 | 74.2 | 280 | 2 | T27758 | hypothetical prote | 495 | 23 | 74.2 | 411 | 2 | T40538 | hypothetical prote |
| 423 | 23 | 74.2 | 280 | 2 | T49142 | CCR4-associated fa | 496 | 23 | 74.2 | 412 | 2 | T21419 | hypothetical prote |
| 424 | 23 | 74.2 | 280 | 2 | A12548 | hypothetical prote | 497 | 23 | 74.2 | 413 | 2 | AF1427 | an hypothetical pr |
| 425 | 23 | 74.2 | 281 | 2 | AG1369 | conserved hypothet | 498 | 23 | 74.2 | 413 | 2 | AD1801 | hypothetical prote |
| 426 | 23 | 74.2 | 282 | 2 | T37491 | dnaJ protein - fis | 499 | 23 | 74.2 | 414 | 2 | T27045 | hypothetical prote |
| 427 | 23 | 74.2 | 286 | 2 | S50855 | neurotrophin-6 - s | 500 | 23 | 74.2 | 415 | 2 | G72335 | hypothetical prote |
| 428 | 23 | 74.2 | 287 | 2 | G64504 | hypothetical prote | 501 | 23 | 74.2 | 421 | 2 | AH3627 | probable trehalose |
| 429 | 23 | 74.2 | 288 | 2 | H84282 | GTP-binding protei | 502 | 23 | 74.2 | 423 | 2 | G95880 | hypothetical prote |
| 430 | 23 | 74.2 | 291 | 2 | T74914 | hypothetical prote | 503 | 23 | 74.2 | 424 | 2 | T20692 | hypothetical prote |
| 431 | 23 | 74.2 | 292 | 1 | A36748 | insulin-like growt | 504 | 23 | 74.2 | 424 | 2 | AD2238 | hypothetical prote |
| 432 | 23 | 74.2 | 292 | 2 | T34529 | hypothetical prote | 505 | 23 | 74.2 | 427 | 2 | G84347 | glycerol-3-phospha |
| 433 | 23 | 74.2 | 292 | 2 | T52257 | CCR4-associated fa | 506 | 23 | 74.2 | 427 | 2 | E83801 | GTP-binding protei |
| 434 | 23 | 74.2 | 292 | 2 | D83494 | hypothetical prote | 507 | 23 | 74.2 | 430 | 2 | T21060 | hypothetical prote |
| 435 | 23 | 74.2 | 299 | 2 | T05680 | hypothetical prote | 508 | 23 | 74.2 | 432 | 2 | G72456 | probable glutamate |
| 436 | 23 | 74.2 | 299 | 2 | A87530 | phosphorylase fami | 509 | 23 | 74.2 | 439 | 2 | E83511 | flagellar hook-ass |
| 437 | 23 | 74.2 | 299 | 2 | G90578 | hypothetical prote | 510 | 23 | 74.2 | 439 | 2 | T03444 | protein kinase hom |
| 438 | 23 | 74.2 | 301 | 2 | F70121 | hypothetical prote | 511 | 23 | 74.2 | 441 | 2 | A72058 | glucose-1-phosphat |
| 439 | 23 | 74.2 | 306 | 2 | G95999 | probable transcrip | 512 | 23 | 74.2 | 441 | 2 | D86566 | glucose-1-P adeny |
| 440 | 23 | 74.2 | 308 | 2 | S73847 | yabc protein homol | 513 | 23 | 74.2 | 442 | 2 | S19712 | ubiquitin-protein |
| 441 | 23 | 74.2 | 309 | 2 | B96602 | hypothetical prote | 514 | 23 | 74.2 | 443 | 2 | D71935 | probable zinc prot |
| 442 | 23 | 74.2 | 311 | 2 | S13808 | protein-tyrosine k | 515 | 23 | 74.2 | 444 | 2 | D64646 | proteinase (EC 3.4 |
| 443 | 23 | 74.2 | 314 | 2 | JC4951 | troponin T - scall | 516 | 23 | 74.2 | 446 | 2 | F71069 | hypothetical prote |
| 444 | 23 | 74.2 | 315 | 2 | T46993 | hypothetical prote | 517 | 23 | 74.2 | 447 | 2 | S59742 | SUFl protein - yea |
| 445 | 23 | 74.2 | 315 | 2 | F90589 | conserved hypothet | 518 | 23 | 74.2 | 450 | 2 | I48756 | gene Sbx protein - |
| 446 | 23 | 74.2 | 317 | 2 | T00500 | probable elicitor | 519 | 23 | 74.2 | 452 | 2 | A12966 | hypothetical prote |
| 447 | 23 | 74.2 | 320 | 2 | T25271 | hypothetical prote | 520 | 23 | 74.2 | 452 | 2 | B98316 | thuD protein (AF17 |
| 448 | 23 | 74.2 | 323 | 2 | A53845 | replication factor | 521 | 23 | 74.2 | 457 | 2 | G82925 | hypothetical prote |
| 449 | 23 | 74.2 | 332 | 2 | D83519 | probable transcrip | 522 | 23 | 74.2 | 458 | 2 | T43643 | smg-7 protein - Ca |
| 450 | 23 | 74.2 | 333 | 2 | C86854 | penicillin amidase | 523 | 23 | 74.2 | 465 | 2 | S69038 | hypothetical prote |
| 451 | 23 | 74.2 | 337 | 2 | D72690 | hypothetical prote | 524 | 23 | 74.2 | 465 | 2 | H64507 | hypothetical prote |
| 452 | 23 | 74.2 | 338 | 2 | H84166 | LPS biosynthesis p | 525 | 23 | 74.2 | 466 | 2 | A13262 | argininosuccinate |
| 453 | 23 | 74.2 | 340 | 1 | R6KWB | GTP-binding regula | 526 | 23 | 74.2 | 466 | 2 | T47789 | hypothetical prote |
| 454 | 23 | 74.2 | 340 | 2 | B86778 | ketol-acid reducto | 527 | 23 | 74.2 | 467 | 2 | B96979 | spore germination |
| 455 | 23 | 74.2 | 340 | 2 | T20830 | hypothetical prote | 528 | 23 | 74.2 | 468 | 2 | H72230 | glutamate synthase |
| 456 | 23 | 74.2 | 341 | 2 | G82014 | dtDPglucose 4,6-de | 529 | 23 | 74.2 | 470 | 2 | T39921 | hypothetical prote |
| 457 | 23 | 74.2 | 344 | 1 | S35140 | probable ketol-ac | 530 | 23 | 74.2 | 472 | 2 | T30831 | hypothetical prote |
| 458 | 23 | 74.2 | 344 | 2 | T34470 | homeobox protein c | 531 | 23 | 74.2 | 472 | 2 | G83335 | outer membrane pro |
| 459 | 23 | 74.2 | 345 | 2 | F84136 | ABC transporter (A | 532 | 23 | 74.2 | 472 | 2 | T43084 | transfer complex p |
| 460 | 23 | 74.2 | 346 | 2 | S47045 | dtDPglucose 4,6-de | 533 | 23 | 74.2 | 473 | 2 | S36241 | penicillin-binding |
| 461 | 23 | 74.2 | 346 | 2 | S13807 | protein-tyrosine k | 534 | 23 | 74.2 | 473 | 2 | S36239 | penicillin-binding |
| 462 | 23 | 74.2 | 349 | 2 | AB1715 | oxidoreductase hom | 535 | 23 | 74.2 | 473 | 2 | S36242 | penicillin-binding |
| 463 | 23 | 74.2 | 349 | 2 | AG1344 | oxidoreductase hom | 536 | 23 | 74.2 | 475 | 2 | S73897 | Mgl23 homolog A65 |
| 464 | 23 | 74.2 | 354 | 2 | D71620 | ubiquinone biosynt | 537 | 23 | 74.2 | 479 | 2 | T06432 | probable protein k |
| 465 | 23 | 74.2 | 355 | 2 | G81242 | dtDPglucose 4,6-de | 538 | 23 | 74.2 | 480 | 2 | A82033 | TLDD protein homol |
| 466 | 23 | 74.2 | 355 | 2 | T00102 | dtDPglucose 4,6-de | 539 | 23 | 74.2 | 480 | 2 | F81010 | tlDD protein NMB20 |
| 467 | 23 | 74.2 | 355 | 2 | AF0470 | dtDP-D-glucose-4,6 | 540 | 23 | 74.2 | 481 | 2 | T36563 | probable ion-trans |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|--------|---------------------|-----|----|------|------|---|--------|--------------------|
| 541 | 23 | 74.2 | 482 | 2 | T43996 | virion protein [im | 614 | 23 | 74.2 | 691 | 2 | C72454 | hypothetical prote |
| 542 | 23 | 74.2 | 484 | 2 | T44183 | probable envelope | 615 | 23 | 74.2 | 698 | 2 | A54796 | regulatory protein |
| 543 | 23 | 74.2 | 486 | 2 | E35965 | penicillin-binding | 616 | 23 | 74.2 | 707 | 2 | T40070 | origin recognition |
| 544 | 23 | 74.2 | 486 | 2 | B35965 | penicillin-binding | 617 | 23 | 74.2 | 707 | 2 | T01502 | probable serine/th |
| 545 | 23 | 74.2 | 490 | 2 | H96911 | uroporphyrinogen I | 618 | 23 | 74.2 | 724 | 2 | S17479 | SEC1 protein - yea |
| 546 | 23 | 74.2 | 492 | 2 | C81379 | probable outer mem | 619 | 23 | 74.2 | 745 | 2 | T12528 | hypothetical prote |
| 547 | 23 | 74.2 | 494 | 2 | A12438 | UDP-N-acetylmuramo | 620 | 23 | 74.2 | 751 | 2 | F83080 | hypothetical prote |
| 548 | 23 | 74.2 | 495 | 2 | T48213 | hypothetical prote | 621 | 23 | 74.2 | 757 | 2 | T42693 | hypothetical prote |
| 549 | 23 | 74.2 | 496 | 2 | T37366 | probable glutathio | 622 | 23 | 74.2 | 772 | 2 | A09997 | ferrous iron trans |
| 550 | 23 | 74.2 | 497 | 2 | F82747 | conserved hypotet | 623 | 23 | 74.2 | 773 | 1 | A36932 | iron(II) transport |
| 551 | 23 | 74.2 | 501 | 2 | A98042 | H+-transporting tw | 624 | 23 | 74.2 | 773 | 2 | C91160 | ferrous iron trans |
| 552 | 23 | 74.2 | 501 | 2 | JC5739 | membrane-bound pro | 625 | 23 | 74.2 | 773 | 2 | B86006 | ferrous iron trans |
| 553 | 23 | 74.2 | 501 | 2 | H95175 | Arp synthase Fl, a | 626 | 23 | 74.2 | 775 | 2 | T30917 | hypothetical prote |
| 554 | 23 | 74.2 | 505 | 1 | D70703 | tld homolog rv231 | 627 | 23 | 74.2 | 787 | 2 | S47245 | ActA protein - Lis |
| 555 | 23 | 74.2 | 505 | 2 | I64189 | amidophosphoribosy | 628 | 23 | 74.2 | 789 | 2 | S28259 | androgen-regulated |
| 556 | 23 | 74.2 | 510 | 2 | T38076 | conserved hypotet | 629 | 23 | 74.2 | 789 | 2 | F82426 | probable phosphogl |
| 557 | 23 | 74.2 | 512 | 2 | T41340 | hypothetical prote | 630 | 23 | 74.2 | 794 | 2 | C87437 | penicillin-binding |
| 558 | 23 | 74.2 | 518 | 1 | A27705 | alpha-amylase (EC | 631 | 23 | 74.2 | 808 | 2 | H64474 | hypothetical prote |
| 559 | 23 | 74.2 | 527 | 2 | G64626 | alginate O-acetyla | 632 | 23 | 74.2 | 811 | 2 | PN0689 | connectin 1 - chic |
| 560 | 23 | 74.2 | 532 | 2 | G84427 | hypothetical prote | 633 | 23 | 74.2 | 822 | 2 | AB3054 | hypothetical prote |
| 561 | 23 | 74.2 | 533 | 2 | G75348 | conserved hypotet | 634 | 23 | 74.2 | 823 | 2 | T34472 | hypothetical prote |
| 562 | 23 | 74.2 | 535 | 2 | B45270 | sensory histidine | 635 | 23 | 74.2 | 832 | 2 | T33490 | hypothetical prote |
| 563 | 23 | 74.2 | 544 | 2 | A13266 | integral membrane | 636 | 23 | 74.2 | 834 | 2 | A97178 | probable permease |
| 564 | 23 | 74.2 | 546 | 2 | T33291 | hypothetical prote | 637 | 23 | 74.2 | 837 | 2 | E87759 | protein D1007.15 [|
| 565 | 23 | 74.2 | 548 | 2 | C70253 | adenine deaminase | 638 | 23 | 74.2 | 840 | 2 | A27832 | cell division cont |
| 566 | 23 | 74.2 | 549 | 2 | S61706 | RNA 5'-triphosphat | 639 | 23 | 74.2 | 842 | 2 | T05400 | hypothetical prote |
| 567 | 23 | 74.2 | 551 | 2 | AC3572 | lysine-tRNA ligase | 640 | 23 | 74.2 | 847 | 2 | S75975 | hypothetical prote |
| 568 | 23 | 74.2 | 561 | 2 | S62552 | hypothetical prote | 641 | 23 | 74.2 | 853 | 2 | T17461 | disease resistance |
| 569 | 23 | 74.2 | 564 | 2 | S57124 | CTP synthase (EC 6 | 642 | 23 | 74.2 | 855 | 2 | T17460 | disease resistance |
| 570 | 23 | 74.2 | 565 | 2 | C86617 | sulfate transporte | 643 | 23 | 74.2 | 856 | 2 | C71956 | probable endopepti |
| 571 | 23 | 74.2 | 565 | 2 | D72006 | sulfate transporte | 644 | 23 | 74.2 | 856 | 2 | H64552 | endopeptidase Clp |
| 572 | 23 | 74.2 | 568 | 2 | F86291 | hypothetical prote | 645 | 23 | 74.2 | 857 | 2 | F81396 | ATP-dependent CLP |
| 573 | 23 | 74.2 | 569 | 2 | T07158 | amidophosphoribosy | 646 | 23 | 74.2 | 871 | 2 | A53429 | acetylglutamate ki |
| 574 | 23 | 74.2 | 569 | 2 | T38627 | hypothetical dna b | 647 | 23 | 74.2 | 886 | 1 | GNLJSP | pol polyprotein - |
| 575 | 23 | 74.2 | 570 | 2 | B96776 | hypothetical prote | 648 | 23 | 74.2 | 886 | 2 | S73184 | Phycobilisome link |
| 576 | 23 | 74.2 | 572 | 2 | B84648 | hypothetical prote | 649 | 23 | 74.2 | 891 | 2 | T30812 | ubiquitin-protein |
| 577 | 23 | 74.2 | 590 | 2 | T49672 | related to a-agglu | 650 | 23 | 74.2 | 891 | 2 | T40417 | hypothetical prote |
| 578 | 23 | 74.2 | 594 | 2 | S00961 | hypothetical prote | 651 | 23 | 74.2 | 892 | 2 | G84693 | probable proline-r |
| 579 | 23 | 74.2 | 597 | 2 | S76209 | probable flavoprot | 652 | 23 | 74.2 | 892 | 2 | S57055 | probable membrane |
| 580 | 23 | 74.2 | 598 | 1 | A37192 | excinuclease ABC, | 653 | 23 | 74.2 | 896 | 2 | S48761 | trehalose-phosphat |
| 581 | 23 | 74.2 | 601 | 2 | T11190 | NADH2 dehydrogenas | 654 | 23 | 74.2 | 896 | 2 | S43074 | epidermal growth f |
| 582 | 23 | 74.2 | 603 | 2 | T28278 | ORF MSV117 probabl | 655 | 23 | 74.2 | 905 | 2 | T38944 | probable coatomer |
| 583 | 23 | 74.2 | 604 | 2 | T15504 | hypothetical prote | 656 | 23 | 74.2 | 907 | 2 | AB1885 | hypothetical prote |
| 584 | 23 | 74.2 | 606 | 2 | AC2508 | hypothetical prote | 657 | 23 | 74.2 | 918 | 2 | G88545 | protein F5982.12 [|
| 585 | 23 | 74.2 | 609 | 2 | T25120 | hypothetical prote | 658 | 23 | 74.2 | 926 | 2 | S48463 | SEC24 protein - ye |
| 586 | 23 | 74.2 | 610 | 2 | A41315 | hypothetical prote | 659 | 23 | 74.2 | 940 | 2 | S19702 | fibronectin-bindin |
| 587 | 23 | 74.2 | 616 | 2 | S50998 | transporter protei | 660 | 23 | 74.2 | 943 | 2 | S31132 | hypothetical prote |
| 588 | 23 | 74.2 | 620 | 2 | T39074 | yeast chs5 homolog | 661 | 23 | 74.2 | 950 | 2 | A71655 | hypothetical prote |
| 589 | 23 | 74.2 | 622 | 2 | A26981 | regulatory protein | 662 | 23 | 74.2 | 957 | 2 | S44748 | C0604.1 protein - |
| 590 | 23 | 74.2 | 625 | 2 | C86955 | hypothetical prote | 663 | 23 | 74.2 | 964 | 2 | S57379 | MSH2 protein - yea |
| 591 | 23 | 74.2 | 625 | 2 | S72993 | glutamine-fructose | 664 | 23 | 74.2 | 978 | 2 | T40803 | probable pre-tRNA |
| 592 | 23 | 74.2 | 625 | 2 | D83753 | PTS system, fructo | 665 | 23 | 74.2 | 986 | 2 | G65116 | hypothetical prote |
| 593 | 23 | 74.2 | 625 | 2 | H90533 | hypothetical prote | 666 | 23 | 74.2 | 986 | 2 | T38205 | hypothetical prote |
| 594 | 23 | 74.2 | 626 | 2 | A42891 | beta-galactosidase | 667 | 23 | 74.2 | 991 | 2 | C98232 | RanBP7/importin-be |
| 595 | 23 | 74.2 | 627 | 2 | E95377 | probable two-compo | 668 | 23 | 74.2 | 993 | 2 | A97334 | type II restrictio |
| 596 | 23 | 74.2 | 633 | 2 | T27499 | hypothetical prote | 669 | 23 | 74.2 | 1008 | 2 | C97726 | acriflavin resista |
| 597 | 23 | 74.2 | 635 | 2 | S64025 | hypothetical prote | 670 | 23 | 74.2 | 1008 | 2 | T18508 | hypothetical prote |
| 598 | 23 | 74.2 | 641 | 2 | G85043 | hypothetical prote | 671 | 23 | 74.2 | 1011 | 2 | T50344 | poly(A)+ RNA trans |
| 599 | 23 | 74.2 | 643 | 2 | A96636 | unknown protein, 7 | 672 | 23 | 74.2 | 1012 | 2 | T24384 | hypothetical prote |
| 600 | 23 | 74.2 | 646 | 2 | C86441 | probable ABC trans | 673 | 23 | 74.2 | 1012 | 2 | T25200 | poly(A)+ RNA trans |
| 601 | 23 | 74.2 | 650 | 2 | JC7088 | heat shock protein | 674 | 23 | 74.2 | 1021 | 2 | AC2202 | hypothetical prote |
| 602 | 23 | 74.2 | 659 | 2 | G82365 | methyl-accepting c | 675 | 23 | 74.2 | 1039 | 2 | T38447 | tetratricopeptide |
| 603 | 23 | 74.2 | 661 | 1 | A69048 | ferrous iron trans | 676 | 23 | 74.2 | 1055 | 2 | A87364 | OmpA-related prote |
| 604 | 23 | 74.2 | 670 | 2 | A11847 | two-component sens | 677 | 23 | 74.2 | 1058 | 2 | A48195 | ubiquitin-protein |
| 605 | 23 | 74.2 | 678 | 2 | H82379 | methyl-accepting c | 678 | 23 | 74.2 | 1058 | 2 | A38564 | ubiquitin-protein |
| 606 | 23 | 74.2 | 679 | 2 | S06000 | penicillin-binding | 679 | 23 | 74.2 | 1058 | 2 | JC1254 | ubiquitin-protein |
| 607 | 23 | 74.2 | 680 | 2 | G95194 | penicillin-binding | 680 | 23 | 74.2 | 1068 | 2 | H96769 | hypothetical prote |
| 608 | 23 | 74.2 | 682 | 2 | T43292 | G protein-linked a | 681 | 23 | 74.2 | 1080 | 2 | T43164 | IactA protein - Li |
| 609 | 23 | 74.2 | 682 | 2 | D40270 | hypothetical prote | 682 | 23 | 74.2 | 1111 | 2 | T01078 | hypothetical prote |
| 610 | 23 | 74.2 | 685 | 2 | P98061 | penicillinbinding p | 683 | 23 | 74.2 | 1113 | 2 | T20004 | hypothetical prote |
| 611 | 23 | 74.2 | 688 | 2 | T27020 | hypothetical prote | 684 | 23 | 74.2 | 1113 | 2 | S48495 | probable membrane |
| 612 | 23 | 74.2 | 689 | 2 | T29772 | hypothetical prote | 685 | 23 | 74.2 | 1115 | 1 | IGMSNL | neural cell adhesi |
| 613 | 23 | 74.2 | 691 | 2 | H71405 | hypothetical prote | 686 | 23 | 74.2 | 1166 | 1 | S06142 | protein-tyrosine k |

| | | | | | | | | | | | | | |
|-----|----|------|------|---|--------|--------------------|-----|----|------|-----|---|--------|---------------------|
| 687 | 23 | 74.2 | 1167 | 2 | B11924 | cag island protein | 760 | 22 | 71.0 | 105 | 2 | B70716 | hypothetical prote |
| 688 | 23 | 74.2 | 1170 | 2 | A57650 | repair protein XPG | 761 | 22 | 71.0 | 105 | 2 | S36266 | Ig lambda chain v |
| 689 | 23 | 74.2 | 1183 | 2 | S65236 | probable membrane | 762 | 22 | 71.0 | 107 | 2 | PL0262 | Ig kappa chain v r |
| 690 | 23 | 74.2 | 1184 | 2 | T00253 | Gene Ankhzn protei | 763 | 22 | 71.0 | 106 | 2 | S36275 | Ig lambda chain v |
| 691 | 23 | 74.2 | 1184 | 2 | H86190 | hypothetical prote | 764 | 22 | 71.0 | 107 | 2 | S40366 | Ig kappa chain v-J |
| 692 | 23 | 74.2 | 1190 | 2 | T00842 | probable histidine | 765 | 22 | 71.0 | 108 | 1 | K1HUDE | Ig kappa chain v-I |
| 693 | 23 | 74.2 | 1207 | 2 | T24559 | sensory transducti | 766 | 22 | 71.0 | 108 | 1 | K1HUSE | Ig kappa chain v-I |
| 694 | 23 | 74.2 | 1242 | 2 | S51246 | probable DNA repai | 767 | 22 | 71.0 | 108 | 2 | S19674 | Ig kappa chain v r |
| 695 | 23 | 74.2 | 1252 | 1 | S77037 | hypothetical prote | 768 | 22 | 71.0 | 108 | 2 | S36279 | Ig lambda chain v |
| 696 | 23 | 74.2 | 1260 | 2 | H89984 | hypothetical prote | 769 | 22 | 71.0 | 109 | 2 | JN0296 | Ig kappa chain v-J |
| 697 | 23 | 74.2 | 1266 | 2 | AF0911 | probable exported | 770 | 22 | 71.0 | 110 | 2 | A53481 | orlp binding prote |
| 698 | 23 | 74.2 | 1266 | 2 | A85989 | hypothetical prote | 771 | 22 | 71.0 | 111 | 1 | K7MS85 | Ig kappa chain v r |
| 699 | 23 | 74.2 | 1266 | 2 | F91143 | hypothetical prote | 772 | 22 | 71.0 | 117 | 1 | K1HUI2 | Ig kappa chain pre |
| 700 | 23 | 74.2 | 1322 | 2 | B71440 | hypothetical prote | 773 | 22 | 71.0 | 117 | 2 | S41812 | Ig kappa chain v r |
| 701 | 23 | 74.2 | 1323 | 1 | S73723 | probable lipoprote | 774 | 22 | 71.0 | 117 | 2 | S11700 | Ig kappa chain pre |
| 702 | 23 | 74.2 | 1411 | 2 | S55123 | hypothetical prote | 775 | 22 | 71.0 | 119 | 2 | A82473 | conserved hypotHet |
| 703 | 23 | 74.2 | 1459 | 2 | G86457 | unknown protein, 4 | 776 | 22 | 71.0 | 123 | 2 | F82461 | conserved phosphogl |
| 704 | 23 | 74.2 | 1462 | 2 | T06819 | DNA topoisomerase | 777 | 22 | 71.0 | 123 | 2 | T50142 | probable phosphogl |
| 705 | 23 | 74.2 | 1468 | 2 | T05672 | hypothetical prote | 778 | 22 | 71.0 | 123 | 2 | E71163 | hypothetical prote |
| 706 | 23 | 74.2 | 1490 | 2 | E84726 | probable unconvent | 779 | 22 | 71.0 | 124 | 2 | S40318 | Ig kappa chain v r |
| 707 | 23 | 74.2 | 1583 | 2 | T00727 | myosin heavy chain | 780 | 22 | 71.0 | 124 | 2 | S40336 | Ig kappa chain v-J |
| 708 | 23 | 74.2 | 1692 | 2 | G01449 | probable mucin G2 | 781 | 22 | 71.0 | 125 | 2 | S40333 | Ig kappa chain v-J |
| 709 | 23 | 74.2 | 1711 | 2 | T18429 | hypothetical prote | 782 | 22 | 71.0 | 125 | 2 | S40349 | Ig kappa chain v-J |
| 710 | 23 | 74.2 | 1744 | 2 | F86161 | Fl003.10 protein - | 783 | 22 | 71.0 | 126 | 2 | E69201 | hypothetical prote |
| 711 | 23 | 74.2 | 1767 | 2 | H97912 | conserved hypotHet | 784 | 22 | 71.0 | 127 | 2 | S11240 | Ig kappa chain v r |
| 712 | 23 | 74.2 | 1804 | 2 | S56247 | probable membrane | 785 | 22 | 71.0 | 128 | 2 | S46372 | Ig light chain var |
| 713 | 23 | 74.2 | 1817 | 2 | AD2165 | two-component hybr | 786 | 22 | 71.0 | 131 | 2 | S40352 | Ig kappa chain v-J |
| 714 | 23 | 74.2 | 1837 | 2 | T41023 | probable nuclear p | 787 | 22 | 71.0 | 132 | 2 | S38646 | Ig kappa chain v r |
| 715 | 23 | 74.2 | 1852 | 1 | VJCH2 | vitellogenin II pr | 788 | 22 | 71.0 | 134 | 1 | XMEBFC | flagellar basal bo |
| 716 | 23 | 74.2 | 1857 | 2 | T50513 | hypothetical prote | 789 | 22 | 71.0 | 134 | 2 | XH0639 | probable flagellar |
| 717 | 23 | 74.2 | 1976 | 2 | AS9252 | hypothetical prote | 790 | 22 | 71.0 | 134 | 2 | H85669 | flagellar basal bo |
| 718 | 23 | 74.2 | 2051 | 2 | T30938 | myosin heavy chain | 791 | 22 | 71.0 | 134 | 2 | G64850 | flagellar rod prot |
| 719 | 23 | 74.2 | 2098 | 2 | T18397 | receptor tyrosine | 792 | 22 | 71.0 | 134 | 2 | D90810 | flagellar basal bo |
| 720 | 23 | 74.2 | 2180 | 2 | A47651 | protein CRP - mal | 793 | 22 | 71.0 | 134 | 2 | B84903 | hypothetical prote |
| 721 | 23 | 74.2 | 2273 | 2 | T09083 | zinc-finger protei | 794 | 22 | 71.0 | 140 | 2 | H81253 | probable bacterial |
| 722 | 23 | 74.2 | 2346 | 2 | T13829 | hemagglutinin/hemo | 795 | 22 | 71.0 | 142 | 2 | E81087 | FrpA/C-related pro |
| 723 | 23 | 74.2 | 2386 | 2 | T39911 | Tpr homolog - frui | 796 | 22 | 71.0 | 142 | 2 | S76162 | hypothetical prote |
| 724 | 23 | 74.2 | 2609 | 2 | T44808 | rad3 checkpoint pr | 797 | 22 | 71.0 | 143 | 2 | H70022 | hypothetical prote |
| 725 | 23 | 74.2 | 2895 | 2 | T08437 | mycosubtilin synth | 798 | 22 | 71.0 | 145 | 2 | AG2617 | conserved hypotHet |
| 726 | 23 | 74.2 | 3421 | 1 | W2BBB6 | hyperplastic discs | 799 | 22 | 71.0 | 146 | 1 | GGZLB | bacterial hemoglob |
| 727 | 23 | 74.2 | 3534 | 2 | T42567 | 367K tegument prot | 800 | 22 | 71.0 | 147 | 2 | S01655 | alpha-amylase/tryp |
| 728 | 23 | 74.2 | 3591 | 1 | S21010 | tegument protein 2 | 801 | 22 | 71.0 | 148 | 2 | S23414 | hypothetical prote |
| 729 | 23 | 74.2 | 3712 | 2 | S18253 | filamentous hemagg | 802 | 22 | 71.0 | 153 | 2 | A82157 | hypothetical prote |
| 730 | 23 | 74.2 | 4092 | 1 | S38128 | laminin alpha-1 ch | 803 | 22 | 71.0 | 153 | 2 | C64858 | probable dNTP pyro |
| 731 | 23 | 74.2 | 4162 | 2 | T42633 | dynein heavy chain | 804 | 22 | 71.0 | 153 | 2 | F90829 | probable phosphoty |
| 732 | 23 | 74.2 | 4436 | 2 | E71086 | connectin/titin - | 805 | 22 | 71.0 | 153 | 2 | D85687 | probable phosphoty |
| 733 | 23 | 74.2 | 4450 | 2 | JX0340 | hypothetical prote | 806 | 22 | 71.0 | 154 | 2 | T32841 | hypothetical prote |
| 734 | 23 | 74.2 | 4452 | 1 | YGBSG2 | gramicidin S synth | 807 | 22 | 71.0 | 155 | 2 | D70623 | hypothetical prote |
| 735 | 22 | 71.0 | 56 | 2 | PQ0432 | genome polypotein | 808 | 22 | 71.0 | 157 | 2 | H95845 | conserved hypotHet |
| 736 | 22 | 71.0 | 56 | 2 | PQ0429 | genome polypotein | 809 | 22 | 71.0 | 159 | 2 | T10826 | probable resistanc |
| 737 | 22 | 71.0 | 56 | 2 | PQ0428 | genome polypotein | 810 | 22 | 71.0 | 162 | 2 | C33739 | hypothetical 17.8K |
| 738 | 22 | 71.0 | 56 | 2 | PQ0431 | genome polypotein | 811 | 22 | 71.0 | 163 | 2 | C96763 | protein calmodulin |
| 739 | 22 | 71.0 | 56 | 2 | PQ0427 | genome polypotein | 812 | 22 | 71.0 | 164 | 2 | B47207 | phycoerythrin alph |
| 740 | 22 | 71.0 | 56 | 2 | PQ0430 | genome polypotein | 813 | 22 | 71.0 | 165 | 2 | AG0207 | conserved hypotHet |
| 741 | 22 | 71.0 | 63 | 2 | C70250 | hypothetical prote | 814 | 22 | 71.0 | 170 | 2 | T43441 | hypothetical prote |
| 742 | 22 | 71.0 | 71 | 2 | S21526 | Ig kappa chain v r | 815 | 22 | 71.0 | 175 | 2 | T15067 | hypothetical prote |
| 743 | 22 | 71.0 | 71 | 2 | F82606 | hypothetical prote | 816 | 22 | 71.0 | 179 | 2 | A28992 | apolipoprotein iii |
| 744 | 22 | 71.0 | 75 | 2 | T01621 | hypothetical prote | 817 | 22 | 71.0 | 181 | 2 | D90218 | LSU ribosomal prot |
| 745 | 22 | 71.0 | 87 | 2 | S21523 | hypothetical prote | 818 | 22 | 71.0 | 181 | 2 | AC0686 | hypothetical prote |
| 746 | 22 | 71.0 | 88 | 2 | S21525 | Ig kappa chain v r | 819 | 22 | 71.0 | 183 | 2 | B83441 | potassium-transport |
| 747 | 22 | 71.0 | 88 | 2 | S21520 | Ig kappa chain v r | 820 | 22 | 71.0 | 185 | 2 | G69322 | hypothetical prote |
| 748 | 22 | 71.0 | 88 | 2 | S34104 | Ig kappa chain v r | 821 | 22 | 71.0 | 194 | 2 | AG0728 | conserved hypotHet |
| 749 | 22 | 71.0 | 88 | 2 | S21524 | Ig kappa chain v r | 822 | 22 | 71.0 | 203 | 2 | T32829 | hypothetical prote |
| 750 | 22 | 71.0 | 92 | 2 | T47167 | hypothetical prote | 823 | 22 | 71.0 | 204 | 2 | H90750 | outer membrane lip |
| 751 | 22 | 71.0 | 95 | 2 | S69898 | Ig kappa chain v r | 824 | 22 | 71.0 | 204 | 2 | S57828 | outer membrane lip |
| 752 | 22 | 71.0 | 95 | 2 | PH0863 | Ig kappa chain v r | 825 | 22 | 71.0 | 204 | 2 | F85614 | outer membrane lip |
| 753 | 22 | 71.0 | 98 | 2 | S41813 | Ig kappa chain v r | 826 | 22 | 71.0 | 204 | 2 | AG0611 | outer membrane lip |
| 754 | 22 | 71.0 | 98 | 2 | F70511 | probable PE protei | 827 | 22 | 71.0 | 207 | 2 | T20296 | hypothetical prote |
| 755 | 22 | 71.0 | 101 | 2 | S44117 | Ig kappa chain v-J | 828 | 22 | 71.0 | 207 | 2 | S77728 | type 4 fimbrial bi |
| 756 | 22 | 71.0 | 102 | 2 | T01033 | hypothetical prote | 829 | 22 | 71.0 | 209 | 2 | T37764 | probable phosphogl |
| 757 | 22 | 71.0 | 102 | 2 | AB1516 | hypothetical prote | 830 | 22 | 71.0 | 212 | 1 | F65054 | L-fucose-phospha |
| 758 | 22 | 71.0 | 102 | 2 | AE1157 | hypothetical prote | 831 | 22 | 71.0 | 215 | 2 | A52892 | hypothetical prote |
| 759 | 22 | 71.0 | 103 | 2 | S44121 | Ig kappa chain v-J | 832 | 22 | 71.0 | 218 | 2 | T07609 | GTP-binding protei |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|--------|----------------------|-----|----|------|-----|---|--------|---------------------|
| 833 | 22 | 71.0 | 224 | 2 | JC4719 | toxin co-regulated | 906 | 22 | 71.0 | 350 | 2 | T21106 | hypothetical prote |
| 834 | 22 | 71.0 | 226 | 2 | C70078 | hypothetical prote | 907 | 22 | 71.0 | 350 | 2 | T24810 | hypothetical prote |
| 835 | 22 | 71.0 | 226 | 2 | T19921 | hypothetical prote | 908 | 22 | 71.0 | 352 | 2 | G81921 | hypothetical prote |
| 836 | 22 | 71.0 | 227 | 2 | S09641 | variant surface gl | 909 | 22 | 71.0 | 353 | 2 | JC7128 | pleckstrin 2 - mou |
| 837 | 22 | 71.0 | 228 | 2 | H97336 | uncharacterized co | 910 | 22 | 71.0 | 362 | 2 | T35287 | probable secreted |
| 838 | 22 | 71.0 | 231 | 2 | T24669 | hypothetical prote | 911 | 22 | 71.0 | 362 | 2 | AF3443 | geranyltransferase |
| 839 | 22 | 71.0 | 234 | 2 | AF2224 | hypothetical prote | 912 | 22 | 71.0 | 363 | 2 | G84385 | diptetide ABC tran |
| 840 | 22 | 71.0 | 235 | 2 | G97399 | hypothetical prote | 913 | 22 | 71.0 | 363 | 2 | T37630 | protein disulfide- |
| 841 | 22 | 71.0 | 236 | 2 | AE1578 | precorrin-2 methyl | 914 | 22 | 71.0 | 363 | 2 | AC0244 | conserved hypotet |
| 842 | 22 | 71.0 | 238 | 2 | T15817 | hypothetical prote | 915 | 22 | 71.0 | 368 | 2 | F98282 | histidinol-phospha |
| 843 | 22 | 71.0 | 242 | 2 | A95180 | conserved hypotet | 916 | 22 | 71.0 | 368 | 2 | AB3001 | histidinol-phospha |
| 844 | 22 | 71.0 | 242 | 2 | E87356 | hypothetical prote | 917 | 22 | 71.0 | 371 | 2 | B84982 | aspartate-semialde |
| 845 | 22 | 71.0 | 242 | 2 | D98047 | conserved hypotet | 918 | 22 | 71.0 | 373 | 2 | T46425 | hypothetical prote |
| 846 | 22 | 71.0 | 243 | 2 | A96744 | hypothetical prote | 919 | 22 | 71.0 | 377 | 2 | B70140 | hypothetical prote |
| 847 | 22 | 71.0 | 244 | 2 | T36797 | hypothetical prote | 920 | 22 | 71.0 | 379 | 2 | E81334 | Ni/Fe-hydrogenase |
| 848 | 22 | 71.0 | 247 | 2 | H83176 | probable transcrip | 921 | 22 | 71.0 | 379 | 2 | JC4843 | ATP-gated ionchann |
| 849 | 22 | 71.0 | 247 | 2 | H82518 | hypothetical prote | 922 | 22 | 71.0 | 380 | 2 | H70144 | ATP-binding protei |
| 850 | 22 | 71.0 | 253 | 2 | C86325 | T29M8.5 protein - | 923 | 22 | 71.0 | 382 | 2 | AG1310 | conserved hypotet |
| 851 | 22 | 71.0 | 256 | 2 | A45921 | chorismate mutase | 924 | 22 | 71.0 | 382 | 2 | AF1682 | conserved hypotet |
| 852 | 22 | 71.0 | 256 | 2 | C83367 | probable exopolyase | 925 | 22 | 71.0 | 383 | 2 | S76146 | hypothetical prote |
| 853 | 22 | 71.0 | 258 | 2 | F64248 | hypothetical prote | 926 | 22 | 71.0 | 384 | 2 | C81043 | hypothetical prote |
| 854 | 22 | 71.0 | 260 | 2 | G87349 | conserved hypotet | 927 | 22 | 71.0 | 386 | 2 | G97722 | hypothetical prote |
| 855 | 22 | 71.0 | 260 | 2 | S65174 | vanadate resistanc | 928 | 22 | 71.0 | 388 | 2 | D72740 | hypothetical prote |
| 856 | 22 | 71.0 | 264 | 2 | AF2123 | ATP-binding protei | 929 | 22 | 71.0 | 390 | 1 | E48563 | 16 protein - fowlp |
| 857 | 22 | 71.0 | 267 | 2 | B83705 | phosphonates trans | 930 | 22 | 71.0 | 390 | 2 | T46028 | hypothetical prote |
| 858 | 22 | 71.0 | 267 | 2 | T37689 | hypothetical prote | 931 | 22 | 71.0 | 390 | 2 | F82789 | hypothetical prote |
| 859 | 22 | 71.0 | 267 | 2 | AE0615 | SmtA protein [impo | 932 | 22 | 71.0 | 391 | 2 | F72552 | hypothetical prote |
| 860 | 22 | 71.0 | 268 | 2 | B97254 | ABC-type iron (III | 933 | 22 | 71.0 | 392 | 2 | C87428 | hypothetical prote |
| 861 | 22 | 71.0 | 273 | 2 | H97312 | nitroreductase fam | 934 | 22 | 71.0 | 393 | 2 | S49759 | probable membrane |
| 862 | 22 | 71.0 | 275 | 2 | S76233 | transcription term | 935 | 22 | 71.0 | 396 | 1 | S15992 | flavohemoglobin hm |
| 863 | 22 | 71.0 | 276 | 2 | A84813 | hypothetical prote | 936 | 22 | 71.0 | 396 | 2 | AC0826 | dihydropteridine r |
| 864 | 22 | 71.0 | 277 | 2 | T29268 | hypothetical prote | 937 | 22 | 71.0 | 396 | 2 | F85900 | dihydropteridine r |
| 865 | 22 | 71.0 | 282 | 2 | AI0186 | probable iron-side | 938 | 22 | 71.0 | 396 | 2 | B91056 | dihydropteridine r |
| 866 | 22 | 71.0 | 285 | 2 | D84197 | branched-chain ami | 939 | 22 | 71.0 | 398 | 2 | C95378 | hypothetical prote |
| 867 | 22 | 71.0 | 288 | 2 | AH0247 | probable binding-p | 940 | 22 | 71.0 | 400 | 2 | D72697 | hypothetical prote |
| 868 | 22 | 71.0 | 290 | 2 | F69697 | transcriptional regu | 941 | 22 | 71.0 | 400 | 2 | B81087 | PrpA/C-related pro |
| 869 | 22 | 71.0 | 291 | 2 | S27721 | hypothetical prote | 942 | 22 | 71.0 | 409 | 2 | AE6240 | protein F20B24.10 |
| 870 | 22 | 71.0 | 295 | 2 | S68974 | tetrahydromethanop | 943 | 22 | 71.0 | 410 | 2 | F69965 | multidrug resistan |
| 871 | 22 | 71.0 | 295 | 2 | A69022 | tetrahydromethanop | 944 | 22 | 71.0 | 411 | 1 | C64783 | probable N-carbamyl |
| 872 | 22 | 71.0 | 297 | 2 | T50015 | hypothetical prote | 945 | 22 | 71.0 | 411 | 2 | B90701 | allantoate amidohy |
| 873 | 22 | 71.0 | 297 | 2 | T34141 | hypothetical prote | 946 | 22 | 71.0 | 411 | 2 | E85551 | probable hydantoin |
| 874 | 22 | 71.0 | 301 | 2 | C72493 | probable ribose AB | 947 | 22 | 71.0 | 411 | 2 | T47951 | hypothetical prote |
| 875 | 22 | 71.0 | 306 | 2 | B84105 | diptetide ABC tran | 948 | 22 | 71.0 | 412 | 2 | B97077 | diverged AAA-famil |
| 876 | 22 | 71.0 | 310 | 2 | S07522 | capsid assembly pr | 949 | 22 | 71.0 | 412 | 2 | A57468 | P-selectin glycopo |
| 877 | 22 | 71.0 | 312 | 2 | B55461 | NAD(P)-arginine AD | 950 | 22 | 71.0 | 416 | 2 | F83197 | probable porin PA3 |
| 878 | 22 | 71.0 | 312 | 2 | D83239 | probable lauroyl a | 951 | 22 | 71.0 | 417 | 2 | S77042 | hypothetical prote |
| 879 | 22 | 71.0 | 312 | 2 | T37922 | hypothetical prote | 952 | 22 | 71.0 | 418 | 2 | AB1170 | ATP/GTP-binding pr |
| 880 | 22 | 71.0 | 312 | 2 | AF2513 | hypothetical prote | 953 | 22 | 71.0 | 418 | 2 | AD1527 | ATP/GTP-binding pr |
| 881 | 22 | 71.0 | 319 | 2 | JH0135 | genome polypeptide | 954 | 22 | 71.0 | 418 | 2 | T00154 | hypothetical prote |
| 882 | 22 | 71.0 | 322 | 2 | AH2192 | hypothetical prote | 955 | 22 | 71.0 | 420 | 1 | AJBYSR | argininosuccinate |
| 883 | 22 | 71.0 | 324 | 2 | D84315 | aryl-alcohol dehyd | 956 | 22 | 71.0 | 421 | 2 | T51809 | succinate-CoA liga |
| 884 | 22 | 71.0 | 324 | 2 | T23876 | hypothetical prote | 957 | 22 | 71.0 | 422 | 1 | JGAGLR | lactose-binding pr |
| 885 | 22 | 71.0 | 326 | 2 | AB3607 | 3-oxoacyl-facyl-ca | 958 | 22 | 71.0 | 422 | 2 | C97569 | hypothetical prote |
| 886 | 22 | 71.0 | 327 | 2 | H97667 | hypothetical prote | 959 | 22 | 71.0 | 429 | 2 | AC2248 | enolase [imported] |
| 887 | 22 | 71.0 | 331 | 2 | T02343 | glucan endo-1,3-be | 960 | 22 | 71.0 | 431 | 2 | S25196 | mitochondrial impo |
| 888 | 22 | 71.0 | 331 | 2 | D88986 | protein C50H11.12 | 961 | 22 | 71.0 | 437 | 2 | S05357 | hypothetical prote |
| 889 | 22 | 71.0 | 333 | 2 | I40791 | acetoin dehydrogen | 962 | 22 | 71.0 | 437 | 2 | A31142 | geloslin, ovarian |
| 890 | 22 | 71.0 | 333 | 2 | T23324 | hypothetical prote | 963 | 22 | 71.0 | 441 | 2 | B86252 | hypothetical prote |
| 891 | 22 | 71.0 | 335 | 2 | H86455 | probable beta-1,3- | 964 | 22 | 71.0 | 443 | 1 | DEIQHN | (R)-6-hydroxynicot |
| 892 | 22 | 71.0 | 336 | 2 | E72591 | hypothetical prote | 965 | 22 | 71.0 | 443 | 2 | A27793 | methyl coenzyme M |
| 893 | 22 | 71.0 | 337 | 2 | D87354 | conserved hypotet | 966 | 22 | 71.0 | 443 | 2 | D72383 | NADH oxidase - The |
| 894 | 22 | 71.0 | 341 | 2 | S04137 | genome polypeptide | 967 | 22 | 71.0 | 444 | 2 | T29820 | hypothetical prote |
| 895 | 22 | 71.0 | 342 | 2 | S76447 | hypothetical prote | 968 | 22 | 71.0 | 444 | 2 | S54039 | hypothetical prote |
| 896 | 22 | 71.0 | 342 | 2 | AB7389 | hypothetical prote | 969 | 22 | 71.0 | 452 | 2 | T37899 | hypothetical prote |
| 897 | 22 | 71.0 | 342 | 2 | AD3360 | Protein gp19 [Bact | 970 | 22 | 71.0 | 453 | 2 | S18597 | tubulin beta chain |
| 898 | 22 | 71.0 | 345 | 2 | C45456 | NADH2 dehydrogenas | 971 | 22 | 71.0 | 454 | 2 | T44878 | 3-oxoacyl-facyl-ca |
| 899 | 22 | 71.0 | 345 | 2 | T21485 | hypothetical prote | 972 | 22 | 71.0 | 454 | 2 | F70938 | probable fabG4 pro |
| 900 | 22 | 71.0 | 346 | 2 | E86715 | transcription regu | 973 | 22 | 71.0 | 458 | 2 | F86433 | protein T17H7.5 [i |
| 901 | 22 | 71.0 | 347 | 2 | T24921 | hypothetical prote | 974 | 22 | 71.0 | 461 | 2 | C98120 | glycerol-3-phospha |
| 902 | 22 | 71.0 | 349 | 1 | S52763 | hypothetical prote | 975 | 22 | 71.0 | 461 | 1 | S47454 | amidase homolog YM |
| 903 | 22 | 71.0 | 349 | 2 | AF3401 | enoyl-CoA hydratase | 976 | 22 | 71.0 | 466 | 2 | T49756 | related to berberl |
| 904 | 22 | 71.0 | 349 | 2 | T49843 | hypothetical prote | 977 | 22 | 71.0 | 466 | 2 | E70183 | purine-binding che |
| 905 | 22 | 71.0 | 349 | 2 | AH2039 | hypothetical prote | 978 | 22 | 71.0 | 468 | 2 | S75389 | probable phenylala |

979 22 71.0 468 2 AS5116
980 22 71.0 469 2 F82232
981 22 71.0 473 2 H69761
982 22 71.0 474 2 S39475
983 22 71.0 480 1 F70174
984 22 71.0 483 2 S36470
985 22 71.0 483 2 E90159
986 22 71.0 483 2 F71684
987 22 71.0 484 2 T10668
988 22 71.0 485 2 H83938
989 22 71.0 485 2 T24677
990 22 71.0 486 2 B86460
991 22 71.0 488 1 JC2385
992 22 71.0 488 2 AT2554
993 22 71.0 491 2 T43673
994 22 71.0 492 2 T26936
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996 22 71.0 493 2 B72704
997 22 71.0 494 2 S57539
998 22 71.0 496 2 AF0165
999 22 71.0 496 2 S61966
1000 22 71.0 499 2 AC2068

vacuolar ATPase (E
indole-3-glycerol
conserved hypothe
embryonic protein
cysteine-TRNA liga
E2 protein - human
hypotheical prote
virB10 protein (vi
hypotheical prote
methylmalonate-sem
hypotheical prote
hypotheical prote
protein disulfide-
probable glu-TRNA
dUTP diphosphatase
hypotheical prote
glutamyl-TRNA amid
hypotheical prote
probable membrane
probable membrane
hypotheical prote
cell death suppres

ALIGNMENTS

RESULT 1
Ig kappa chain V region (7D4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
C:Accession: B38601
J.Goshorn, S.C.; Retzel, E.; Jemmerson, R.
R. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same antigen
A:Reference number: A38601; MUID:91115823; PMID:1703527
A:Accession: B38601
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-65 <GOS>
A:Cross-references: UNIPARC:UPI0000115176; GB:M57979; NID:G196404; PIDN:AAAG3360.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 31; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 7 AASNLES 13

RESULT 2
C38601
Ig kappa chain V region (2B5) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
C:Accession: C38601
J.Goshorn, S.C.; Retzel, E.; Jemmerson, R.
R. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same antigen
A:Reference number: A38601; MUID:91115823; PMID:1703527
A:Accession: C38601
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-65 <GOS>
A:Cross-references: UNIPARC:UPI0000115177; GB:M57980; NID:G196406; PIDN:AAAG3361.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 31; DB 2; Length 65;

Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 7 AASNLES 13

RESULT 3
A38601
Ig kappa chain V region (1G3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
C:Accession: A38601
J.Goshorn, S.C.; Retzel, E.; Jemmerson, R.
R. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same antigen
A:Reference number: A38601; MUID:91115823; PMID:1703527
A:Accession: A38601
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-93 <GOS>
A:Cross-references: UNIPARC:UPI0000115175; GB:M57978; NID:G196402; PIDN:AAAG3359.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 31; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 35 AASNLES 41

RESULT 4
KVMS10
Ig kappa chain V region (PC7210) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: D01937; A01937
R.Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152; PMID:103003
A:Accession: D01937
A:Molecule type: protein
A:Residues: 1-110 <WEI>
A:Cross-references: UNIPROT:P01668; UNIPARC:UPI000002A103
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger aggregates.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 54 AASNLES 60

RESULT 5
KVMS43
Ig kappa chain V region (PC7043) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C:Accession: A01937; S42187; S42194; S42189; S42188; S42191; S42192
R.Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978

A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
A;Accession: A01937
A;Molecule type: protein
A;Residues: 1-111 <WEI>
A;Cross-references: UNIPROT:P01665; UNIPARC:UPI000002A100
R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec
A;Reference number: S42176; MUID:94009207; PMID:7691608
A;Accession: S42187
A;Molecule type: DNA
A;Residues: 10-99 <MOJ>
A;Cross-references: UNIPARC:UPI000011655C; EMBL:Z25444; NID:g407832; PIDN:CAA80931.1; PI
A;Note: V-kappa-2IE; anti-collagen
A;Accession: S42194
A;Molecule type: DNA
A;Residues: 12-99 <MOJ>
A;Cross-references: UNIPARC:UPI000011655B; EMBL:Z25458; NID:g407844; PIDN:CAA80945.1; PI
A;Note: V-kappa-2IE; anti-collagen
A;Accession: S42190
A;Molecule type: DNA
A;Residues: 13-99 <MOF>
A;Cross-references: UNIPARC:UPI0000116562; EMBL:Z25450; NID:g407838; PIDN:CAA80937.1; PI
A;Note: V-kappa-2IE; anti-collagen
A;Accession: S42189
A;Molecule type: DNA
A;Residues: 15-99 <MOA>
A;Cross-references: UNIPARC:UPI0000116560; EMBL:Z25448; NID:g407836; PIDN:CAA80935.1; PI
A;Note: V-kappa-2IE; anti-collagen
A;Accession: S42188
A;Molecule type: DNA
A;Residues: 12-99 <MOZ>
A;Cross-references: UNIPARC:UPI000011655B; EMBL:Z25446; NID:g407834; PIDN:CAA80933.1; PI
A;Note: V-kappa-2IE; anti-collagen
A;Accession: S42191
A;Molecule type: DNA
A;Residues: 10-99 <MOY>
A;Cross-references: UNIPARC:UPI000011655C; EMBL:Z25452; NID:g407840; PIDN:CAA80939.1; PI
A;Note: V-kappa-2IE; anti-collagen
A;Accession: S42192
A;Molecule type: DNA
A;Residues: 10-99 <MOO>
A;Cross-references: UNIPARC:UPI000011655C; EMBL:Z25454; NID:g407842; PIDN:CAA80941.1; PI
A;Note: V-kappa-2IE; anti-collagen
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IGM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>
F;23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 54 AASNLES 60

RESULT 6
KVMS69
IG kappa chain V region (PC7769) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: E01937; A01937
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
A;Accession: E01937
A;Molecule type: protein

A;Residues: 1-111 <WEI>
A;Cross-references: UNIPROT:P01669; UNIPARC:UPI000002A104
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IGM, the subunits associate into 1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>
F;23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 54 AASNLES 60

RESULT 7
KVMS83
IG kappa chain V region (PC7183) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: B01937; A01937
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
A;Accession: B01937
A;Molecule type: protein
A;Residues: 1-111 <WEI>
A;Cross-references: UNIPROT:P01666; UNIPARC:UPI000002A101
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IGM, the subunits associate into 1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>
F;23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 54 AASNLES 60

RESULT 8
KVMSCI
IG kappa chain V region (CBPC 101) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 09-Jul-2004
C;Accession: A01936
R;McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A;Title: Mechanisms of antibody diversity: multiple genes encode structurally related m
A;Reference number: A93822; MUID:79012520; PMID:99744
A;Accession: A01936
A;Molecule type: protein
A;Residues: 1-111 <MCK>
A;Cross-references: UNIPROT:P01664; UNIPARC:UPI000002A0FF
C;Comment: This chain was isolated from a myeloma protein.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IGM, the subunits associate into 1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-94/Domain: immunoglobulin homology <IMM>
F;23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||||||
Db 54 AASNLES 60

RESULT 9

S19976
Ig kappa chain V region (M-T413) - mouse (fragment)
A:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S19976
R:Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: S19963
A:Accession: S19976
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <WEI>
A:Cross-references: UNIPARC:UPI0000116031; EMBL:X65093; NID:g52298; PIDN:CAA46221.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||||||
Db 54 AASNLES 60

RESULT 10

S19971
Ig kappa chain V region (CD4 mAb clone M-T310 and others) - mouse (fragment)
A:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S19971; S19973
R:Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: S19963
A:Accession: S19971
A:Molecule type: mRNA
A:Residues: 1-112 <WEI>
A:Cross-references: UNIPARC:UPI0000116030; EMBL:X65091; NID:g52288; PIDN:CAA46219.1; PID
A:Experimental source: clone M-T310
A:Accession: S19973

Query Match 100.0%; Score 31; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||||||
Db 54 AASNLES 60

RESULT 11

PH1226
Ig kappa chain precursor V region (M-T310) - mouse (fragment)
A:Species: Mus musculus (house mouse)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
C:Accession: PH1226

R:Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; Lenz
Gene 121, 271-278, 1992
A:Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and on
A:Reference number: PH1224; MUID:93077041; PMID:1446824

A:Accession: PH1226
A:Molecule type: mRNA
A:Residues: 1-131 <WEI>
A:Cross-references: UNIPARC:UPI00001153EE; GB:S50265; NID:g260765; PIDN:AAB24320.1; PID:
A:Note: This mouse sequence was hybridized and fused with a human constant region gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-131/Product: Ig light chain V region #status predicted <MAT>
F:36-114/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||||||
Db 74 AASNLES 80

RESULT 12

B64160
Hypothetical protein HI0852 - Haemophilus influenzae (strain Rd KW20)
A:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C:Accession: B64160
R:Flischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.F.; Glodek, A.; Kelley, J.M.; Weidman, J
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: B64160
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-463 <TIGR>
A:Cross-references: UNIPROT:P44903; UNIPARC:UPI000013B3CF; GB:U32766; GB:L42023; NID:915
A:Note: best homolog was a hypothetical protein from Escherichia coli
C:Superfamily: multidrug-efflux transporter
C:Keywords: antibiotic resistance; transmembrane protein

Query Match 100.0%; Score 31; DB 2; Length 463;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||||||
Db 94 AASNLES 100

RESULT 13

T39624
6-phosphofructokinase beta subunit - fission yeast (Schizosaccharomyces pombe)
A:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T39624
R:Wood, V.; Rajadream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
submitted to the EMBL Data Library, March 1998
A:Reference number: Z21843
A:Accession: T39624
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-942 <WOO>
A:Cross-references: UNIPROT:O42938; UNIPARC:UPI00000697AB; EMBL:AL022104; PIDN:CAAL7900
A:Experimental source: strain 972h-; cosmid c16H5
C:Genetics:
A:Gene: SPDB:SPBCL6H5.02
A:Map position: 2

C:Superfamily: ATP-dependent phosphofructokinase, eukaryotic type; 6-phosphofructokinase

Query Match 100.0%; Score 31; DB 2; Length 942;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNL5 7
DB 165 AASNL5 171

RESULT 14
T00362
hypothetical protein KIAA0675 - human
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C:Accession: T00362
R:Ikishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.
DNA Res. 5, 169-176, 1998
A:Title: Prediction of the coding sequences of unidentified human genes. X. The complete
A:Reference number: Z14142; MUID:98403880; PMID:9734811
A:Accession: T00362
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1208 <ISH>
A:Cross-references: UNIPROT:O75162; UNIPARC:UPI00000657D4; EMBL:AB014575; NID:G3327163;
A:Experimental source: brain; clone HK02566
C:Genetics:
A:Note: KIAA0675
F:1144-1193/Domain: RING finger homology <RRN>

Query Match 100.0%; Score 31; DB 2; Length 1208;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNL5 7
DB 896 AASNL5 902

RESULT 15
AH3440
cold shock protein csps [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 31-Dec-2004
C:Accession: AH3440
R:DelVecchio, V.G.; Kaputal, V.; Redkar, R.J.; Patra, G.; Mujar, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess,
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756688
A:Accession: AH3440
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-69 <KUR>
A:Cross-references: UNIPROT:Q8YFLO; UNIPARC:UPI00000580CC; GB:AE008917; PIDN:AAL52691.1;
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI1510
A:Map position: 1
C:Superfamily: cold shock protein, CspA type; cold shock domain homology

Query Match 90.3%; Score 28; DB 2; Length 69;
Best Local Similarity 85.7%; Pred. No. 5.9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNL5 7
DB 62 AASNL5 68

RESULT 16
K1HUGL

Ig kappa chain V-I region (Gal) - human (tentative sequence)
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C:Accession: A01867
R:Laure, C.J.; Watanabe, S.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 354, 1503-1504, 1973
A:Title: The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal),
A:Reference number: A01867; MUID:75059122; PMID:4215718
A:Accession: A01867
A:Molecule type: protein
A:Residues: 1-108 <LAU>
A:Cross-references: UNIPROT:P01599; UNIPARC:UPI000012E142
A:Note: the C region of this chain has the Inv (3) marker
C:Comment: This chain was isolated from a Waldenström's macroglobulin.
C:Genetics:
A:Gene: GDB:IGKV1
A:Cross-references: GDB:136264
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka)
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-30/Domain: immunoglobulin homology <IMM>
F:23-88/Disulfide bonds: #status predicted

Query Match 90.3%; Score 28; DB 1; Length 108;
Best Local Similarity 85.7%; Pred. No. 9.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNL5 7
DB 50 AASNL5 56

RESULT 17
S19972
Ig kappa chain V region (M-T321) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S19972
R:Weissenhorn, W.; Riethmüller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: S19963
A:Accession: S19972
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <WEI>
A:Cross-references: UNIPARC:UPI0000116032; EMBL:X65094; NID:G52290; PIDN:CAA46222.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 90.3%; Score 28; DB 2; Length 112;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNL5 7
DB 54 AASNL5 60

RESULT 18
S06731
Ig kappa chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jul-2000
C:Accession: S06731
R:Alanen, A.; Weiss, S.
Eur. J. Immunol. 19, 1961-1963, 1989
A:Title: Sequence and linkage of the V(kappa)21A and G germ-line gene segments in the m
A:Reference number: S06731; MUID:90060210; PMID:2583230
A:Accession: S06731

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-120 <ALA>
A;Cross-references: UNIPARC:UPI0000116D68; EMBL:X16955; NID:g55315; PIDN:CAB38573.1; PIDN:18/1
C;Genetics:
A;Introns: 18/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F:37-115/Domain: immunoglobulin homology <IMM>

Query Match 90.3%; Score 28; DB 2; Length 120;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||:|
Db 75 AASNVES 81

RESULT 19
S40370
IG kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40370
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40370
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-122 <KLE>
A;Cross-references: UNIPARC:UPI0000116178; EMBL:X72480; NID:g441428; PIDN:CAA51148.1; PIDN:1148.1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F:30-104/Domain: immunoglobulin homology <IMM>

Query Match 90.3%; Score 28; DB 2; Length 122;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||:|
Db 64 AASNLSQS 70

RESULT 20
C87521
hypothetical protein CC2196 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: C87521
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.; Lau, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: C87521
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-209 <STO>
A;Cross-references: UNIPROT:Q9A698; UNIPARC:UPI00000C763E; GB:AE005673; NID:g13423697; F:30-104/Domain: immunoglobulin homology <IMM>
C;Genetics:
A;Gene: CC2196

Query Match 90.3%; Score 28; DB 2; Length 209;
Best Local Similarity 85.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||:|

Db 151 AASNLEA 157

RESULT 21
A98166
hypothetical protein AGR_L_563 [imported] - Agrobacterium tumefaciens (strain C58, Cerec)
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: A98166
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: A98166
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-228 <KUR>
A;Cross-references: UNIPROT:Q8U760; UNIPARC:UPI00000D261B; GB:AE007870; PIDN:AAK88851.1;
C;Genetics:
A;Gene: AGR_L_563
A;Map position: linear chromosome

Query Match 90.3%; Score 28; DB 2; Length 228;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||:|
Db 156 AASNLET 162

RESULT 22
AF3121
hypothetical protein Atu4594 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AF3121
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, J.; Karp, P.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan, S.; Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, S.; E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AF3121
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-228 <KUR>
A;Cross-references: UNIPROT:Q8U760; UNIPARC:UPI00000D261B; GB:AE008689; PIDN:AAL45388.1;
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu4594
A;Map position: linear chromosome

Query Match 90.3%; Score 28; DB 2; Length 228;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||:|
Db 156 AASNLET 162

RESULT 23
QMYRW
nonstructural protein Pns11 - wound tumor virus (strain NJ)
N;Alternate names: segment 11 protein
C;Species: wound tumor virus, WTV
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C;Accession: C41705
R;Hillman, B.I.; Anzola, J.V.; Halpern, B.T.; Cavileer, T.D.; Nuss, D.L.

Virology 185, 896-900, 1991
A;Title: First field isolation of wound tumor virus from a plant host: minimal sequence
A;Reference number: A41705; MUID:92074261; PMID:1962460
A;Accession: C41705
A;Molecule type: genomic RNA
A;Residues: 1-313 <HLL>
A;Cross-references: UNIPROT:P31611; UNIPARC:UPI00000138CA4; GB:M77020; NID:G336172; PIDN:
C;Genetics:
A;Map position: segment 11
C;Superfamily: phytoeovirus nonstructural protein Pns9
C;Keywords: nonstructural protein

Query Match 90.3%; Score 28; DB 1; Length 313;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||||:
Db 294 AASNLDLS 300

RESULT 24
OMXRTW
C;Species: wound tumor virus, WTV
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C;Accession: S04139
R;Dall, D.J.; Anzola, J.V.; Xu, Z.; Nuss, D.L.
Nucleic Acids Res. 17, 3599, 1989
A;Title: Complete nucleotide sequence of wound tumor virus genomic segment S11.
A;Reference number: S04139; MUID:89263810; PMID:2726499
A;Accession: S04139
A;Molecule type: Genomic RNA
A;Residues: 1-313 <DAL>
A;Cross-references: UNIPROT:P12326; UNIPARC:UPI0000061DB1; GB:X14219; NID:G62264; PIDN:
C;Genetics:
A;Map position: segment 11
C;Superfamily: phytoeovirus nonstructural protein Pns9

Query Match 90.3%; Score 28; DB 1; Length 313;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||||:
Db 294 AASNLDLS 300

RESULT 25
AB2177
hypothetical protein all2969 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AB2177
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AB2177
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-579 <KUR>
A;Cross-references: UNIPROT:Q8YSW1; UNIPARC:UPI00000CE60E; GB:BA0000019; PIDN:BAB74668.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all2969

Query Match 90.3%; Score 28; DB 2; Length 579;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||||:
Db 378 AASNLDLS 384

RESULT 26

D71941
ATP-dependent zinc metalloproteinase - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: D71941
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric patho
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: D71941
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-632 <ARN>
A;Cross-references: UNIPROT:Q9ZM66; UNIPARC:UPI000012ACCF; GB:AE001471; GB:AE001439; NI
A;Experimental source: strain J99
C;Genetics:

A;Gene: ftsH_2
C;Superfamily: cell division protein ftsH; FtsH/SEC18/CDC48-type ATP-binding domain hom
F;184-395/Domain: FtsH/SEC18/CDC48-type ATP-binding domain homology <VAT>

Query Match 90.3%; Score 28; DB 2; Length 632;
Best Local Similarity 85.7%; Pred. No. 71;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||||:
Db 616 AANNLES 622

RESULT 27

A55236
kinesin-related protein KLP68D - fruit fly (Drosophila melanogaster)
N;Alternate names: kinesin-like protein 5; KLP5
C;Species: Drosophila melanogaster
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C;Accession: A55236; E41298
R;Pesavento, P.A.; Stewart, R.J.; Goldstein, L.S.B.
J. Cell Biol. 127, 1041-1048, 1994
A;Title: Characterization of the KLP68D kinesin-like protein in Drosophila: possible ro
A;Reference number: A55236; MUID:95050960; PMID:7525600
A;Accession: A55236
A;Molecule type: mRNA
A;Residues: 1-784 <PES>
A;Cross-references: UNIPROT:P46867; UNIPARC:UPI000012DECS; GB:U15974; NID:G595912; PIDN:
R;Stewart, R.J.; Pesavento, P.A.; Woerpel, D.N.; Goldstein, L.S.B.
Proc. Natl. Acad. Sci. U.S.A. 88, 8470-8474, 1991

A;Title: Identification and partial characterization of six members of the kinesin supe
A;Reference number: A41298; MUID:92020874; PMID:1924306
A;Accession: E41298

A;Molecule type: DNA
A;Residues: 'TC', 222-337, 'VRGQV' <STE>
A;Cross-references: UNIPARC:UPI000016BC5B; GB:M74431; NID:g157791; PIDN:AAA28658.1; PID

C;Genetics:

A;Gene: FlyBase:Klp68D; KLP5
A;Cross-references: FlyBase:Flyg00004381

C;Function:

A;Description: may be part of a motor protein that provides anterograde fast axonal tra
C;Superfamily: kinesin-related protein KIF3; kinesin motor domain homology
C;Keywords: ATP; coiled coil; microtubule binding; nucleotide binding; P-loop
F;1-349/Domain: head globular #status predicted <HGL>
F;20-350/Domain: kinesin motor domain homology <KMT>
F;106-113/Region: nucleotide-binding motif A (P-loop)
F;350-580/Domain: helical rod #status predicted <ROD>
F;581-784/Domain: tail globular #status predicted <TGL>
F;112/Binding site: ATP (Lys) #status predicted

Query Match 90.3%; Score 28; DB 1; Length 784;
 Best Local Similarity 85.7%; Pred. No. 90;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 |||||:|
 Db 751 AASNLD 757

RESULT 28
 S42193
 Ig kappa chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 07-Oct-1994 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
 C:Accession: S42193
 R:Mo, J.A.; Bona, C.A.; Holmdahl, R.
 Eur. J. Immunol. 23, 2503-2510, 1993
 A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec
 A:Reference number: S42176; MUID:94009207; PMID:7691608
 A:Accession: S42193
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-81 <MOJ>
 A:Cross-references: UNIPARC:UPI0000116566; EMBL:X67623; NID:G407846; PIDN:CAA80943.1; PI
 A>Note: the authors translated the codon GGT for residue 36 as Ala
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 87.1%; Score 27; DB 2; Length 81;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
 |||||
 Db 37 ASNLES 42

RESULT 29
 S25462
 Ig kappa chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
 C:Accession: S25462
 R:Monestier, M.; Fasy, T.M.; Loeman, M.J.; Novick, K.E.; Muller, S.
 submitted to the EMBL Data Library, July 1992
 A:Description: Structure and binding properties of monoclonal antibodies to core histone
 A:Reference number: S25174
 A:Accession: S25462
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-91 <MON>
 A:Cross-references: UNIPARC:UPI00001160C5; EMBL:X67623; NID:G52188; PIDN:CAA47881.1; PID
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 87.1%; Score 27; DB 2; Length 91;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
 |||||
 Db 55 ASNLES 60

RESULT 30
 S25177
 Ig kappa chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
 C:Accession: S25177; S33134
 R:Monestier, M.; Fasy, T.M.; Loeman, M.J.; Novick, K.E.; Muller, S.
 submitted to the EMBL Data Library, July 1992

A:Description: Structure and binding properties of monoclonal antibodies to core histone
 A:Reference number: S25174
 A:Accession: S25177
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-95 <MON>
 A:Cross-references: UNIPARC:UPI00001160C7; EMBL:X67625; NID:G52146; PIDN:CAA47883.1; PI
 A:Accession: S33134
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-95 <MO2>
 A:Cross-references: UNIPARC:UPI00001160C7; EMBL:X67625; NID:G52146; PIDN:CAA47883.1; PI
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-93/Domain: immunoglobulin homology <IMM>

Query Match 87.1%; Score 27; DB 2; Length 95;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
 |||||
 Db 54 ASNLES 59

RESULT 31
 SS9640
 Ig light chain V region N10 - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
 C:Accession: SS9640
 R:Bosart-Whitaker, P.; Chang, C.Y.Y.; Novotny, J.; Benjamin, D.C.; Sheriff, S.
 J. Mol. Biol. 253, 559-575, 1995
 A:Title: The crystal structure of the antibody N10-staphylococcal nuclease complex at 2.
 A:Reference number: SS9639; MUID:96068846; PMID:7473734
 A:Accession: SS9640
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-101 <BOS>
 A:Cross-references: UNIPROT:Q920E9; UNIPARC:UPI00001767CD; EMBL:U25122
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:6-84/Domain: immunoglobulin homology <IMM>

Query Match 87.1%; Score 27; DB 2; Length 101;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
 |||||
 Db 45 ASNLES 50

RESULT 32
 PH1077
 Ig light chain V region (clone 17s-c4) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
 C:Accession: PH1077
 R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
 A:Reference number: PH0971; MUID:92381444; PMID:1512540
 A:Accession: PH1077
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-102 <TIL>
 A:Cross-references: UNIPARC:UPI00001767CC
 A:Experimental source: B cell, strain [NZB x NZW]F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 87.1%; Score 27; DB 2; Length 102;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
 Db 55 ASNLES 60
 |||||

RESULT 33

PH1076
 Ig light chain V region (clone 74-c2) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
 C;Accession: PH1076
 R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cells
 A;Reference number: PH0971; MUID:92381444; PMID:1512540
 A;Accession: PH1076
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-102 <TIL>
 A;Cross-references: UNIPARC:UPI00001767C6
 A;Experimental source: B cell, strain [NZB x NZW]F1
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: immunoglobulin
 F;16-94/Domain: immunoglobulin homology <IMM>

Query Match 87.1%; Score 27; DB 2; Length 102;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
 Db 55 ASNLES 60
 |||||

RESULT 34

S26343
 Ig kappa chain V region - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
 C;Accession: S26343
 R;Stark, S.E.; Caton, A.J.
 J. Exp. Med. 174, 613-624, 1991
 A;Title: Antibodies that are specific for a single amino acid interchange in a protein
 A;Reference number: S26309; MUID:91341421; PMID:1908510
 A;Accession: S26343
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-107 <STA>
 A;Cross-references: UNIPARC:UPI0000115F8A; EMBL:X59207; NID:G52334; PIDN:CAA41917.1; PFI
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;15-93/Domain: immunoglobulin homology <IMM>

Query Match 87.1%; Score 27; DB 2; Length 107;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
 Db 54 ASNLES 59
 |||||

RESULT 35

S26344
 Ig kappa chain V region - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
 C;Accession: S26344
 R;Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991
 A;Title: Antibodies that are specific for a single amino acid interchange in a protein
 A;Reference number: S26309; MUID:91341421; PMID:1908510
 A;Accession: S26344
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-107 <STA>
 A;Cross-references: UNIPARC:UPI0000115F8C; EMBL:X59209; NID:G52336; PIDN:CAA41919.1; PFI
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;15-93/Domain: immunoglobulin homology <IMM>

Query Match 87.1%; Score 27; DB 2; Length 107;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
 Db 54 ASNLES 59
 |||||

RESULT 36

KIHUAV
 Ig kappa chain V-I region (Au) - human
 C;Species: Homo sapiens (man)
 C;Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
 C;Accession: A91653; A01862; S02573
 R;Schiechl, H.; Hilechmann, N.
 Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
 A;Title: Die Primärstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Su
 A;Reference number: A91653; MUID:72189444; PMID:5028201
 A;Accession: A91653
 A;Molecule type: protein
 A;Residues: 1-108 <SCH>
 A;Cross-references: UNIPROT:P01594; UNIPARC:UPI000012E13E
 A;Note: the C region of this chain has the Inv (3) marker
 R;Fehlhammer, H.; Schiffer, M.; Epp, O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; Ste
 Biophys. Struct. Mech. 1, 139-146, 1975
 A;Title: The structure determination of the variable portion of the Bence-Jones protein
 A;Reference number: A90729; MUID:77022433; PMID:1234024
 A;Contents: annotation; X-ray crystallography
 A;Note: the structure of the V region was determined by molecular replacement methods u
 R;Steiner, V.; Chang, J.Y.
 FEBS Lett. 222, 6-10, 1987
 A;Title: Chemical modification of the carboxyl groups of protein substrates enhances th
 A;Reference number: S02572; MUID:88005152; PMID:3115831
 A;Contents: annotation
 C;Comment: This is a Bence Jones protein.
 C;Genetics:
 A;Gene: GDB:IGKV1
 A;Cross-references: GDB:136264
 A;Map position: 2p12-2p12
 C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (ka
 hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into 1
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;16-90/Domain: immunoglobulin homology <IMM>
 F;23-88/Disulfide bonds: #status predicted

Query Match 87.1%; Score 27; DB 1; Length 108;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
 Db 51 ASNLES 56
 |||||

RESULT 37

KVMS54
 Ig kappa chain V region (PC2154) - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004

C:Accession: A01940
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152; PMID:103003
A:Accession: A01940
A:Molecule type: protein
A:Residues: 1-108 <WEI>
A:Cross-references: UNIPROT:P01674; UNIPARC:UPI000002A10F
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 87.1%; Score 27; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
|||||
Db 55 ASNLES 60

RESULT 38
KWS08
Ig kappa chain V region (PC6308) - mouse (tentative sequence)
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
A:Accession: C01937; A01937
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152; PMID:103003
A:Accession: C01937
A:Molecule type: protein
A:Residues: 1-111 <WEI>
A:Cross-references: UNIPROT:P01667; UNIPARC:UPI000002A102
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 87.1%; Score 27; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
|||||
Db 55 ASNLES 60

RESULT 39
KWS37
Ig kappa chain V regions (PC3741, T111) - mouse (tentative sequence)
C:Species: Mus musculus (house mouse)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
A:Accession: A93204; A93822; A01934
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152; PMID:103003
A:Accession: A93204
A:Molecule type: protein
A:Residues: 1-111 <WEI>
A:Cross-references: UNIPROT:P01660; UNIPARC:UPI000002A0FB
R:McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related mo

A:Reference number: A93822; MUID:79012520; PMID:99744
A:Contents: T111
A:Accession: A93822
A:Molecule type: protein
A:Residues: 1-111 <MCK>
A:Cross-references: UNIPARC:UPI000002A0FB
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 87.1%; Score 27; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
|||||
Db 55 ASNLES 60

RESULT 40
KWS40
Ig kappa chain V region (PC7940) - mouse (tentative sequence)
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
A:Accession: C01938; A01938
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152; PMID:103003
A:Accession: C01938
A:Molecule type: protein
A:Residues: 1-111 <WEI>
A:Cross-references: UNIPROT:P01672; UNIPARC:UPI000002A109
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 87.1%; Score 27; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
|||||
Db 55 ASNLES 60

RESULT 41
KWS75
Ig kappa chain V region (PC7175) - mouse (tentative sequence)
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
A:Accession: B01938; A01938
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152; PMID:103003
A:Accession: B01938
A:Molecule type: protein
A:Residues: 1-111 <WEI>
A:Cross-references: UNIPROT:P01671; UNIPARC:UPI000002A108
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 87.1%; Score 27; DB 1; Length 111;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
 |||||
 DB 55 ASNLES 60

RESULT 42
 KMS84
 Ig kappa chain V region (PC6684) - mouse (tentative sequence)
 C:Species: Mus musculus (house mouse)
 C>Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
 C:Accession: A01938
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
 Nature 276, 785-790, 1978
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
 A:Reference number: A93204; MUID:79073152; PMID:103003
 A:Accession: A01938
 A:Molecule type: protein
 A:Residues: 1-111 <WEI>
 A:Cross-references: UNIPROT:P01670; UNIPARC:UPI000002A107
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer
 F:16-94/Domain: immunoglobulin homology <IMM>
 F:23-92/Disulfide bonds: #status predicted

Query Match 87.1%; Score 27; DB 1; Length 111;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
 |||||
 DB 55 ASNLES 60

RESULT 43
 S09965
 Ig kappa chain V-J region (106-108) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
 C:Accession: S09965
 R:Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jatton, J.C.; Izui, S.
 Eur. J. Immunol. 20, 771-777, 1990
 A:Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies
 A:Reference number: S09955; MUID:90269328; PMID:2347362
 A:Accession: S09965
 A:Molecule type: mRNA
 A:Residues: 1-111 <REI>
 A:Cross-references: UNIPARC:UPI0000115B64; EMBL:X51853; NID:g55394; PIDN:CAA36146.1; PID
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 87.1%; Score 27; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
 |||||
 DB 55 ASNLES 60

RESULT 44
 D45722
 anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 109) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: D45722
 R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasquez

J. Virol. 67, 489-496, 1993
 A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on h
 A:Reference number: A45722; MUID:93100833; PMID:7677958
 A:Accession: D45722
 A>Status: Preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-111 <SIM>
 A:Cross-references: UNIPARC:UPI0000176D43
 A:Note: sequence extracted from NCBI backbone (NCBIP:120592)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: glycoprotein
 F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 87.1%; Score 27; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
 |||||
 DB 55 ASNLES 60

RESULT 45
 S09966
 Ig kappa chain V-J region (1810) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
 C:Accession: S09966
 R:Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jatton, J.C.; Izui, S.
 Eur. J. Immunol. 20, 771-777, 1990
 A:Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies
 A:Reference number: S09955; MUID:90269328; PMID:2347362
 A:Accession: S09966
 A:Molecule type: mRNA
 A:Residues: 1-111 <REI>
 A:Cross-references: UNIPARC:UPI0000115B65; EMBL:X51854; NID:g55397; PIDN:CAA36147.1; PID
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 87.1%; Score 27; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
 |||||
 DB 55 ASNLES 60

RESULT 46
 S09963
 Ig kappa chain V-J region (103-78) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
 C:Accession: S09963
 R:Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jatton, J.C.; Izui, S.
 Eur. J. Immunol. 20, 771-777, 1990
 A:Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies
 A:Reference number: S09955; MUID:90269328; PMID:2347362
 A:Accession: S09963
 A:Molecule type: mRNA
 A:Residues: 1-111 <REI>
 A:Cross-references: UNIPROT:Q920E9; UNIPARC:UPI00001767C4; EMBL:X51851
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 87.1%; Score 27; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
 |||||

Db 55 ASNLES 60

RESULT 47

S45715
Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 14-Nov-1997 #text_change 07-May-1999
C:Accession: S45715
R:Kim, H.H.; Kato, K.; Yamato, S.; Igarashi, T.; Matsunaga, C.; Ohtsuka, H.; Higuchi, A.
FEBS Lett. 346, 246-250, 1994
A:Title: Application of (13)C NMR spectroscopy to paratope mapping for larger antigen-Pa
A:Reference number: S45714; MUID:94283606; PMID:8013642
A:Accession: S45715
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-112 <KIM>
A:Cross-references: UNIPARC:UPI00001767D8
A:Experimental source: cell line Ex-3C7
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 87.1%; Score 27; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASNLES 7

Db 55 ASNLES 60

RESULT 48

S63596
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S63596
R:Verdaguer, N.; Mateu, M.G.; Bravo, J.; Domingo, E.; Fita, I.
J. Mol. Biol. 256, 364-376, 1996
A:Title: Induced pocket to accommodate the cell attachment Arg-Gly-Asp motif in a neutra
A:Reference number: S63596; MUID:96174482; PMID:8594203
A:Accession: S63596
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-115 <VER>
A:Cross-references: UNIPARC:UPI00001154DD; GB:S81196; NID:gl336821; PIDN:AAB36171.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 87.1%; Score 27; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASNLES 7

Db 55 ASNLES 60

RESULT 49

S46374
Ig kappa chain V-J region (T33-4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C:Accession: S46374; S38651
R:Benison, C.; Chaetagnez, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rea
A:Reference number: S46369; MUID:94313975; PMID:8039491
A:Accession: S46374
A:Molecule type: mRNA
A:Residues: 1-120 <BEN>

A:Cross-references: UNIPARC:UPI00001165A7; EMBL:Z27175; NID:g415965; PIDN:CAA81699.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:31-105/Domain: immunoglobulin homology <IMM>

Query Match 87.1%; Score 27; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASNLES 7

Db 66 ASNLES 71

RESULT 50

KVMSM6
Ig kappa chain precursor V regions (M63, AB22, PC9245, PC4050) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C:Accession: B90412; B90374; B93822; C93822; C93204; D93204; PH1078; A01935
R:Burstein, Y.; Schechter, I.
Biochemistry 17, 2392-2400, 1978
A:Title: Primary structures of N-terminal extra peptide segments linked to the variable
expression of immunoglobulin genes
A:Reference number: A90412; MUID:78235887; PMID:98179
A:Contents: M63
A:Accession: B90412
A:Molecule type: protein
A:Residues: 1-35 <BUR>
A:Cross-references: UNIPROT:P01661; UNIPARC:UPI0000017371A
R:McKean, D.; Potter, M.; Hood, L.
Biochemistry 12, 760-771, 1973
A:Title: Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains w
A:Reference number: A90374; MUID:73140225; PMID:4691517
A:Contents: M63
A:Accession: B90374
A:Molecule type: protein
A:Residues: 1-53; 59-107 <MC2>
A:Cross-references: UNIPARC:UPI000017371C; UNIPARC:UPI000017371D
A:Accession: C93822
A:Molecule type: protein
A:Residues: 21-119; 'Y', 121-131 <WE1>
A:Cross-references: UNIPARC:UPI000017371C; UNIPARC:UPI000017371D
R:Wiegert, M.; Gatnaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152; PMID:103003
A:Contents: PC9245; PC4050
A:Accession: C93204
A:Molecule type: protein
A:Residues: 21-119; 'Y', 121-131 <WE1>
A:Cross-references: UNIPARC:UPI000002A0FD
A:Accession: D93204
A:Molecule type: protein
A:Residues: 21-119; 'L', 121-123; 'A', 125-129; 'L', 131 <WE2>
A:Cross-references: UNIPARC:UPI000002A0FD
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1078
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA

A;Residues: 21-122 <TIL>
A;Cross-references: UNIPARC:UPI00017371E
A;Experimental source: B cell, strain [NZB x NZW]F1, clone 17p.73
C;Comment: The M63 precursor sequence is shown.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status experimental <SIG>
F;21-131/Domain: Ig kappa chain precursor V region #status experimental <MAT>
F;36-114/Domain: immunoglobulin homology <IMM>
F;43-112/Disulfide bonds: #status predicted

Query Match 87.1%; Score 27; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
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Db 75 ASNLES 80

Search completed: February 23, 2006, 09:51:04
Job time : 31.9077 secs

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|-----|----|------|------|---|--------------|---------------------|-----|----|------|-------|---|----------------|---------------------|
| 105 | 27 | 87.1 | 1195 | 2 | Q9PUM2_XENLA | Q9pum2 xenopus lae | 178 | 26 | 83.9 | 601 | 2 | Q5VYAL_HUMAN | Q5vyal homo sapien |
| 106 | 27 | 87.1 | 1425 | 2 | O85662_SPHAR | O85662 sphingomona | 179 | 26 | 83.9 | 606 | 2 | Q5ZLR8_CHICK | Q5zlr8 gallus gall |
| 107 | 27 | 87.1 | 1700 | 2 | Q6BZD3_DEBAR | Q6bzdz3 debaromyce | 180 | 26 | 83.9 | 624 | 1 | UBQL2_HUMAN | Q5zlr8 gallus gall |
| 108 | 27 | 87.1 | 1906 | 2 | Q6C359_YARLI | Q6c359 yarrowia li | 181 | 26 | 83.9 | 624 | 1 | UBQL2_HUMAN | Q5zlr8 gallus gall |
| 109 | 27 | 87.1 | 2186 | 2 | Q6DQW3_CERN | Q6dqw3 cercospora | 182 | 26 | 83.9 | 624 | 2 | Q5A788_CANAL | Q5a788 candida alb |
| 110 | 27 | 87.1 | 4600 | 2 | Q6QW3_CERN | Q6qwd3 trypanosoma | 183 | 26 | 83.9 | 637 | 2 | Q5D027_HUMAN | Q5d027 homo sapien |
| 111 | 27 | 87.1 | 5085 | 1 | PCLO_RAT | Q6gzd0 cyanoosoma | 184 | 26 | 83.9 | 638 | 2 | Q5CL28_CHYHO | Q5cl28 cryptospori |
| 112 | 27 | 83.9 | 112 | 1 | KV3G_MOUSE | Q9jks6 rattus norv | 185 | 26 | 83.9 | 638 | 1 | UBQL2_MOUSE | Q9qzm0 mus musculus |
| 113 | 26 | 83.9 | 132 | 1 | KV3F_MOUSE | P01659 mus musculus | 186 | 26 | 83.9 | 650 | 2 | Q6CBAB_YARLI | Q6cba8 yarrowia li |
| 114 | 26 | 83.9 | 163 | 2 | Q5N2J6_AZOSE | Q8ytf5 mus musculus | 187 | 26 | 83.9 | 658 | 1 | UBQL3_MOUSE | Q8cbs9 mus musculus |
| 115 | 26 | 83.9 | 173 | 2 | Q8YTF5_ANASP | Q8ytf5 azoarcus sp | 188 | 26 | 83.9 | 664 | 2 | Q8JS04_9BACU | Q8js04 phthorimaea |
| 116 | 26 | 83.9 | 180 | 2 | Q6OCJ3_METCA | Q6ocj3 anabaena sp | 189 | 26 | 83.9 | 664 | 2 | Q22834_ARATH | Q22834 arabidopsis |
| 117 | 26 | 83.9 | 195 | 2 | Q4HDS9_CAMCO | Q6ocj3 methylococc | 190 | 26 | 83.9 | 699 | 2 | Q64JU9_PLAVI | Q64ju9 plasmodium |
| 118 | 26 | 83.9 | 211 | 2 | Q5O3D0_BRARE | Q4hds9 campylobact | 191 | 26 | 83.9 | 699 | 2 | Q64JU9_PLAVI | Q64ju9 plasmodium |
| 119 | 26 | 83.9 | 222 | 2 | Q4UFF0_THEAN | Q5o3d0 brachydanio | 192 | 26 | 83.9 | 750 | 2 | O01348_DROME | O01348 drosophila |
| 120 | 26 | 83.9 | 225 | 2 | Q5SHH8_CRYNE | Q4uff0 theileria a | 193 | 26 | 83.9 | 803 | 2 | Q9VTD3_DROME | Q9vtd3 drosophila |
| 121 | 26 | 83.9 | 225 | 2 | Q5K7L5_CRYNE | Q5shh8 cryptococc | 194 | 26 | 83.9 | 803 | 2 | Q5BIH1_DROME | Q5bih1 drosophila |
| 122 | 26 | 83.9 | 251 | 2 | Q5HRX3_STAEO | Q5k7l5 cryptococc | 195 | 26 | 83.9 | 893 | 2 | Q7XUD7_ORYSA | Q7xud7 oryza sativ |
| 123 | 26 | 83.9 | 254 | 2 | Q8CMQ4_STAEP | Q5hrx3 staphylococ | 196 | 26 | 83.9 | 894 | 2 | Q6D7X1_ERWCT | Q6d7x1 erwinia car |
| 124 | 26 | 83.9 | 292 | 1 | SNAP_DROME | Q8cmq4 staphylococ | 197 | 26 | 83.9 | 900 | 2 | Q64JW4_PLAVI | Q64jw4 plasmodium |
| 125 | 26 | 83.9 | 292 | 2 | Q541G5_DROME | Q23983 drosophila | 198 | 26 | 83.9 | 927 | 2 | Q64JW1_PLAVI | Q64jw1 plasmodium |
| 126 | 26 | 83.9 | 292 | 2 | Q42XY7_PGESY | Q541g5 drosophila | 199 | 26 | 83.9 | 928 | 2 | Q5P971_AZOSE | Q5p971 azoarcus sp |
| 127 | 26 | 83.9 | 297 | 2 | Q5O805_BORBU | Q42xy7 pseudomonas | 200 | 26 | 83.9 | 1114 | 2 | Q6RYH8_CRYNE | Q6ryh8 cryptococc |
| 128 | 26 | 83.9 | 299 | 2 | Q5SD01_DICDI | Q5o805 borrelia bu | 201 | 26 | 83.9 | 1193 | 2 | Q5KIB7_CRYNE | Q5kib7 cryptococc |
| 129 | 26 | 83.9 | 299 | 2 | Q6VY02_ORYSA | Q5sd01 dictyosteli | 202 | 26 | 83.9 | 1245 | 2 | Q55U25_CRYNE | Q55u25 cryptococc |
| 130 | 26 | 83.9 | 309 | 2 | Q88GV9_PSEPK | Q6vy02 oryza sativ | 203 | 26 | 83.9 | 1355 | 2 | Q7X971_ORYSA | Q7x971 oryza sativ |
| 131 | 26 | 83.9 | 325 | 2 | Q59FJ2_HUMAN | Q88gv9 pseudomonas | 204 | 26 | 83.9 | 1407 | 1 | CYAA_DICDI | Cyaa dictyosteli |
| 132 | 26 | 83.9 | 326 | 2 | Q4HV12_GIBZE | Q59fj2 homo sapien | 205 | 26 | 83.9 | 1484 | 2 | Q8TGV4_9PEZI | Q8tgv4 dictyosteli |
| 133 | 26 | 83.9 | 335 | 2 | Q4ORH7_BRARE | Q4hv12 gibberella | 206 | 26 | 83.9 | 1487 | 2 | Q8TGV4_9PEZI | Q8tgv4 diaporthe p |
| 134 | 26 | 83.9 | 345 | 2 | Q89BF6_BRAJA | Q4orh7 brachydanio | 207 | 26 | 83.9 | 1971 | 2 | Q59E58_DROME | Q59e58 drosophila |
| 135 | 26 | 83.9 | 346 | 2 | Q663E3_YERPS | Q89bf6 bradyrhizob | 208 | 26 | 83.9 | 2016 | 2 | Q59E59_DROME | Q59e59 drosophila |
| 136 | 26 | 83.9 | 367 | 2 | Q9SE32_ORYSA | Q663e3 yersinia ps | 209 | 26 | 83.9 | 2057 | 1 | MYSN_DROME | Q93323 drosophila |
| 137 | 26 | 83.9 | 371 | 2 | Q661G8_XENTR | Q9se32 oryza sativ | 210 | 26 | 83.9 | 2127 | 2 | Q57VW6_TRYNOMA | Q57vw6 trypanosoma |
| 138 | 26 | 83.9 | 373 | 2 | Q8W516_HORVU | Q661g8 xenopus tro | 211 | 26 | 83.9 | 2401 | 2 | Q55XB4_CRYNE | Q55xb4 cryptococc |
| 139 | 26 | 83.9 | 388 | 2 | Q5B4L8_VIBF1 | Q8w516 hordeum vul | 212 | 26 | 83.9 | 2401 | 2 | Q5KML9_CRYNE | Q5kml9 cryptococc |
| 140 | 26 | 83.9 | 390 | 2 | Q7VMG0_HAEDU | Q5b4l8 vibrio fisc | 213 | 26 | 83.9 | 2465 | 2 | Q6CB66_YARLI | Q6cb66 yarrowia li |
| 141 | 26 | 83.9 | 396 | 2 | Q41659_GIBZE | Q7vmg0 haemophilus | 214 | 26 | 83.9 | 2573 | 2 | Q93CG8_PHOPR | Q93cg8 photobacter |
| 142 | 26 | 83.9 | 400 | 2 | Q527J2_MAGGR | Q41659 gibberella | 215 | 26 | 83.9 | 2581 | 2 | Q8LS55_PHOPR | Q8lss5 photobacter |
| 143 | 26 | 83.9 | 402 | 2 | Q4T159_TETNG | Q527j2 magnaporthe | 216 | 26 | 83.9 | 2922 | 2 | Q81PU3_DROME | Q81pu3 drosophila |
| 144 | 26 | 83.9 | 423 | 2 | Q4WXQ1_ASPFU | Q4t159 tetraodon n | 217 | 26 | 83.9 | 3699 | 2 | Q9HFB8_SCHPO | Q9hfb8 schizosach |
| 145 | 26 | 83.9 | 457 | 1 | CHKA_HUMAN | Q4wxq1 aspergillus | 218 | 26 | 83.9 | 3834 | 2 | Q600K9_MYCHY | Q600k9 mycoplasma |
| 146 | 26 | 83.9 | 486 | 2 | Q6F960_ACTAD | P35790 homo sapien | 219 | 26 | 83.9 | 15281 | 2 | Q09164_TOLIN | Q09164 tolypocladi |
| 147 | 26 | 83.9 | 493 | 2 | Q9AXF0_ORYSA | Q6f960 acinetobact | 220 | 25 | 80.6 | 94 | 2 | Q6D316_ERWCT | Q6d316 erwinia car |
| 148 | 26 | 83.9 | 497 | 2 | Q7SXA2_BRARE | Q9axf0 oryza sativ | 221 | 25 | 80.6 | 94 | 2 | Q7LZLO_CHICK | Q7lzl0 gallus gall |
| 149 | 26 | 83.9 | 498 | 2 | Q7Y0Y7_ORYSA | Q7sxa2 brachydanio | 222 | 25 | 80.6 | 103 | 2 | Q6LVT8_PHOPR | Q6lvt8 photobacter |
| 150 | 26 | 83.9 | 509 | 2 | Q6TV04_ORYSA | Q7y0y7 oryza sativ | 223 | 25 | 80.6 | 106 | 2 | Q416P1_GIBZE | Q416p1 gibberella |
| 151 | 26 | 83.9 | 510 | 2 | Q7Y0Y6_ORYSA | Q6tv04 oryza sativ | 224 | 25 | 80.6 | 117 | 1 | RL18_METCA | Q605c8 methylococc |
| 152 | 26 | 83.9 | 514 | 2 | Q5P3P3_AZOSE | Q7y0y6 oryza sativ | 225 | 25 | 80.6 | 120 | 2 | Q93HP8_STRAW | Q93hp8 streptomyce |
| 153 | 26 | 83.9 | 524 | 2 | Q7UM24_RHOBA | Q5p3p3 azoarcus sp | 226 | 25 | 80.6 | 132 | 2 | Q4W6W2_9HERP | Q4w6w2 koi herpesv |
| 154 | 26 | 83.9 | 538 | 2 | Q7QAD3_ANOGA | Q7um24 rhodopirell | 227 | 25 | 80.6 | 134 | 2 | Q9Z0W8_RAT | Q9z0w8 rattus norv |
| 155 | 26 | 83.9 | 547 | 2 | Q9VMD9_DROME | Q7qad3 anopheles g | 228 | 25 | 80.6 | 135 | 2 | Q5T8P0_HUMAN | Q5t8p0 homo sapien |
| 156 | 26 | 83.9 | 560 | 2 | Q5GH39_BRARE | Q9vmd9 drosophila | 229 | 25 | 80.6 | 135 | 2 | Q4W6U6_9HERP | Q4w6u6 koi herpesv |
| 157 | 26 | 83.9 | 561 | 2 | Q5T6J5_HUMAN | Q5gh39 brachydanio | 230 | 25 | 80.6 | 135 | 2 | Q4W6U7_9HERP | Q4w6u7 koi herpesv |
| 158 | 26 | 83.9 | 564 | 2 | Q6DCM1_XENLA | Q5t6j5 homo sapien | 231 | 25 | 80.6 | 136 | 2 | Q4W6U3_9HERP | Q4w6u3 koi herpesv |
| 159 | 26 | 83.9 | 564 | 2 | Q6F4Z3_XENTR | Q6dcm1 xenopus lae | 232 | 25 | 80.6 | 136 | 2 | Q4W6U4_9HERP | Q4w6u4 koi herpesv |
| 160 | 26 | 83.9 | 568 | 2 | Q5NLH0_ZYMMO | Q6f4z3 xenopus tro | 233 | 25 | 80.6 | 136 | 2 | Q4W6U5_9HERP | Q4w6u5 koi herpesv |
| 161 | 26 | 83.9 | 582 | 1 | UBQL1_MOUSE | Q5nlh0 zymomonas m | 234 | 25 | 80.6 | 136 | 2 | Q4W6U8_9HERP | Q4w6u8 koi herpesv |
| 162 | 26 | 83.9 | 582 | 2 | Q66K07_MOUSE | Q66k07 mus musculus | 235 | 25 | 80.6 | 136 | 2 | Q4W6U9_9HERP | Q4w6u9 koi herpesv |
| 163 | 26 | 83.9 | 582 | 2 | Q6IN34_RAT | Q6in34 rattus norv | 236 | 25 | 80.6 | 138 | 2 | Q4W6W5_9HERP | Q4w6w5 koi herpesv |
| 164 | 26 | 83.9 | 585 | 2 | Q9PVN8_XENLA | Q6in34 mus musculus | 237 | 25 | 80.6 | 141 | 2 | Q4W6W3_9HERP | Q4w6w3 koi herpesv |
| 165 | 26 | 83.9 | 589 | 1 | UBQL1_HUMAN | Q9pvn8 xenopus lae | 238 | 25 | 80.6 | 142 | 2 | Q6C869_YARLI | Q6c869 yarrowia li |
| 166 | 26 | 83.9 | 589 | 2 | Q5T6J9_HUMAN | Q5t6j9 homo sapien | 239 | 25 | 80.6 | 146 | 2 | Q7USR3_RHOBA | Q7usr3 rhodopirell |
| 167 | 26 | 83.9 | 589 | 2 | Q5R684_PONPY | Q5r684 pongo pygma | 240 | 25 | 80.6 | 155 | 2 | Q52UN9_9HERP | Q52un9 cyprinid he |
| 168 | 26 | 83.9 | 595 | 2 | Q95M59_BOVIN | Q95m59 bos taurus | 241 | 25 | 80.6 | 156 | 2 | Q4W6W4_9HERP | Q4w6w4 koi herpesv |
| 169 | 26 | 83.9 | 596 | 1 | UBQL4_MOUSE | Q95nb8 mus musculus | 242 | 25 | 80.6 | 167 | 2 | Q9CD40_MYCLE | Q9cd40 mycobacteri |
| 170 | 26 | 83.9 | 596 | 2 | Q8AVI8_XENLA | Q8avi8 xenopus lae | 243 | 25 | 80.6 | 173 | 2 | Q8E9R1_SHEON | Q8e9r1 shewanella |
| 171 | 26 | 83.9 | 596 | 2 | Q6P1T0_XENTR | Q6p1t0 xenopus tro | 244 | 25 | 80.6 | 182 | 2 | Q7QG05_ANOGA | Q7qg05 anopheles g |
| 172 | 26 | 83.9 | 599 | 2 | Q801P8_XENLA | Q801p8 xenopus lae | 245 | 25 | 80.6 | 201 | 2 | Q6BTV9_DEBHA | Q6btv9 debaryomyce |
| 173 | 26 | 83.9 | 599 | 2 | Q4G000_BRARE | Q4g000 brachydanio | 246 | 25 | 80.6 | 201 | 2 | Q6M111_BDEBA | Q6m111 bdellovibri |
| 174 | 26 | 83.9 | 600 | 2 | Q59F94_HUMAN | Q59f94 homo sapien | 247 | 25 | 80.6 | 202 | 2 | Q51QW3_MAGGR | Q51qw3 magnaporthe |
| 175 | 26 | 83.9 | 600 | 2 | Q6GN89_XENLA | Q6gn89 xenopus lae | 248 | 25 | 80.6 | 207 | 2 | Q9A6K5_CAUCR | Q9a6k5 caulobacter |
| 176 | 26 | 83.9 | 600 | 2 | Q4VBE0_XENTR | Q4vbe0 xenopus tro | 249 | 25 | 80.6 | 214 | 2 | Q657Y6_ORYSA | Q657y6 oryza sativ |
| 177 | 26 | 83.9 | 601 | 1 | UBQL4_HUMAN | Q9nrr5 homo sapien | 250 | 25 | 80.6 | 216 | 2 | Q8SQB5_BOVIN | Q8sqb5 bos taurus |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|--------------|----------------------|-----|----|------|-----|---|---------------|---------------------|
| 543 | 24 | 77.4 | 181 | 2 | Q8PS18_METWA | Q8pa18 methanosarc | 616 | 24 | 77.4 | 199 | 2 | Q8QZH8_9ORTO | Q8qzh8 influenza c |
| 544 | 24 | 77.4 | 182 | 2 | Q8Y365_RALSO | Q8y365 lactostonia s | 617 | 24 | 77.4 | 199 | 2 | Q8QZH9_9ORTO | Q8qzh9 influenza c |
| 545 | 24 | 77.4 | 182 | 2 | Q88YX2_LACPL | Q88yx2 lactobacill | 618 | 24 | 77.4 | 199 | 2 | Q8QZ10_9ORTO | Q8qz10 influenza c |
| 546 | 24 | 77.4 | 186 | 1 | NADM_PYRAB | Q9uyd4 pyrococcus | 619 | 24 | 77.4 | 199 | 2 | Q8QZ11_9ORTO | Q8qz11 influenza c |
| 547 | 24 | 77.4 | 186 | 1 | NADM_PYRHO | O58z11 pyrococcus | 620 | 24 | 77.4 | 199 | 2 | Q91Q50_9ORTO | Q91q50 influenza c |
| 548 | 24 | 77.4 | 188 | 1 | NADM_PYRFU | Q8u3k8 pyrococcus | 621 | 24 | 77.4 | 199 | 2 | Q91Q51_9ORTO | Q91q51 influenza c |
| 549 | 24 | 77.4 | 188 | 1 | NADM_PYRKO | O5jef8 pyrococcus | 622 | 24 | 77.4 | 199 | 2 | Q91Q51_9ORTO | Q91q51 influenza c |
| 550 | 24 | 77.4 | 192 | 2 | Q38383_9CAUD | Q38383 bacterioph | 623 | 24 | 77.4 | 199 | 2 | Q901Y7_9ORTO | Q901y7 influenza c |
| 551 | 24 | 77.4 | 192 | 2 | Q8YZA9_ANASP | Q8yza9 anabaena sp | 624 | 24 | 77.4 | 199 | 2 | Q901Y9_9ORTO | Q901y9 influenza c |
| 552 | 24 | 77.4 | 193 | 1 | IP13_BPT4 | PI1302 bacterioph | 625 | 24 | 77.4 | 199 | 2 | Q901Z3_9ORTO | Q901z3 influenza c |
| 553 | 24 | 77.4 | 193 | 2 | Q38387_BPK3 | Q38387 bacterioph | 626 | 24 | 77.4 | 199 | 2 | Q901Z9_INCNB | Q901z9 influenza c |
| 554 | 24 | 77.4 | 194 | 2 | CSF3_FELCA | O02708 felis silve | 627 | 24 | 77.4 | 199 | 2 | Q90217_9ORTO | Q90217 influenza c |
| 555 | 24 | 77.4 | 195 | 1 | Q5AQDI_EMENI | O5aqd1 aspergillus | 628 | 24 | 77.4 | 199 | 2 | Q901Z1_9ORTO | Q901z1 influenza c |
| 556 | 24 | 77.4 | 195 | 2 | Q9GJU0_FELCA | O9gju0 felis silve | 629 | 24 | 77.4 | 199 | 2 | Q901Z5_9ORTO | Q901z5 influenza c |
| 557 | 24 | 77.4 | 199 | 2 | Q5PBE6_9ORTO | O5fbeb6 influenza c | 630 | 24 | 77.4 | 199 | 2 | Q901Z7_9ORTO | Q901z7 influenza c |
| 558 | 24 | 77.4 | 199 | 2 | Q68C48_9ORTO | Q68c48 influenza c | 631 | 24 | 77.4 | 199 | 2 | Q90201_9ORTO | Q90201 influenza c |
| 559 | 24 | 77.4 | 199 | 2 | Q68C49_9ORTO | Q68c49 influenza c | 632 | 24 | 77.4 | 199 | 2 | Q90203_9ORTO | Q90203 influenza c |
| 560 | 24 | 77.4 | 199 | 2 | Q68C50_9ORTO | Q68c50 influenza c | 633 | 24 | 77.4 | 199 | 2 | Q90205_9ORTO | Q90205 influenza c |
| 561 | 24 | 77.4 | 199 | 2 | Q68C51_9ORTO | Q68c51 influenza c | 634 | 24 | 77.4 | 199 | 2 | Q902P4_9ORTO | Q902p4 influenza c |
| 562 | 24 | 77.4 | 199 | 2 | Q68C52_9ORTO | Q68c52 influenza c | 635 | 24 | 77.4 | 199 | 2 | Q4U6X1_9ORTO | Q4u6x1 influenza c |
| 563 | 24 | 77.4 | 199 | 2 | Q68C53_9ORTO | Q68c53 influenza c | 636 | 24 | 77.4 | 199 | 2 | Q4U6X2_9ORTO | Q4u6x2 influenza c |
| 564 | 24 | 77.4 | 199 | 2 | Q68C54_9ORTO | Q68c54 influenza c | 637 | 24 | 77.4 | 199 | 2 | Q4U6X3_9ORTO | Q4u6x3 influenza c |
| 565 | 24 | 77.4 | 199 | 2 | Q68C55_9ORTO | Q68c55 influenza c | 638 | 24 | 77.4 | 199 | 2 | Q4U6X4_9ORTO | Q4u6x4 influenza c |
| 566 | 24 | 77.4 | 199 | 2 | Q68C56_9ORTO | Q68c56 influenza c | 639 | 24 | 77.4 | 200 | 2 | Q8GC67_ECOLI | Q8gc67 escherichia |
| 567 | 24 | 77.4 | 199 | 2 | Q68C57_9ORTO | Q68c57 influenza c | 640 | 24 | 77.4 | 202 | 2 | Q5F4P9_BOTLU | Q5f4p9 botrychium |
| 568 | 24 | 77.4 | 199 | 2 | Q68C58_9ORTO | Q68c58 influenza c | 641 | 24 | 77.4 | 204 | 2 | Q5FFJ5_ARATH | Q5ffj5 arabidopsis |
| 569 | 24 | 77.4 | 199 | 2 | Q68C59_9ORTO | Q68c59 influenza c | 642 | 24 | 77.4 | 205 | 2 | Q5KGZ4_CRYNE | Q5kgz4 cryptococcu |
| 570 | 24 | 77.4 | 199 | 2 | Q68C60_9ORTO | Q68c60 influenza c | 643 | 24 | 77.4 | 205 | 2 | Q6GKX1_ARATH | Q6gkx1 arabidopsis |
| 571 | 24 | 77.4 | 199 | 2 | Q68C61_9ORTO | Q68c61 influenza c | 644 | 24 | 77.4 | 206 | 2 | Q8YRWO_ANASP | Q8yryw0 anabaena sp |
| 572 | 24 | 77.4 | 199 | 2 | Q68C62_9ORTO | Q68c62 influenza c | 645 | 24 | 77.4 | 208 | 2 | Q5Z7X0_MAGGR | Q5z7x0 magnaporthe |
| 573 | 24 | 77.4 | 199 | 2 | Q68C63_9ORTO | Q68c63 influenza c | 646 | 24 | 77.4 | 209 | 2 | Q4XFB7_PLACH | Q4xfb7 plasmodium |
| 574 | 24 | 77.4 | 199 | 2 | Q68C64_9ORTO | Q68c64 influenza c | 647 | 24 | 77.4 | 211 | 2 | Q5V8K1_PAXIN | Q5v8k1 paxillus in |
| 575 | 24 | 77.4 | 199 | 2 | Q68C65_9ORTO | Q68c65 influenza c | 648 | 24 | 77.4 | 212 | 1 | Y014_MYCPN | P75099 mycoplasma |
| 576 | 24 | 77.4 | 199 | 2 | Q68C66_9ORTO | Q68c66 influenza c | 649 | 24 | 77.4 | 213 | 2 | Q5SSK4_CRYNE | Q5ssk4 cryptococcu |
| 577 | 24 | 77.4 | 199 | 2 | Q68C67_9ORTO | Q68c67 influenza c | 650 | 24 | 77.4 | 213 | 2 | Q23053_CABEL | Q23053 caenorhabdi |
| 578 | 24 | 77.4 | 199 | 2 | Q68C68_9ORTO | Q68c68 influenza c | 651 | 24 | 77.4 | 217 | 2 | Q4YK84_PLABE | Q4yk84 plasmodium |
| 579 | 24 | 77.4 | 199 | 2 | Q68C69_9ORTO | Q68c69 influenza c | 652 | 24 | 77.4 | 218 | 2 | Q60TV1_CAEBR | Q60tv1 caenorhabdi |
| 580 | 24 | 77.4 | 199 | 2 | Q68C70_9ORTO | Q68c70 influenza c | 653 | 24 | 77.4 | 218 | 2 | Q7TMB9_MYCBO | Q7tmb9 mycobacteri |
| 581 | 24 | 77.4 | 199 | 2 | Q68C71_9ORTO | Q68c71 influenza c | 654 | 24 | 77.4 | 218 | 2 | O53558_MYCTU | O53558 mycobacteri |
| 582 | 24 | 77.4 | 199 | 2 | Q8AZX8_9ORTO | Q8azx8 influenza c | 655 | 24 | 77.4 | 220 | 1 | VIRB5_AGR9 | PI7795 agrobacteri |
| 583 | 24 | 77.4 | 199 | 2 | Q8AZX9_9ORTO | Q8azx9 influenza c | 656 | 24 | 77.4 | 220 | 1 | VIRB5_AGR9 | P0a3w3 agrobacteri |
| 584 | 24 | 77.4 | 199 | 2 | Q8AZY0_9ORTO | Q8azy0 influenza c | 657 | 24 | 77.4 | 220 | 1 | VIRB5_AGR9 | P0a3w2 agrobacteri |
| 585 | 24 | 77.4 | 199 | 2 | Q8AZY1_9ORTO | Q8azy1 influenza c | 658 | 24 | 77.4 | 220 | 2 | Q4JC56_SULAC | Q4jc56 sulfolobus |
| 586 | 24 | 77.4 | 199 | 2 | Q8AZY2_9ORTO | Q8azy2 influenza c | 659 | 24 | 77.4 | 220 | 2 | O66285_9RHIZ | O66285 agrobacteri |
| 587 | 24 | 77.4 | 199 | 2 | Q8AZY3_9ORTO | Q8azy3 influenza c | 660 | 24 | 77.4 | 220 | 2 | O7DKC8_9RHIZ | O7dkc8 agrobacteri |
| 588 | 24 | 77.4 | 199 | 2 | Q8AZY4_9ORTO | Q8azy4 influenza c | 661 | 24 | 77.4 | 220 | 2 | O7BLQ2_9RHIZ | O7blq2 agrobacteri |
| 589 | 24 | 77.4 | 199 | 2 | Q8AZY5_9ORTO | Q8azy5 influenza c | 662 | 24 | 77.4 | 221 | 2 | Q96Y73_SULTO | Q96y73 sulfolobus |
| 590 | 24 | 77.4 | 199 | 2 | Q8AZY6_9ORTO | Q8azy6 influenza c | 663 | 24 | 77.4 | 221 | 2 | Q55QX7_CRYNE | Q55qx7 cryptococcu |
| 591 | 24 | 77.4 | 199 | 2 | Q8AZY7_9ORTO | Q8azy7 influenza c | 664 | 24 | 77.4 | 221 | 2 | Q5KF91_CRYNE | Q5kf91 cryptococcu |
| 592 | 24 | 77.4 | 199 | 2 | Q8AZY8_9ORTO | Q8azy8 influenza c | 665 | 24 | 77.4 | 221 | 2 | Q5N866_ORYSA | Q5n866 oryza sativ |
| 593 | 24 | 77.4 | 199 | 2 | Q8AZY9_9ORTO | Q8azy9 influenza c | 666 | 24 | 77.4 | 222 | 2 | Q4N423_THERPA | Q4n423 theileria p |
| 594 | 24 | 77.4 | 199 | 2 | Q8AZZ0_9ORTO | Q8azzo influenza c | 667 | 24 | 77.4 | 222 | 2 | O7XZM1_ORYSA | O7xzm1 oryza sativ |
| 595 | 24 | 77.4 | 199 | 2 | Q8AZZ1_9ORTO | Q8azzi influenza c | 668 | 24 | 77.4 | 227 | 2 | Q6AH86_LEIXX | Q6ah86 leifsonia x |
| 596 | 24 | 77.4 | 199 | 2 | Q8AZZ2_9ORTO | Q8azzz influenza c | 669 | 24 | 77.4 | 227 | 2 | P73547_SYNY3 | P73547 synochocet |
| 597 | 24 | 77.4 | 199 | 2 | Q8AZZ3_9ORTO | Q8azzz influenza c | 670 | 24 | 77.4 | 231 | 2 | Q9YQF5_ANASP | Q9yqf5 anabaena sp |
| 598 | 24 | 77.4 | 199 | 2 | Q8AZZ4_9ORTO | Q8azzz influenza c | 671 | 24 | 77.4 | 236 | 2 | Q9FQ99_MAIZE | Q9fq99 zea mays (m |
| 599 | 24 | 77.4 | 199 | 2 | Q8OHM2_9ORTO | Q8ohm2 influenza c | 672 | 24 | 77.4 | 237 | 2 | Q5I745_BACNO | Q5i745 bacteroides |
| 600 | 24 | 77.4 | 199 | 2 | Q8QZG7_9ORTO | Q8qzgm2 influenza c | 673 | 24 | 77.4 | 237 | 2 | Q4K7U0_PSEF5 | Q4k7u0 pseudomonas |
| 601 | 24 | 77.4 | 199 | 2 | Q8QZG8_9ORTO | Q8qzgm2 influenza c | 674 | 24 | 77.4 | 239 | 2 | Q61WU2_CAEBR | Q61wu2 caenorhabdi |
| 602 | 24 | 77.4 | 199 | 2 | Q8QZG9_9ORTO | Q8qzgm2 influenza c | 675 | 24 | 77.4 | 242 | 2 | Q8K322_MOUSE | Q8k322 mus musculu |
| 603 | 24 | 77.4 | 199 | 2 | Q8QZG4_9ORTO | Q8qzgm4 influenza c | 676 | 24 | 77.4 | 243 | 1 | KAD2_ORYSA | Q8480 oryza sativ |
| 604 | 24 | 77.4 | 199 | 2 | Q8QZG5_9ORTO | Q8qzgm5 influenza c | 677 | 24 | 77.4 | 243 | 2 | Q53MA3_ORYSA | Q53ma3 oryza sativ |
| 605 | 24 | 77.4 | 199 | 2 | Q8QZG6_9ORTO | Q8qzgm6 influenza c | 678 | 24 | 77.4 | 244 | 2 | O54WE0_DICDI | Q54we0 dictyosteli |
| 606 | 24 | 77.4 | 199 | 2 | Q8QZG7_9ORTO | Q8qzgm7 influenza c | 679 | 24 | 77.4 | 244 | 2 | O92480_NPVB | O92480 bombyx mori |
| 607 | 24 | 77.4 | 199 | 2 | Q8QZG8_9ORTO | Q8qzgm8 influenza c | 680 | 24 | 77.4 | 247 | 1 | Y1423_PROMM | Q7v5w3 prochloroco |
| 608 | 24 | 77.4 | 199 | 2 | Q8QZG9_9ORTO | Q8qzgm9 influenza c | 681 | 24 | 77.4 | 251 | 2 | Q6ASF1_BORGA | Q6asf1 borrelia ga |
| 609 | 24 | 77.4 | 199 | 2 | Q8QZH1_9ORTO | Q8qzh1 influenza c | 682 | 24 | 77.4 | 254 | 2 | Q8CSN2_STAEP | Q8csn2 staphylococ |
| 610 | 24 | 77.4 | 199 | 2 | Q8QZH2_9ORTO | Q8qzh2 influenza c | 683 | 24 | 77.4 | 256 | 2 | Q5TS58_ANOGA | Q5ts58 anopheles g |
| 611 | 24 | 77.4 | 199 | 2 | Q8QZH3_9ORTO | Q8qzh3 influenza c | 684 | 24 | 77.4 | 256 | 2 | Q4PP47_9BACT | Q4pp47 uncultured |
| 612 | 24 | 77.4 | 199 | 2 | Q8QZH4_9ORTO | Q8qzh4 influenza c | 685 | 24 | 77.4 | 256 | 2 | Q4PNF2_9BACT | Q4pnf2 uncultured |
| 613 | 24 | 77.4 | 199 | 2 | Q8QZH5_9ORTO | Q8qzh5 influenza c | 686 | 24 | 77.4 | 257 | 1 | ZUPT_ECOL6 | P0a8h5 escherichia |
| 614 | 24 | 77.4 | 199 | 2 | Q8QZH6_9ORTO | Q8qzh6 influenza c | 687 | 24 | 77.4 | 257 | 1 | ZUPT_ECOLI | P0a8h3 escherichia |
| 615 | 24 | 77.4 | 199 | 2 | Q8QZH7_9ORTO | Q8qzh7 influenza c | 688 | 24 | 77.4 | 257 | 1 | ZUPT_SALTI | P67471 salmonella |


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981 24 77.4 523 2 Q96DU2 homo sapien
982 24 77.4 523 2 Q8CYB8 pongo pygma
983 24 77.4 524 1 K2C6G MOUSE
984 24 77.4 526 1 HRG RABIT
985 24 77.4 526 2 Q6L4M5 ORYSA
986 24 77.4 527 2 Q8AVV1 9GAMA
987 24 77.4 530 2 Q6CY22 KLULA
988 24 77.4 531 2 Q4Q8X2 LEIMA
989 24 77.4 536 2 Q5CXT4 CRYPV
990 24 77.4 537 2 Q5CG62 CRYHO
991 24 77.4 538 2 Q9SII9 ARATH
992 24 77.4 541 2 Q6CTA8 KLULA
993 24 77.4 541 2 Q4T2C9 TETNG
994 24 77.4 542 2 Q4ZR42 PSESY
995 24 77.4 543 2 Q5A3G5 CANAL
996 24 77.4 543 2 Q64391 SOLTU
997 24 77.4 543 2 Q8G491 BIFLO
998 24 77.4 544 2 Q52BZ1 MAGGR
999 24 77.4 545 2 Q87PC7 VIBPA
1000 24 77.4 546 2 Q85963 SPHAR

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ALIGNMENTS

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RESULT 1
KV3P_MOUSE
ID KV3P_MOUSE STANDARD; PRT; 110 AA.
AC P01668;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region PC 7210.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Murioidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790 (1978).
-----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
DR PIR; D01937; KVM510.
DR HSP; P01665; IQNZ.
DR SMR; P01668; 1-110.
DR Ensembl; ENSMUSG00000053225; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 38
FT REGION 39 53
FT REGION 54 60
FT REGION 61 92
FT REGION 93 100
FT REGION 101 110
FT DISULFID 23 92
FT NON_TER 110 110
SQ SEQUENCE 110 AA; 69FIA5CE886B1249 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 110;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
DB 54 AASNLES 60

RESULT 3
KV3M_MOUSE
ID KV3M_MOUSE STANDARD; PRT; 111 AA.
AC P01665;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)

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Query Match 100.0%; Score 31; DB 1; Length 110;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
DB 54 AASNLES 60

RESULT 2
KV3L_MOUSE
ID KV3L_MOUSE STANDARD; PRT; 111 AA.
AC P01664;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region CBPC 101.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Murioidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=79012520; PubMed=93744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917 (1978).
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein.
-----
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-----
DR PIR; A01936; KVMSC1.
DR HSP; P01665; IQNZ.
DR SMR; P01664; 1-111.
DR Ensembl; ENSMUSG00000053225; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 38
FT REGION 39 53
FT REGION 54 60
FT REGION 61 92
FT REGION 93 101
FT REGION 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11964 MW; E2B1AD98AD965962 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
DB 54 AASNLES 60

RESULT 3
KV3M_MOUSE
ID KV3M_MOUSE STANDARD; PRT; 111 AA.
AC P01665;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)

```

DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Ig kappa chain V-III region PC 7043.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN PROTEIN SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790 (1978).
[2]
RN NUCLEOTIDE SEQUENCE OF 10-99.
RX MEDLINE=94009207; PubMed=7691608;
RA Mo J.A., Bona C.A., Holmdahl R.;
RT "Variable region gene selection of immunoglobulin G-expressing B cells
with specificity for a defined epitope on type II collagen.";
RL Eur. J. Immunol. 23:2503-2510 (1993).
[3]
RN STRUCTURE BY NMR OF 1-111.
RX MEDLINE=20264305; PubMed=10801487; DOI=10.1016/S0969-2126(00)00119-2;
RA Tugarinov V., Zvi A., Levy R., Hayek Y., Matsushita S., Angliester J.;
RT "NMR structure of an anti-gp120 antibody complex with a V3 peptide
reveals a surface important for co-receptor binding.";
RL Structure 8:385-395 (2000).
[4]
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CC
DR EMBL; Z25444; CAA80931.1; -; mRNA.
DR EMBL; Z25446; CAA80933.1; -; mRNA.
DR EMBL; Z25448; CAA80935.1; -; mRNA.
DR EMBL; Z25450; CAA80937.1; -; mRNA.
DR EMBL; Z25452; CAA80939.1; -; mRNA.
DR EMBL; Z25454; CAA80941.1; -; mRNA.
DR EMBL; Z25456; CAA80945.1; -; mRNA.
DR PIR; A01937; KWSM343.
DR PDB; 1QNZ; NMR; L=1-111.
DR Ensembl; ENSMUSG00000053225; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 38
FT REGION 39 53
FT REGION 54 60
FT REGION 61 92
FT REGION 93 101
FT REGION 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB596C306D29 CRC64;
Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AASNLRS 7
Db 54 AASNLRS 60
RESULT 4
KV3N_MOUSE

ID KV3N_MOUSE STANDARD; PRT; 111 AA.
AC P01666;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region PC 7183.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN PROTEIN SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790 (1978).
[2]
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CC
DR PIR; B01937; KWSM83.
DR HSSP; P01665; 1QNZ.
DR SMR; P01666; 1-111.
DR Ensembl; ENSMUSG00000053225; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 38
FT REGION 39 53
FT REGION 54 60
FT REGION 61 92
FT REGION 93 101
FT REGION 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;
Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AASNLRS 7
Db 54 AASNLRS 60
RESULT 5
KV3Q_MOUSE STANDARD; PRT; 111 AA.
ID KV3Q_MOUSE
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region PC 7769.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN PROTEIN SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin

RT diversity";
RL Nature 276:785-790(1978).
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; E01937; KMS669.
DR HSP; P01665; 1QNZ.
DR SMR; P01669; 1-111.
DR Ensembl; ENSMUSG0000053225; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 38 Complementarity-determining-1.
FT REGION 39 53 Framework-2.
FT REGION 54 60 Complementarity-determining-2.
FT REGION 61 92 Framework-3.
FT REGION 93 101 Complementarity-determining-3.
FT REGION 102 111 Framework-4.
FT DISULFID 23 92 By similarity.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
DB 54 AASNLES 60
|||||
RESULT 6
Y852 HAEIN
ID Y852 HAEIN STANDARD; PRT; 463 AA.
AC P44503;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Hypothetical transport protein HI0852.
GN OrderedLocusNames=HI0852;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]_TaxID=727;
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G.G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.W., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT rd";
RL Science 269:496-512(1995).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Probable).
CC -!- SIMILARITY: Belongs to the major facilitator superfamily. EmrB
CC family.
CC -----

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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U32766; AAC22509.1; -; Genomic_DNA.
DR TIGR; B64160; B64160.
DR TIGR; HI0852; -.
DR InterPro; IPR004638; Efflux_EmrB.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR011701; MFS 1.
DR InterPro; IPR001958; TCR_TetA.
DR InterPro; IPR001411; TCR_TetB.
DR Pfam; PF07690; MFS_1; 1.
DR PRINTS; PR01035; TCR_TetA.
DR PRINTS; PR01036; TCR_TetB.
DR TIGRFAMs; TIGR00711; efflux_EmrB; 1.
DR PROSITE; PS50850; MFS; 1.
KW Complete proteome; Hypothetical protein; Inner membrane; Membrane;
KW Transmembrane; Transport.
FT TRANSMEM 10 30 Potential.
FT TRANSMEM 49 69 Potential.
FT TRANSMEM 82 102 Potential.
FT TRANSMEM 107 127 Potential.
FT TRANSMEM 139 159 Potential.
FT TRANSMEM 165 185 Potential.
FT TRANSMEM 197 217 Potential.
FT TRANSMEM 225 245 Potential.
FT TRANSMEM 267 287 Potential.
FT TRANSMEM 298 318 Potential.
FT TRANSMEM 328 348 Potential.
FT TRANSMEM 354 374 Potential.
FT TRANSMEM 393 413 Potential.
FT TRANSMEM 429 449 Potential.
SQ SEQUENCE 463 AA; 50003 MW; D725EPFD50F9F23F CRC64;

Query Match 100.0%; Score 31; DB 1; Length 463;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
DB 94 AASNLES 100
|||||
RESULT 7
Q4QM49 HAEI8
ID Q4QM49 HAEI8 PRELIMINARY; PRT; 463 AA.
AC Q4QM49;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=NH11020;
OS Haemophilus influenzae (Strain 86-028NP).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=281310;
RN [1]_TaxID=281310;
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15968074; DOI=10.1128/JB.187.13.4627-4636.2005;
RA Harrison A., Dyer D.W., Gillaspay A., Ray W.C., Mungur R., Carson M.B.,
RA Zhong H., Gipson J., Gipson M., Johnson L.S., Lewis L., Bakaletz L.O.,
RA Munson R.S. Jr.;
RT "Genomic sequence of an otitis media isolate of nontypeable
RT Haemophilus influenzae: comparative study with H. influenzae serotype
RT d, strain KW20";
RL J. Bacteriol. 187:4627-4636(2005).
DR EMBL; CP000057; AAX87898.1; -; Genomic_DNA.
DR InterPro; IPR004638; Efflux_EmrB.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR011701; MFS_1.

DR InterPro: IPR006162; Ppantne.S.
 DR InterPro: IPR001958; TCR_TetA.
 DR InterPro: IPR001411; TCR_TetB.
 DR Pfam: PF07690; MFS 1; 1.
 DR PRINTS: PR01035; TCR_TetA.
 DR PRINTS: PR01036; TCR_TetB.
 DR TIGRFAMs: TIGR00711; efflux_EmrB; 1.
 DR PROSITE: PS00850; MFS; 1.
 DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 463 AA; 50036 MW; AF67B6A23E621266 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 463;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNL5 7
 |||||
 Db 94 AASNL5 100

RESULT 8

O4X0E9 ASPFU PRELIMINARY; PRT; 519 AA.

AC O4X0E9;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE NADH-ubiquinone oxidoreductase 49 kDa subunit, putative.
 GN ORFNames=Afu2g13710;
 OS Aspergillus fumigatus Af293.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=330879;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Af293;
 RA Nierman W., Pain A., Anderson M.J., Wortman J.J., Kim H. Stanley.,
 RA Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
 RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
 RA Farman N., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
 RA Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
 RA Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,
 RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
 RA Kellier N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
 RA Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
 RA Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
 RA Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
 RA Penava M.A., Pertea M., Price C., Pritchard B.L., Quail M.A.,
 RA Rabinowitz E., Rawlins N., Rajandream M.-A., Reichard U.,
 RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
 RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
 RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
 RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
 RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
 RA Machida M., Hall N., Barrell B., Denning D.W.,
 RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
 Aspergillus fumigatus";
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; AAH01000001; EAL93666.1; -; Genomic_DNA.

DR InterPro: IPR010219; Nuod.
 DR InterPro: IPR001135; Oxidored 49kDa.
 DR Pfam: PF00346; Complex1_49kDa; 1.
 DR TIGRFAMs: TIGR01962; Nuod; 1.
 DR PROSITE: PS00535; COMPLEX1_49K; 1.
 KW NAD; Oxidoreductase; Ubiquinone.

SQ SEQUENCE 519 AA; 58230 MW; 21646F55AF8687A6 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 519;
 Best Local Similarity 100.0%; Pred. No. 86;

QY 1 AASNL5 7
 |||||
 Db 121 AASNL5 127

RESULT 9

K6PF SCHPO STANDARD; PRT; 942 AA.

AC O42938; P78762;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE 6-phosphofructokinase (EC 2.7.1.11) (Phosphofructokinase)
 GN (Phosphohexokinase) (6PF-1-K).
 DE Name=pfk1; ORFNames=SPBCL16H5.02;
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M.H., Lyne R., Stewart A.,
 RA Sgouros J.G., Peat N., Hayles J., Baker S.G., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D.E., Hidaigo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagals K.,
 RA James K.D., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K.L., Murphy L.D., Niblett D., Odell C.,
 RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitz E.,
 RA Rutherford K.M., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M.N., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J.R., Volckaert G., Aert R., Robben J., Grymonprez B.,
 RA Weljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Duesterhoeft A., Frizc C., Holzer E., Moestl D.,
 RA Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R.,
 RA Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Furnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomycetes pombe";
 RL Nature 415:871-880 (2002).

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 583-942.

RC STRAIN=PR745;
 RX MEDLINE=98162722; PubMed=9501991;
 RA Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H.;
 RT "Identification of open reading frames in Schizosaccharomycetes pombe
 cDNAs";
 RL DNA Res. 4:363-369 (1997).

RN [3]

RP FUNCTION IN CELL CYCLE REGULATION.

RX MEDLINE=22232329; PubMed=12237855; DOI=10.1002/yea.902;
 RA Tallada V.A., Daga R.R., Palomeque C., Garzon A., Jimenez J.;
 RT "Genome-wide search of Schizosaccharomycetes pombe genes causing
 overexpression-mediated cell cycle defects";
 RL Yeast 19:1139-1151 (2002).

CC -!- FUNCTION: May also have a role in cell cycle regulation.

CC -!- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
 fructose 1,6-bisphosphate.

CC -!- PATHWAY: Key control step of glycolysis.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -!- SIMILARITY: Belongs to the phosphofructokinase family. Two domains

```
CC subfamily.
CC -! CAUTION: Ref.2 sequence differs from that shown due to a
CC frameshift in position 836.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AL022104; CAAL7900.1; -; Genomic DNA.
CC EMBL; D89110; BAAL3773.1; ALT_FRAME; mRNA.
CC PIR; T39624; T39624.
CC HSP; P00512; 3PKF.
CC -----
CC GeneDB Spombe; SPEIC16H5.02; -.
CC GO; GO:0003872; F:6-phosphofructokinase activity; TAS.
CC GO; GO:0006096; P:glycolysis; TAS.
CC GO; GO:0000074; P:regulation of cell cycle; IDA.
CC InterPro; IPR009161; PFK_euk.
CC InterPro; IPR000023; Ppfuckinase.
CC PANTHER; PTHR13697; Ppfuckinase; 1.
CC Pfam; PF00365; PFK; 2.
CC PIRSF; PIRSF000533; ATP_PFK_euk; 1.
CC PRINTS; PR00476; PPFCKINASE.
CC ProDom; PD000707; Ppfuckinase; 2.
CC TIGRFAWs; TIGR02478; 6PFK_euk; 1.
CC PROSITE; PS00433; PHOSPHOFRUCTOKINASE; 2.
CC KW Allosteric enzyme; ATP-binding; Complete proteome; Glycolysis; Kinase;
CC Magnesium; Metal-binding; Nucleotide-binding; Repeat; Transferase.
CC FT NP_BIND 214 218 ATP (By similarity).
CC FT NP_BIND 372 376 ATP (By similarity).
CC FT NP_BIND 389 405 ATP (By similarity).
CC FT ACT_SITE 345 345 Proton acceptor (By similarity).
CC FT METAL 403 403 Magnesium (via carbonyl oxygen) (By
CC similarity).
CC FT BINDING 380 380 Substrate (By similarity).
CC FT BINDING 472 472 Substrate (By similarity).
CC FT BINDING 478 478 Substrate (By similarity).
CC FT BINDING 481 481 Substrate (By similarity).
CC SQ SEQUENCE 942 AA; 102555 MW; C6052AF7C1DB75B4 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 942;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 165 AASNLES 171

RESULT 10
DZIP3 MOUSE STANDARD; PRT; 1204 AA.
AC Q7TPV2; Q8OTU4; Q8BYK7;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Ubiquitin ligase protein DZIP3 (EC 6.3.2.-) (DAZ-interacting protein 3
DE homolog).
GN Name=Dzip3; Synonyms=Kiaa0675;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).
RC TISSUE=Brain;
RX MEDLINE=22579291; PubMed=12693553;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
RA Nakajima D., Nagase T., Ohara O., Koga H.;
RT "prediction of the coding sequences of mouse homologues of KIAA gene:
CC -!- FUNCTION: E3 Ubiquitin ligase proteins mediate ubiquitination and
CC subsequent proteasomal degradation of target proteins. E3
```

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RT CDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries."
RN DNA Res. 10:35-48 (2003).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 1-787 (ISOFORM 1).
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kaeukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmer S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RN Nature 420:563-573 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 1-664 (ISOFORM 2).
RC STRAIN=C3H/He; TISSUE=Osteoblast;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 767-1133 (ISOFORM 1).
RC TISSUE=Head, and Retina;
RA Strausberg R.L.;
RN Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE OF 1062-1204 (ISOFORM 1).
RA Tanaka T.S., Jaradat S.A., Lim M.K., Kargul G.J., Wang X., Doi H.,
RA Grabovac M.J., Pantano S., Sano Y., Piao Y., Nagaraja R., Doi H.,
RA Wood W.H. III, Becker K.G., Ko M.S.H.;
RN Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: E3 Ubiquitin ligase proteins mediate ubiquitination and
CC subsequent proteasomal degradation of target proteins. E3
```

ubiquitin ligases accept ubiquitin from an E2 ubiquitin-conjugating enzyme in the form of a thioester and then directly transfers the ubiquitin to targeted substrates. Able to specifically bind RNA (By similarity).

-!- PATHWAY: Ubiquitin conjugation; third step.

-!- SUBUNIT: Probably interacts with DAZL (By similarity).

-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=3;

Name=1;

isoId=Q7TPV2-1; Sequence=Displayed;

Name=2;

isoId=Q7TPV2-2; Sequence=VSP_010977;

Note=No experimental confirmation available;

Name=3;

isoId=Q7TPV2-3; Sequence=VSP_010973, VSP_010974, VSP_010975, VSP_010976;

Note=No experimental confirmation available;

-!- SIMILARITY: Contains 1 RING-type zinc finger.

-!- CAUTION: This is a conceptual translation.

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EMBL; AK123144; BAC5626.1; ALT INIT; mRNA.

DR EMBL; AK031972; BAC30265.1; -; mRNA.

DR EMBL; BC052893; AH52893.1; -; mRNA.

DR EMBL; BT136207; -; NOT ANNOTATED CDS; mRNA.

DR EMBL; CN535823; -; NOT ANNOTATED CDS; mRNA.

DR EMBL; BG070132; -; NOT ANNOTATED CDS; mRNA.

DR Ensembl; ENSMUSG0000054061; Mus_musculus.

DR MGI; MGI:1917433; 2310047C04Rik.

DR InterPro; IPR011990; Tpr-like_helical.

DR Pfam; PF00097; zf-C3HC4; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.

DR PROSITE; PS00589; ZF_RING_2; 1.

KW Alternative splicing; Coiled coil; Ligase; Metal-binding; RNA-binding;

KW Ub1 conjugation pathway; Zinc; Zinc-finger.

FT ZN FING 1144 1184 RING-type; atypical.

FT COILED 746 861 Potential.

FT COILED 906 941 Potential.

FT COMBIAS 657 684 Poly-Lys.

FT COMBIAS 954 960 Poly-Pro.

FT COMBIAS 1137 1142 Poly-Glu.

FT VARSPLIC 1 889 Missing (in isoform 3).

FT VARSPLIC 382 587 Missing (in isoform 2).

FT VARSPLIC 890 899 /FTId=VSP_010977.

FT VARSPLIC 1135 1153 /FTId=VSP_010974.

FT VARSPLIC 1154 1204 /FTId=VSP_010975.

FT VARSPLIC 1154 1204 Missing (in isoform 3).

FT CONFLICT 306 306 D -> G (in Ref. 3).

FT CONFLICT 650 650 V -> I (in Ref. 3).

SQ SEQUENCE 1204 AA; 138021 MW; 9522730708DB570C CRC64;

Query Match 100.0%; Score 31; DB 1; Length 1204;

Best Local Similarity 100.0%; Pred. No. 2.2e-02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLLES 7

DB 898 AASNLLES 904

RESULT 11

ID DZIP3 HUMAN STANDARD; PRT: 1208 AA.

AC Q86VL3; O75162; Q6P3R9; Q6PH82; Q86YL4; Q86YL5; Q86YL6; Q8IWI0;

AC Q96RS9;

DT 25-OCT-2004 (Rel. 45, Created)

DT 25-OCT-2004 (Rel. 45, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Ubiquitin ligase protein DZIP3 (EC 6.3.2.-) (DAZ-interacting protein

DE 3) (RNA-binding ubiquitin ligase of 138 kDa) (HRUL138).

GN Name=DZIP3; Synonyms=KIAA0675;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2), FUNCTION, SUBCELLULAR

RP LOCATION, RNA-BINDING, TISSUE SPECIFICITY, AND MUTAGENESIS OF

RP 662-LYS--LYS-666 AND CYS-1187.

RC TISSUE=Liver, and Uterus;

RX MEDLINE=22426342; PubMed=12538761; DOI=10.1242/jcs.00261;

RA Krefl S.G., Nassal M.;

RT "hrUL138, a novel human RNA-binding RING-H2 ubiquitin-protein

RT ligase.";

RL J. Cell Sci. 116:605-616(2003).

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RC TISSUE=Brain;

RX MEDLINE=98403880; PubMed=9734811;

RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,

RA Kotani H., Nomura N., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. X.

RT The complete sequences of 100 new cDNA clones from brain which can

RT code for large proteins in vitro.";

RL DNA Res. 5:169-176(1998).

RN [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).

RC TISSUE=Skin, and Testis;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,

RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [4]

RP NUCLEOTIDE SEQUENCE OF 641-1208, AND INTERACTION WITH DAZ.

RX PubMed=12511597; DOI=10.1073/pnas.0234478100;

RA Moore F.L., Jaruzelska J., Fox M.S., Urano J., Firpo M.T., Turek P.J.,

RA Dorfman D.M., Reijo Pera R.A.;

RT "Human Pumilio-2 is expressed in embryonic stem cells and germ cells

RT and interacts with DAZ (Deleted in Azoospermia) and DAZ-like

RT proteins.";

RL Proc. Natl. Acad. Sci. U.S.A. 100:538-543(2003).

CC -!- FUNCTION: E3 Ubiquitin ligase proteins mediate ubiquitination and

CC subsequent proteasomal degradation of target proteins. E3

CC ubiquitin ligases accept ubiquitin from an E2 ubiquitin-

CC conjugating enzyme in the form of a thioester and then directly

```
CC transfers the ubiquitin to targeted substrates. Able to
CC specifically bind RNA.
CC -!- PATHWAY: Ubiquitin conjugation; third step.
CC -!- SUBUNIT: Interacts with DAZ proteins.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q86Y13-1; Sequences=Displayed;
CC Name=2; Synonyms=Short;
CC IsoId=Q86Y13-2; Sequences=VSP 010971, VSP 010972;
CC -!- TISSUE SPECIFICITY: Widely expressed at low level. Highly
CC expressed in skeletal muscle, kidney and heart. Expressed at low
CC level in placenta, lung, brain, liver and pancreas.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -!- CAUTION: Ref.4 sequence differs from that shown due to a
CC frameshift in position 1127.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AY227651; AA072967.1; -; mRNA.
CC EMBL; AY227652; AA072968.1; -; mRNA.
CC EMBL; AY227653; AA072969.1; -; Other RNA.
CC EMBL; AY227654; AA072970.1; -; mRNA.
CC EMBL; AB014575; BAA31650.2; ALT INIT; mRNA.
CC EMBL; BC039018; AAH39018.1; ALT TERM; mRNA.
CC EMBL; BC056674; AAH56674.1; ALT TERM; mRNA.
CC EMBL; BC063882; AAH63882.1; -; mRNA.
CC EMBL; AF279370; AAK69484.1; ALT_FRAME; mRNA.
CC PIR; T00362; T00362.
CC HSSP; P28990; 1CHC.
CC Ensembl; ENSG00000198919; Homo sapiens.
CC MIM; 608672; -.
CC InterPro; IPR001841; ZnF_RING.
CC Pfam; PF00097; zf-C3HC4; 1.
CC SMART; SM00184; RING; 1.
CC PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
CC PROSITE; PS00518; ZF_RING_2; 1.
CC Alternative splicing; Coiled coil; Ligase; Metal-binding; RNA-binding;
KW Ubl conjugation pathway; Zinc; Zinc-finger.
FT ZN_FING 1148 1188 RING-type; atypical.
FT COILED 14 43 Potential.
FT COILED 647 676 Potential.
FT COILED 792 853 Potential.
FT COILED 904 939 Potential.
FT COMPBIA5 607 610 Poly-Glu.
FT COMPBIA5 661 671 Poly-Lys.
FT COMPBIA5 952 958 Poly-Pro.
FT COMPBIA5 1140 1146 Poly-Glu.
FT VARSPLIC 302 303 GE -> EF (in isoform 2).
FT VARSPLIC 304 1208 /FTId=VSP 010971.
FT MUTAGEN 662 666 Missing (in isoform 2).
FT MUTAGEN 662 666 KKTKK->SGSTK: Strongly decreases RNA-
FT MUTAGEN 1187 1187 binding activity.
FT MUTAGEN 1187 1187 C->S: Abolishes ubiquitin ligase
FT activity.
FT CONFLICT 368 368 D -> G (in Ref. 3; AAH56674).
FT CONFLICT 1208 AA; 138604 MW; 76945A63AF85207E CRC64;
SQ SEQUENCE 1208 AA; 138604 MW; 76945A63AF85207E CRC64;
Query Match 100.0%; Score 31; DB 1; Length 1208;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AASNLES 7
DB 896 AASNLES 902
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RESULT 12
Q57EU3 BRUAB
ID Q57EU3 BRUAB PRELIMINARY; PRT; 69 AA.
AC Q57EU3;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Cold-shock family protein.
GN OrderedLocusNames=Brubi_0445;
OS Brucella abortus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=235;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=9-941 / Biovar 1;
RX PubMed=15805518; DOI=10.1128/JB.187.8.2715-2726.2005;
RA Halling S.M., Peterson-Burch B.D., Bricker B.J., Zuerner R.L.,
RA Qing Z., Li L.-L., Kapur V., Alt D.P., Olsen S.C.;
RT "Completion of the genome sequence of Brucella abortus and comparison
RT to the highly similar genomes of Brucella melitensis and Brucella
RT suis.";
RL J. Bacteriol. 187:2715-2726(2005).
DR EMBL; AE017223; AAX73841.1; -; Genomic_DNA.
SQ SEQUENCE 69 AA; 7301 MW; D6142414631FDEBA CRC64;
Query Match 90.3%; Score 28; DB 2; Length 69;
Best Local Similarity 85.7%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AASNLES 7
DB 62 AASNLES 68

RESULT 13
Q8YFLO BRUME
ID Q8YFLO BRUME PRELIMINARY; PRT; 69 AA.
AC Q8YFLO;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE COLD SHOCK PROTEIN CSPA.
GN OrderedLocusNames=BME11510;
OS Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=21642680; PubMed=11756688; DOI=10.1073/pnas.221575398;
RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mijer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
RA Jablonki L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyprides N.C., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Contains 1 CSD (cold-shock) domain.
DR EMBL; AE009587; AAL52691.1; -; Genomic_DNA.
DR PIR; AH3440; AH3440.
DR HSSP; P15277; 1MJC.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR002059; Cold_shock.
DR InterPro; IPR012156; Cold_shock_Cspa.
DR InterPro; IPR011129; CSP.
DR InterPro; IPR012340; NA-bind_OB_sub.
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DR Pfam; PF00313; CSD; 1.
DR PIRSP; PIRSF002599; Cold_shock_A; 1.
DR PRINTS; PR00050; COLDSHOCK.
DR ProDom; PD000621; Cold_shock; 1.
DR SMART; SM00357; CSP; 1; SHOCK; 1.
DR PROSITE; PS00352; COLD_SHOCK; 1.
KW Activator; Complete proteome; DNA-binding; Transcription;
SQ SEQUENCE 69 AA; 7301 MW; D6142414631FDEBA CRC64;

Query Match          90.3%; Score 28; DB 2; Length 69;
Best Local Similarity 85.7%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNL5 7
Db 62 AANLES 68

RESULT 14
Q9JL80 MOUSE
ID Q9JL80_MOUSE PRELIMINARY; PRT; 103 AA.
AC Q9JL80_
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Anti-myosin immunoglobulin light chain variable region
DE (Fragment).
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=BALB/c;
RC MEDLINE=20448942; PubMed=10992488;
RX DOI=10.1128/IAI.168.10.5803-5808.2000;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206026; AAF69324.1; -; mRNA.
DR HSSP; P01665; 1QN2.
DR SMR; Q9JL80; 1-103.
DR Ensembl; ENSMUSG00000053225; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1_1
FT NON_TER 103_103
SQ SEQUENCE 103 AA; 11224 MW; EC87D653DB3AB21 CRC64;

Query Match          90.3%; Score 28; DB 2; Length 103;
Best Local Similarity 85.7%; Pred. No. 79;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNL5 7
Db 46 AASNL5 52

RESULT 15
KVIG_HUMAN
ID KVIG_HUMAN STANDARD; PRT; 108 AA.
AC P01599;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region Gal.
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=75059122; PubMed=4215718;
RA Laure C.J., Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
RT (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
RT kappa-type, subgroup Ia.";
RT Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This chain was isolated from a Waldenström's
CC macroglobulin.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A01867; KIHUGL.
CC HSSP; P01607; LBWW.
CC SMR; P01599; 1-107.
CC GO; GO:0005576; C:extracellular region; NAS.
CC GO; GO:0003823; P:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1_23
FT REGION 24_34
FT REGION 35_49
FT REGION 50_56
FT REGION 57_88
FT REGION 89_97
FT REGION 98_107
FT DISULFID 23_88
FT NON_TER 108_108
SQ SEQUENCE 108 AA; 11814 MW; C1AD3CB0F600FF73 CRC64;

Query Match          90.3%; Score 28; DB 1; Length 108;
Best Local Similarity 85.7%; Pred. No. 84;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNL5 7
Db 50 AASNLQS 56

RESULT 16
Q4QIM4 LEIMA
ID Q4QIM4_LEIMA PRELIMINARY; PRT; 166 AA.
AC Q4QIM4_
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=LmjF07_0670;
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Friedlin;
RA Peacock C.S, Murphy L., Ivens A.C, Berriman M., Blackwell J.;
RA Smith D., Collins M., Fosker N., Harris D., Oliver K., O'Neil S.;
RA Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.

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DR EMBL; CT005246; CAJ07029.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 166 AA; 17847 MW; 0721B8C4E1F2D8CF CRC64;

  Query Match          90.3%; Score 28; DB 2; Length 166;
  Best Local Similarity 85.7%; Pred. No. 1.4e+02;
  Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 43 AASNLOS 49

RESULT 17
ID Q9U2Y4_CABEL PRELIMINARY; PRT; 204 AA.
AC Q9U2Y4;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE Hypothetical protein Y113G7A.14.
OS ORFNames=Y113G7A.14;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; AL132858; CAB60484.1; -; Genomic DNA.
DR Ensembl; Y113G7A.14; Caenorhabditis elegans.
DR WormBase; WBGene00013751; Y113G7A.14.
DR WormPep; Y113G7A.14; CE23283.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 204 AA; 23067 MW; 8968065DF2EA9C7E CRC64;

  Query Match          90.3%; Score 28; DB 2; Length 204;
  Best Local Similarity 85.7%; Pred. No. 1.7e+02;
  Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 134 SASNLES 140

RESULT 18
ID Q9A698_CAUCR PRELIMINARY; PRT; 209 AA.
AC Q9A698;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DE Hypothetical protein CC2196.
OS OrderedLocustNames=CC2196;
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 13089 / CB15;
RX MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
RA Eisen J.A., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Nierman W.C., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,
RA Berry K.J., Uterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
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RA Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
RA Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE005891; AAK24167.1; -; Genomic_DNA.
DR PIR; C87521; C87521.
DR TIGR; CC2196; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 209 AA; 22181 MW; D0200247FF7E9E2D CRC64;

  Query Match          90.3%; Score 28; DB 2; Length 209;
  Best Local Similarity 85.7%; Pred. No. 1.8e+02;
  Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 151 AASNLEA 157

RESULT 19
ID Q701Z5_9CREN PRELIMINARY; PRT; 228 AA.
AC Q701Z5;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS uncultured crenarchaeote.
OC Archaea; Crenarchaeota; environmental samples.
OX NCBI_TaxID=29281;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Treusch A.H., Kletzin A., Raddatz G., Ochsenreiter T., Quaiser A.,
RA Meurer G., Schuster S.C., Schleper C.;
RT "Characterization of Large-Insert DNA Libraries from Soil for
Environmental Genomic Studies of Archaea.";
RL Environ. Microbiol. 9:970-980(2004).
DR EMBL; AJ627421; CAP28729.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 228 AA; 26380 MW; DBD6FCE793855BAA CRC64;

  Query Match          90.3%; Score 28; DB 2; Length 228;
  Best Local Similarity 85.7%; Pred. No. 1.9e+02;
  Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 55 SASNLES 61

RESULT 20
ID Q8U760_AGR75 PRELIMINARY; PRT; 228 AA.
AC Q8U760; Q7CVCS;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Hypothetical protein Atu4594 (AGR L. 563p).
OS OrderedLocustNames=AGR L. 563, Atu4594;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
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RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Neeter E.W.;
 RT "The genome of the natural genetic engineer *Agrobacterium tumefaciens*
 RT C58,";
 RL Science 294:2317-2323(2001).
 RN [2]

RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;

RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Houmlet K., Gordon J., Vaudin M., Tatchouk O., Epp A., Liu F.,
 RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
 RA Flanagan C., Crowell C., Gursun J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 RT *Agrobacterium tumefaciens* C58,";
 RL Science 294:2323-2328(2001).
 DR EMBL; AB009387; AAL45388.1; -; Genomic DNA.
 DR EMBL; AB009228; AAK88951.1; -; Genomic DNA.
 DR PIR; A98166; A98166.
 DR PIR; AF3121; AF3121.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 228 AA; 24816 MW; 4B03E65F8F88A998 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 228;
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 DB 156 AASNLET 162
 |||:|||||

RESULT 21
 Q4NAZ3_9M1CC
 ID Q4NAZ3_9M1CC PRELIMINARY; PRT; 234 AA.
 AC Q4NAZ3;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=ArthDRAFT_0234;
 OS *Arthrobacter* sp. FB24.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Micrococcineae; Micrococcaceae; *Arthrobacter*.
 OX NCBI_TaxID=290399;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FB24;
 RG US DOE Joint Genome Institute (JGI-PGF);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
 RA Hammon N., Israni S., Piluck S., Richardson P.;
 RT "Sequencing of the draft genome assembly of *Arthrobacter* sp. FB24,";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FB24; Genome Institute (PGP-ORNL);
 RG Larimer F., Land M.;
 RA "Annotation of the draft genome assembly of *Arthrobacter* sp. FB24,";
 RT Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; AAR0100026; EAL94496.1; -; Genomic DNA.
 DR EMBL; AAR0100026;
 KW Hypothetical protein.
 SQ SEQUENCE 234 AA; 24889 MW; 79E8F0D08F129ACA CRC64;

Query Match 90.3%; Score 28; DB 2; Length 234;
 Best Local Similarity 85.7%; Pred. No. 2e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 DB 176 AANLES 182
 |||:|||||

RESULT 22
 Q4PKF4_9BACT
 ID Q4PKF4_9BACT PRELIMINARY; PRT; 250 AA.
 AC Q4PKF4;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Proteorhodopsin.
 DE Proteorhodopsins.
 OS uncultured bacterium MedEAC82F10.
 OC Bacteria; environmental samples.
 OX NCBI_TaxID=332272;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RA Sabehi G., Loy A., Jung K.H., Partha R., Spudich J.L., Isaacson T.,
 RA Hirschberg J., Wagner M., Beja O.;
 RT "New Insights into Metabolic Properties of Marine Bacteria Encoding
 RT Proteorhodopsins,";
 RL PLOS Biol. 3:e273-e273(2005).
 DR EMBL; DQ073796; AAY78592.1; -; Genomic DNA.
 DR InterPro; IPR001425; Bac_rhodopsin.
 DR Pfam; PF01036; Bac_rhodopsin; 1.
 DR PROSITE; PS00950; BACTERIAL_OPSIN_1; UNKNOWN 1.
 SQ SEQUENCE 250 AA; 27456 MW; 216112D190DE91A3 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 250;
 Best Local Similarity 85.7%; Pred. No. 2.2e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 DB 21 AANLES 27
 |||:|||||

RESULT 23
 Q5YQH0_NOCPA
 ID Q5YQH0_NOCPA PRELIMINARY; PRT; 289 AA.
 AC Q5YQH0;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=nf47200;
 OS *Nocardia farcinica*.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Nocardaceae; *Nocardia*.
 OX NCBI_TaxID=37329;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=IFM 10152;
 RX PubMed=15466710; DOI=10.1073/pnas.0406410101;
 RA Ishikawa J., Yamashita A., Mikami Y., Hoshino Y., Kurita H., Hotta K.,
 RA Shiba T., Hattori M.;
 RT "The complete genomic sequence of *Nocardia farcinica* IFM 10152,";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).
 DR EMBL; AP006618; BAD59571.1; -; Genomic DNA.
 KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 289 AA; 30105 MW; C03F4CF028534631 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 289;
 Best Local Similarity 85.7%; Pred. No. 2.5e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 DB 42 AASNLS 48
 |||:|||||

RESULT 24

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Q9ATD5_GOSHI PRELIMINARY; PRT; 302 AA.
ID Q9ATD5_GOSHI PRELIMINARY; PRT; 302 AA.
AC Q9ATD5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GHVYB10.
GN Name=ghmyb10;
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Acala Maxxa; TISSUE=Day of anthesis ovule;
RA Matz E.C., Burr B.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DDAJ databases.
CC -1- SURCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AF36282; AAK19615.1; -; mRNA.
DR HSSP; P06876; IMBK.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR001005; MYB DNA bd.
DR Pfam; PF00249; MYB DNA-Binding; 2.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00334; MYB 2; 1.
DR PROSITE; PS00090; MYB 3; 2.
KW Nuclear protein; Repeat.
SQ SEQUENCE 302 AA; 33817 MW; 48BE5D9D921ED2D7 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 302;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLDS 7
| | | | |
DB 286 AASNLQS 292

RESULT 25
VP9_WTV STANDARD; PRT; 313 AA.
ID VP9_WTV
AC P12326;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Structural protein P9 (Capsomere protein P9) (Protein Pns11).
GN Name=S11;
OS Wound tumor virus (WTV).
OC Viruses; dsRNA viruses; Reoviridae; Phytoreovirus.
OX NCBI_TaxID=10987;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC RNA].
RX MEDLINE=89263810; PubMed=2726499;
RA Dall D.J., Anzola J.V., Xu Z., Nuss D.L.;
RT "Complete nucleotide sequence of wound tumor virus genomic segment S11."
RL Nucleic Acids Res. 17:3599-3599(1989).
CC -1- SIMILARITY: Belongs to the phytoreoviruses S11 family.
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CC
CC EMBL; X14219; CAA32439.1; -; Genomic_RNA.
DR PIR; S04139; QMKRW.
DR InterPro; IPR008776; Phyto_Pns9_10.
DR Pfam; PF05878; Phyto_Pns9_10; 1.
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SQ SEQUENCE 313 AA; 35607 MW; 6746P59840AD17F2 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 313;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLDS 7
| | | | |
DB 294 AASNLDS 300

RESULT 26
VP9_WTV STANDARD; PRT; 313 AA.
ID VP9_WTV
AC P31611;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Structural protein P9 (Capsomere protein P9) (Protein Pns11).
OS Wound tumor virus (strain NJ) (WTV).
OC Viruses; dsRNA viruses; Reoviridae; Phytoreovirus.
OX NCBI_TaxID=31595;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENE]
RX MEDLINE=92074261; PubMed=1962460;
RA Hillman B.I., Anzola J.V., Halpern B.T., Cavileer T.D., Nuss D.L.;
RT "First field isolation of wound tumor virus from a plant host: minimal sequence divergence from the type strain isolated from an insect vector."
RL Virology 185:896-900(1991).
CC -1- SIMILARITY: Belongs to the phytoreoviruses S11 family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC
CC EMBL; M77020; AAA48500.1; -; mRNA.
DR PIR; C41705; QMKRW.
DR InterPro; IPR008776; Phyto_Pns9_10.
DR Pfam; PF05878; Phyto_Pns9_10; 1.
SQ SEQUENCE 313 AA; 35552 MW; D9B904785C601C34 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 313;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLDS 7
| | | | |
DB 294 AASNLDS 300

RESULT 27
QSDYJ7_VIBF1 PRELIMINARY; PRT; 362 AA.
ID QSDYJ7_VIBF1 PRELIMINARY; PRT; 362 AA.
AC QSDYJ7;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical membrane spanning protein.
GN OrderedocusNames=VFA1079;
OS Vibrio fischeri (strain ATCC 700601 / ES114).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OX NCBI_TaxID=312309;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15703294; DOI=10.1073/pnas.0409900102;
RA Ruby E.G., Urbanowski M., Campbell J., Dunn A., Faini M., Gunsalus R.,
RA Lostroh P., Lupp C., McCann J., Millikan D., Schaefer A., Stabb E.,
RA Stevens A., Visick K., Whistler C., Greenberg E.P.;
RT "Complete genome sequence of Vibrio fischeri: a symbiotic bacterium
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RT with pathogenic congeners."
RL Proc. Natl. Acad. Sci. U.S.A. 102:3004-3009(2005).
DR EMBL; CP000021; AAW8149.1; -; Genomic_DNA.
DR InterPro; IPR002549; UPF0118.
DR Pfam; PF01594; UPF0118; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 362 AA; 38664 MW; 59943AB0BED91077 CRC64;

Query Match          90.3%; Score 28; DB 2; Length 362;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNL5 7
DB 132 ASSNLS 138

RESULT 28
QBZQV5_STRAW
ID QBZQV5_STRAW PRELIMINARY; PRT; 368 AA.
AC QBZQV5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=SAV390;
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562; DOI=10.1038/nbt820;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RA "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=NA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RA "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
DR EMBL; BA000030; BAC68099.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 368 AA; 39156 MW; B268A4F7DB212E12 CRC64;

Query Match          90.3%; Score 28; DB 2; Length 368;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNL5 7
DB 221 AASNVES 227

RESULT 29
QBYSWI_ANASP
ID QBYSWI_ANASP PRELIMINARY; PRT; 579 AA.
AC QBYSWI;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE All2969 protein.
GN OrderedLocNames=all2969;
OS Anabaena sp. (strain PCC 7120).

OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpō S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; BA000019; BAB74668.1; -; Genomic_DNA.
DR PIR; AB2177; AB2177.
KW Complete proteome.
SQ SEQUENCE 579 AA; 66557 MW; 5C00EBD8CF31BB97 CRC64;

Query Match          90.3%; Score 28; DB 2; Length 579;
Best Local Similarity 85.7%; Pred. No. 5.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNL5 7
DB 378 AASNLDS 384

RESULT 30
FTSH_HELPJ
ID FTSH_HELPJ STANDARD; PRT; 632 AA.
AC Q9ZNM66;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Cell division protein ftsH homolog (EC 3.4.24.-).
GN Name=ftsH; OrderedLocNames=JHP0356;
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deLange B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nikelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Millis S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
CC -!- FUNCTION: Seems to act as an ATP-dependent zinc metallopeptidase
CC (By similarity).
CC -!- COFACTOR: Binds 1 zinc ion (Potential).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: In the N-terminal section; belongs to the AAA ATPase
CC family.
CC -!- SIMILARITY: In the C-terminal section; belongs to the peptidase
CC M41 family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; AE001471; AAD05932.1; -; Genomic_DNA.
DR PIR; D71941; D71941.
DR HSP; O9LCZ4; 11Y0.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003959; AAA_ATPase_cent.
DR InterPro; IPR003960; AAA_sub.
DR InterPro; IPR005936; Pept_M41_FtsH.
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DR InterPro; IPR011546; Pept_M41_FtsH_ex.
 DR InterPro; IPR000642; Peptidase_M41.
 DR Pfam; PF00004; AAA; 1.
 DR Pfam; PF06480; FtsH_ext; 1.
 DR Pfam; PF01434; Peptidase_M41; 1.
 DR SMART; SM00382; AAA; 1.
 DR TIGRFAMs; TIGR01241; FtsH_fam; 1.
 DR PROSITE; PS00674; AAA; 1.
 KW ATP-binding; Cell cycle; Cell division; Complete proteome; Hydrolase;
 KW Metal-binding; Metalloprotease; Nucleotide-binding; Protease;
 KW Transmembrane; Zinc.
 FT TOPO_DOM 1 9 Cytoplasmic (Potential).
 FT TRANSMEM 10 31 Potential.
 FT TOPO_DOM 32 116 Periplasmic (Potential).
 FT TRANSMEM 117 137 Potential.
 FT TOPO_DOM 138 632 Cytoplasmic (Potential).
 FT NP_BIND 210 217 ATP (Potential).
 FT ACT_SITE 435 435 By similarity.
 FT METAL 434 434 Zinc (catalytic) (By similarity).
 FT METAL 438 438 Zinc (catalytic) (By similarity).
 SQ SEQUENCE 632 AA; 69765 MW; 2FB67B43C51559FB CRC64;

Query Match 90.3%; Score 28; DB 1; Length 632;
 Best Local Similarity 85.7%; Pred. No. 6.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLNS 7
 ||:|||||
 Db 616 AANNLES 622

RESULT 31
 Q7RWBI_NEUCR PRELIMINARY; PRT; 701 AA.
 AC Q7RWBI_NEUCR PRELIMINARY;
 DT 01-WAR-2004 (TrEMBLrel. 26, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DE Hypothetical protein (Related to nuclear assembly factor NAF1).
 GN Name=NCU04455.1; Synonyms=G21B4.060;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=OR74A;
 RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
 RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
 RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
 RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
 RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
 RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
 RA Kamal M., Kamysseilis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
 RA Kryotkova S., Raamsen C., Metzberg R.L., Perkins D.D., Kroken S.,
 RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmari S.A.,
 RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
 RA Varden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
 RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
 RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
 RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
 RL Nature 0:0-0(2003).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Schulte U., Algn V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA German Neurospora genome project;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AABX01000782; EAA26677.1; -; Genomic DNA.
 DR EMBL; BX908808; CAF05991.1; -; Genomic DNA.
 DR InterPro; IPR008696; NAF1.
 DR Pfam; PF05492; NAF1; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 701 AA; 75154 MW; 7FF7B9BACC2CF45 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 701;
 Best Local Similarity 85.7%; Pred. No. 6.9e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLNS 7
 ||:|||||
 Db 105 AASNLDLS 111

RESULT 32
 Q51PCS_MAGGR PRELIMINARY; PRT; 747 AA.
 ID Q51PCS_MAGGR PRELIMINARY;
 AC Q51PCS;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=MG00551.4;
 OS Magnaporthe grisea 70-15.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthae.
 OX NCBI_TaxID=242507;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
 RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
 RA Archchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
 RA Bayul T., Blitsheteyn B., Bloom T., Blye J., Boguslavskiy L.,
 RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,
 RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
 RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
 RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
 RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
 RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
 RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
 RA Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
 RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
 RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysseilis M., Karlsson E.,
 RA Kellis C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K.,
 RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
 RA Lindblad-Toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,
 RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
 RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
 RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Menues L.,
 RA Mesirov J., Mihalav A., Mihova T., Mikkelsen T., Mienga V., Moru K.,
 RA Mozes J., Mulrinal L., Munson G., Naylor J., Neues C., Nguyen C.,
 RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
 RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
 RA O'Neill K., Osmari S., Parker S., Perrin D., Phunkhang P., Pigani B.,
 RA Purcell S., Rachupka T., Ramaamy U., Rameau R., Ray V., Raymond C.,
 RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
 RA Rutnan M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
 RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougne C.,
 RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
 RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
 RA Tenzing P., Tesfaye S., Theodore J., Thoulursang Y., Topham K.,
 RA Towey S., Tsamila T., Tsomo N., Vallee D., Vassiliev H.,
 RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
 RA Wangdi T., Whittaker C., Wilkison J., Wu Y., Wyman D., Yadav S.,
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
 RA Zimmer A., Zody M., Lander E.;
 RT "The genome sequence of Magnaporthe grisea.";

RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 [2]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 [3]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=70-15;
 RA Zhu H., Blackmon B.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC -!- COFACTOR: Binds 4 copper ions per monomer (By similarity).
 DR EMBL; AACU01001427; EAA48893.1; -; Genomic_DNA.
 DR InterPro; IPR001117; Cu-oxidase.
 DR InterPro; IPR011706; Cu-oxidase_2.
 DR InterPro; IPR011707; Cu-oxidase_3.
 DR InterPro; IPR023355; Cu-ox_copper_BS.
 DR InterPro; IPR002129; Pyridoxal_deC.
 DR Pfam; PF00394; Cu-oxidase; 1.
 DR Pfam; PF07731; Cu-oxidase; 2; 1.
 DR Pfam; PF07732; Cu-oxidase; 3; 1.
 DR PROSITE; PS00392; DDC_GAD_HDC_YDC; UNKNOWN 1.
 DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
 DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
 KW Copper; Hypothetical protein; Metal-binding; Oxidoreductase; Repeat.
 SQ SEQUENCE 747 AA; 82971 MW; C796B25B74A087BC CRC64;

Query Match 90.3%; Score 28; DB 2; Length 747;
 Best Local Similarity 85.7%; Pred. No. 7.4e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 Db 155 ASSNLES 161
 |:|||||

RESULT 33
 KLP68 DROME
 ID KLP68 DROME STANDARD; PRT; 784 AA.
 AC P46867; Q9VTN8;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Kinesin-like protein KLP68D
 GN Names:KLP68D; Synonyms:KLPF5; ORFNames:CG7293;
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=95050960; PubMed=7525600; DOI=10.1083/jcb.127.4.1041;
 RA Pesavento P.A., Stewart R.J., Goldstein L.S.B.;
 RT "Characterization of the KLP68D kinesin-like protein in Drosophila:
 possible roles in axonal transport.";
 RL J. Cell Biol. 127:1041-1048(1994).
 [2]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Berkely;
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Franknoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen T.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupeki M.P., Smith H.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J., Yao Q.A.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [3]
 RN GENOME REANNOTATION.
 RP MEDLINE=22426069; PubMed=12537572;
 RX Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 [4]
 RN NUCLEOTIDE SEQUENCE OF 220-342.
 RP MEDLINE=92020874; PubMed=1924306;
 RX Stewart R.J., Pesavento P.A., Woerpel D.N., Goldstein L.S.B.;
 RA "Identification and partial characterization of six members of the
 kinesin superfamily in Drosophila.";
 RT Proc. Natl. Acad. Sci. U.S.A. 88:8470-8474(1991).
 CC -!- FUNCTION: Plus-end directed microtubule motor that may be used for
 anterograde axonal transport and could conceivably move cargoes in
 fly neurons different than those moved by kinesin heavy chain or
 other plus-end directed motors.
 CC -!- TISSUE SPECIFICITY: Expressed primarily in the central nervous
 system and in a subset of the peripheral nervous system during
 embryogenesis.
 CC -!- SIMILARITY: Belongs to the kinesin-like protein family. Kinesin II
 subfamily.
 CC -!- SIMILARITY: Contains 1 kinesin-motor domain.
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 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC EMBL; U15974; AAA69929.1; -; mRNA.
 DR EMBL; M74431; AAA28658.1; -; Genomic DNA.
 DR EMBL; AE003543; AAF50008.1; -; Genomic DNA.
 DR PIR; A52336; A55236.
 DR HSSP; F33173; 115S.
 DR Ensembl; FG2293; Drosophila melanogaster.
 DR FlyBase; FBgn0004381; Klp68D.

DR GO; GO:0003774; F: motor activity; IDA.
DR GO; GO:0008089; P: anterograde axon cargo transport; IEPI.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS00667; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Coiled coil; Microtubule; Motor protein;
KW Nucleotide-binding.
KW Nucleotide-binding.

FT DOMAIN 16 275 Kinesin_motor.
FT NP_BIND 106 113 ATP (Potential).
FT COILED 351 385 Potential.
FT COILED 426 582 Potential.
FT CONFLICT 220 221 SS -> TC (in Ref. 4).
FT CONFLICT 338 342 GSRK -> VRQV (in Ref. 4).
FT CONFLICT 338 338 G -> A (in Ref. 2).
SQ SEQUENCE 784 AA; 88193 MW; 94BB9BADF072DFC0 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 784;
Best Local Similarity 85.7%; Pred. No. 7.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||||:
Db 751 AASNLS 757

RESULT 34
Q961H5 DROME PRELIMINARY; PRT; 784 AA.
ID Q961H5; AC Q961H5; DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE GH2307SP.
GN Name=Klp68D; ORFNames=CG7293;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1] NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY051583; AAK93007.1; -; mRNA.
DR HSP; P20480; IN6M.
DR FlyBase; FB00004381; Klp68D.
DR GO; GO:0003774; F: motor activity; IDA.
DR GO; GO:0008089; P: anterograde axon cargo transport; IEPI.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS00667; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
SQ SEQUENCE 784 AA; 88207 MW; 7A3C6716D22BC05D CRC64;

Query Match 90.3%; Score 28; DB 2; Length 784;
Best Local Similarity 85.7%; Pred. No. 7.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||||:
Db 751 AASNLS 757

RESULT 35
RPOB SYNXP STANDARD; PRT; 1097 AA.
ID Q7U8K4;
AC Q7U8K4; DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (RNAP beta subunit) (Transcriptase beta chain) (RNA polymerase beta subunit).
GN Name=rpoB; OrderedLocustNames=SYNW0613;
CN Synecococcus sp. (strain WH8102).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
OX NCBI_TaxID=84586;
RN [1] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;
RA Palenik B., Brahmeha B., Larimer F.W., Land M.L., Hauser L.,
RA Chain P., Lamerdin J.E., Regala W., Allen E.E., McCarran J.,
RA Paulsen I.F., Dufresne A., Partensky F., Webb E.A., Waterbury J.;
RT Nature 424:1037-1042(2003).
RL Nature 424:1037-1042(2003).
CC -!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as substrates.
CC -!- CATALYTIC ACTIVITY: Nucleoside triphosphate + RNA(n) = diphosphate + RNA(n+1).
CC -!- SUBUNIT: In cyanobacteria the RNAP catalytic core is composed of 2 alpha, 1 beta, 1 beta', 1 gamma and 1 omega subunit. When a sigma factor is associated with the core the holoenzyme is formed, which can initiate transcription (By similarity).
CC -!- SIMILARITY: Belongs to the RNA polymerase beta chain family.
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CC EMBL; BX569690; CAE07128.1; -; Genomic_DNA.
DR HAMAP; MF_01321; -; 1.
DR InterPro; IPR007121; RNA_pol_B.
DR InterPro; IPR007644; RNA_pol_Rpb2_1.
DR InterPro; IPR007642; RNA_pol_Rpb2_2.
DR InterPro; IPR007645; RNA_pol_Rpb2_3.
DR InterPro; IPR007120; RNA_pol_Rpb2_6.
DR InterPro; IPR007641; RNA_pol_Rpb2_7.
DR InterPro; IPR010243; RpoB.
DR Pfam; PF04563; RNA_pol_Rpb2_1; 1.
DR Pfam; PF04561; RNA_pol_Rpb2_2; 1.
DR Pfam; PF04565; RNA_pol_Rpb2_3; 1.
DR Pfam; PF00562; RNA_pol_Rpb2_6; 1.
DR Pfam; PF04560; RNA_pol_Rpb2_7; 1.
DR TIGRFAMs; TIGR02013; rpoB; 1.
DR PROSITE; PS01166; RNA_POL_BETA; 1.
KW Complete proteome; DNA-directed RNA polymerase; Nucleotidyltransferase; Transcription; Transferase.
SQ SEQUENCE 1097 AA; 122452 MW; 1FFA1A87DB6079BC CRC64;

Query Match 90.3%; Score 28; DB 1; Length 1097;
Best Local Similarity 85.7%; Pred. No. 1.1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||||:
Db 880 AASNLS 886

RESULT 36
Q6C3I8 YARLI PRELIMINARY; PRT; 1260 AA.
ID Q6C3I8 YARLI PRELIMINARY; PRT; 1260 AA.
AC Q6C3I8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)

```

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similarities with w|NCU06697.1 Neurospora crassa NCU06697.1
DE hypothetical protein.
GN OrderedLocusNames=YALI0E34463g;
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=4952;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrans P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Barovar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolski M., Oztas G.-F., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in Yeasts.";
RL Nature 430:35-44(2004).
DR EMBL; CR382131; CAG80381.1; -; Genomic_DNA.
DR GO; GO:0004519; F:endonuclease activity; IEA.
DR GO; GO:0016787; F:DNA repair; IEA.
DR GO; GO:0006281; P:DNA repair; IEA.
DR InterPro; IPR004843; M-pesterase.
DR Pfam; PF00149; Metallophos; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 1260 AA; 131877 MW; 8A4679A8AC53DFCB CRC64;

Query Match 90.3%; Score 28; DB 2; Length 1260;
Best Local Similarity 85.7%; Pred. No. 1.3e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
DB 1171 AASNLES 1177

RESULT 37
Q60EB9_ORYSA PRELIMINARY; PRT; 73 AA.
AC Q60EB9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Unknown protein.
GN Name=OSNBA0044P19.8;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RT "Oryza sativa BAC OSNBA0044P19 genomic sequence.";
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC135419; AAV25010.1; -; Genomic DNA.
SQ SEQUENCE 73 AA; 8113 MW; 220127E45B8F6A98 CRC64;

Query Match 87.1%; Score 27; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
DB 18 ASNLES 23

RESULT 38
KV1B_HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=72189444; PubMed=5028201;
RA Schiechl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=77022433; PubMed=1234024;
RA Fehlinhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA Schwager P., Steigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the Bence-
RT Jones protein Au.";
RL Biophys. Struct. Mech. 1:139-146(1975).
CC -!- MISCELLANEOUS; The structure of the V region was determined by
CC molecular replacement methods using the known structure of the V
CC region of the kappa chain REI.
CC -!- MISCELLANEOUS; The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS; This is a Bence-Jones protein.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A91653; KIHUAV.
CC PDB; 1JUV5; X-ray; Aa1-107.
CC Ensembl; ENSG00000173782; Homo sapiens.
CC GO; GO:0005576; C:extracellular region; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC SMART; SM00406; Igv; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin domain; Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 34 Complementarity-determining-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Framework-3.
FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
FT STRAND 4 5
FT STRAND 10 13

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 CC removed.

DR PIR; C01937; KVM508.
 DR HSSP; P01665; 1QNZ.
 DR SMR; P01667; 1-111.
 DR Ensembl; ENSMUSG00000053225; Mus musculus.
 DR InterPro; IPR007110; Ig-like.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin domain;
 KW Immunoglobulin V region.
 FT REGION 1 23
 FT REGION 24 38
 FT REGION 24 38
 FT REGION 39 53
 FT REGION 54 60
 FT REGION 54 60
 FT REGION 61 92
 FT REGION 93 101
 FT REGION 102 111
 FT DISULFID 23 92
 FT NON TER 111 111
 SQ SEQUENCE 111 AA; 12071 MW; 7A4AD84D6C256D29 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 111;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
 DB 55 ASNLES 60

RESULT 44

KV3R_MOUSE
 ID KV3R_MOUSE STANDARD; PRT; 111 AA.
 AC P01670;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig kappa chain V-III region PC 6684.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity.";
 RL Nature 276.785-790(1978).

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DR PIR; A01938; KVM584.
 DR HSSP; P01665; 1QNZ.
 DR SMR; P01670; 1-111.
 DR Ensembl; ENSMUSG00000053225; Mus musculus.
 DR InterPro; IPR007110; Ig-like.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin domain;
 KW Immunoglobulin V region.
 FT REGION 1 23
 FT REGION 24 38
 FT REGION 24 38
 FT REGION 39 53
 FT REGION 54 60
 FT REGION 54 60
 FT REGION 61 92
 FT REGION 93 101
 FT REGION 102 111
 FT DISULFID 23 92
 FT NON TER 111 111
 SQ SEQUENCE 111 AA; 12010 MW; F041E89AA7858523 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 111;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
 DB 55 ASNLES 60

FT REGION 39 53
 FT REGION 54 60
 FT REGION 61 92
 FT REGION 93 101
 FT REGION 102 111
 FT DISULFID 23 92
 FT NON TER 111 111
 SQ SEQUENCE 111 AA; 12040 MW; 1E46988341858526 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 111;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
 DB 55 ASNLES 60

RESULT 45

KV3S_MOUSE
 ID KV3S_MOUSE STANDARD; PRT; 111 AA.
 AC P01671;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig kappa chain V-III region PC 7175.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity.";
 RL Nature 276.785-790(1978).

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DR PIR; B01938; KVM575.
 DR HSSP; P01665; 1QNZ.
 DR SMR; P01671; 2-111.
 DR Ensembl; ENSMUSG00000053225; Mus musculus.
 DR InterPro; IPR007110; Ig-like.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin domain;
 KW Immunoglobulin V region.

FT REGION 1 23
 FT REGION 24 38
 FT REGION 39 53
 FT REGION 54 60
 FT REGION 61 92
 FT REGION 93 101
 FT REGION 102 111
 FT DISULFID 23 92
 FT NON TER 111 111
 SQ SEQUENCE 111 AA; 12010 MW; F041E89AA7858523 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 111;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
 DB 55 ASNLES 60

RN NUCLEOTIDE SEQUENCE.
RA Erlandsson A., Holm P., Ullen A., Stigbrand T., Sundstrom B.E.;
RT "Studies of the interactions between the anticytokeratin 8 monoclonal
antibody TSI, its antigen and its anti-idiotypic antibody alphas1.";
RL J. Mol. Recognit. 16:157-163(2003).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RA Erlandsson A.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ880391; CA154295.1; -, mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1 111
SQ SEQUENCE 111 AA; 12198 MW; 65815F785F586E3C CRC64;
Query Match 87.1%; Score 27; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ASNLES 7
DB 55 ASNLES 60
RESULT 48
Q920E9 MOUSE
ID Q920E9 MOUSE PRELIMINARY; PRT; 111 AA.
AC Q920E9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Pterin-mimicking anti-idiotypic kappa chain variable region
DE (Fragment).
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RA Atkin J.D., Ispe A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RN NUCLEOTIDE SEQUENCE.
RX PubMed=2347362;
RA Reininger L., Shibata T., Ozaki S., Shirai T., Jaton J.C., Izui S.;
RT "Variable region sequences of pathogenic anti-mouse red blood cell
autoantibodies from autoimmune NZB mice.";
RL Eur. J. Immunol. 20:771-777(1990).
RN [3]
RN NUCLEOTIDE SEQUENCE.
RX PubMed=7473734;
RA Bossart-Whitaker P., Chang C.Y., Novotny J., Benjamin D.C.,
RA Sheriff S.;
RT "The crystal structure of the antibody N10-staphylococcal nuclease
complex at 2.9 A resolution.";
RL J. Mol. Biol. 253:559-575(1995).
DR EMBL; AF307935; AAL09419.1; -, Genomic_DNA.
DR FIR; PC6027; PC6027.
DR FIR; S09963; S09963.
DR FIR; S59640; S59640.
DR HSP; P01665; IQNZ.
DR SMR; Q920E9; 1-111.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.

RESULT 46
ID Q920E9 MOUSE
ID Q920E9 MOUSE STANDARD; PRT; 111 AA.
AC Q920E9;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-JII region PC 7940.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN PROTEIN SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
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CC removed.
CC -----
DR FIR; C01938; KWS40.
DR HSP; P01665; IQNZ.
DR SMR; P01672; 1-111.
DR Ensembl; ENSMUSG0000053225; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 38
FT REGION 39 53
FT REGION 54 60
FT REGION 61 92
FT REGION 93 101
FT REGION 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12039 MW; EE8A82306084352E CRC64;
Query Match 87.1%; Score 27; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ASNLES 7
DB 55 ASNLES 60
RESULT 47
Q9F217 MOUSE
ID Q9F217 MOUSE PRELIMINARY; PRT; 111 AA.
AC Q9F217;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Kappa light chain variable region (Fragment).
GN Name=IGG1 Ts1 VL;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

```
DR PROSITE, P550835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12046 MW; 1E46988AA6858526 CRC64;

Query Match
Best Local Similarity 87.1%; Score 27; DB 2; Length 111;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
Db 55 ASNLES 60

RESULT 49
KV31 MOUSE
ID KV31 MOUSE STANDARD; PRT; 131 AA.
AC P01661;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region MOPC 63 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE OF 1-35.
RX MEDLINE=78235887; PubMed=98179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to the
RT variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled expression
RT of immunoglobulin genes.";
RL Biochemistry 17:2392-2400(1978).
RN [2]
RP PROTEIN SEQUENCE OF 21-131.
RX MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RT kappa chains with limited sequence differences.";
RL Biochemistry 12:760-771(1973).
RN [3]
RP SEQUENCE REVISION.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; B90412; KVM5M6.
DR HSSP; P01665; 1QN2.
DR SMR; P01661; 21-131.
DR Ensembl; ENSMUSG00000060064; Mus musculus.
DR InterPro; IPR007110; IG-Like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; P550835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 131 Ig kappa chain V-III region MOPC 63.
FT REGION 21 43 Framework-1.
FT REGION 44 58 Complementarity-determining-1.
FT REGION 59 73 Framework-2.
FT REGION 74 80 Complementarity-determining-2.
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FT REGION 81 112 Framework-3.
FT REGION 113 121 Complementarity-determining-3.
FT REGION 122 131 Framework-4.
FT DISULFID 43 112 By similarity.
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;

Query Match
Best Local Similarity 87.1%; Score 27; DB 1; Length 131;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
Db 75 ASNLES 80

RESULT 50
PSS_BACSU
ID PSS_BACSU STANDARD; PRT; 177 AA.
AC P39823;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE CDP-diacylglycerol--serine O-phosphatidyltransferase (EC 2.7.8.8)
DE (Phosphatidylserine synthase).
GN Name=pesA; Synonyms=psse; OrderedLocusNames=BSU02270;
OC Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=168 / Marburg;
RX MEDLINE=95095912; PubMed=8002567;
RA Okada M., Matsuzaki H., Shibuya I., Matsumoto K.;
RT "Cloning, sequencing, and expression in Escherichia coli of the
RT Bacillus subtilis gene for phosphatidylserine synthase.";
RL J. Bacteriol. 176:7456-7461(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=168;
RX MEDLINE=95095912; PubMed=8002567;
RA Okada M., Matsuzaki H., Shibuya I., Matsumoto K.;
RT "Cloning, sequencing, and expression in Escherichia coli of the
RT Bacillus subtilis gene for phosphatidylserine synthase.";
RL J. Bacteriol. 176:7456-7461(1994).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RA Kunst F., Ogasawara N., Mozer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Duysterhoef A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghm S.-Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hulio M.-F., Itaya M.,
RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaer-Blanchard M.,
RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Lazarevic V., Lee S.-M., Levine A., Liu H., Masuda S., Mauel C.,
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Park S.-H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
RA Prescott A.M., Prescan E., Pujic P., Purnelle B., Rapoport G.,
RA Rey M., Reynolds S., Rieger M., Rivoita C., Rocha E., Roche B.,
RA Rose M., Sadale Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Seror P.,
RA Shin B.-S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P.,
RA Tognoni A., Tosato V., Uchiyama S., Vandenberg M., Vannier F.,
```

RA Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
RA Weitzenecker T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zumbstein E.,
RA Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.",
RL Nature 390:249-256(1997).
CC -!- CATALYTIC ACTIVITY: CDP-diacylglycerol + L-serine = CMP + 3-O-sn-
CC phosphatidyl-L-serine.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the CDP-alcohol phosphatidyltransferase
CC class-I family.
CC -----
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CC -----
DR EMBL; D38022; BAA07225.1; -; Genomic DNA.
DR EMBL; AB006424; BAA33124.1; -; Genomic DNA.
DR EMBL; Z99105; CAB12021.1; -; Genomic DNA.
DR PIR; A55537; A55537.
DR Subtilist; BG11012; pssa.
DR InterPro; IPR000462; CDP-OH_P_trans.
DR InterPro; IPR004533; O-phosphatidyl trans.
DR Pfam; PF01066; CDP-OH_P_transf; 1.
DR TIGRFAMs; TIGR00473; pser; 1.
DR PROSITE; PS00379; CDP_ALCOHOL_P_TRANSF; 1.
KW Complete proteome; Phospholipid biosynthesis; Transferase;
KW Transmembrane.
FT TRANSMEM 4 24 Potential.
FT TRANSMEM 28 48 Potential.
FT TRANSMEM 77 97 Potential.
FT TRANSMEM 116 136 Potential.
FT TRANSMEM 140 160 Potential.
SQ SEQUENCE 177 AA; 19613 MW; 55CFDF1F3C18EE8 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 177;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 167 AASNLES 173

Search completed: February 23, 2006, 09:50:10
Job time : 104.308 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 09:29:53 ; Search time 129.231 Seconds
(without alignments)
81.892 Million cell updates/sec

Title: US-10-723-872-16

Perfect score: 79

Sequence: 1 KASQSVYDGDGYMN 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------------|---------------------|
| 1 | 79 | 100.0 | 111 | 1 KV3N MOUSE | P01665 mus musculus |
| 2 | 79 | 100.0 | 111 | 1 KV3M MOUSE | P01666 mus musculus |
| 3 | 79 | 100.0 | 111 | 1 KV3O MOUSE | P01667 mus musculus |
| 4 | 79 | 100.0 | 111 | 1 KV3Q MOUSE | P01668 mus musculus |
| 5 | 76 | 96.2 | 110 | 1 KV3F MOUSE | P01669 mus musculus |
| 6 | 71 | 89.9 | 111 | 2 Q811U6 MOUSE | P01670 mus musculus |
| 7 | 68 | 86.1 | 111 | 1 KV3L MOUSE | P01671 mus musculus |
| 8 | 48 | 60.8 | 282 | 2 Q57HK0 SALCH | P01672 mus musculus |
| 9 | 48 | 60.8 | 282 | 2 Q5PKD6 SALPA | P01673 mus musculus |
| 10 | 48 | 60.8 | 282 | 2 Q822S9 SALTI | P01674 mus musculus |
| 11 | 48 | 60.8 | 282 | 2 Q8ZKU0 SALTI | P01675 mus musculus |
| 12 | 46 | 58.2 | 734 | 2 Q6CWJ5 KLULA | P01676 mus musculus |
| 13 | 45 | 57.0 | 94 | 2 Q81C28 BACCR | P01677 mus musculus |
| 14 | 45 | 57.0 | 111 | 1 KV3C MOUSE | P01678 mus musculus |
| 15 | 45 | 57.0 | 652 | 2 Q4TRC9 9SPHN | P01679 mus musculus |
| 16 | 45 | 57.7 | 294 | 2 Q4PKA4 9BACT | P01680 mus musculus |
| 17 | 44 | 55.7 | 296 | 2 Q6Q940 9GAMM | P01681 mus musculus |
| 18 | 44 | 55.7 | 542 | 2 Q9NJD9 ONCVO | P01682 mus musculus |
| 19 | 44 | 55.7 | 710 | 2 Q6LYG7 METWP | P01683 mus musculus |
| 20 | 44 | 55.7 | 815 | 1 MCL1 SCHPO | P01684 mus musculus |
| 21 | 43 | 54.4 | 137 | 2 P97596 RAT | P01685 mus musculus |
| 22 | 43 | 54.4 | 186 | 2 Q9W2L0 DROME | P01686 mus musculus |
| 23 | 43 | 54.4 | 380 | 2 Q4SMD4 TETNG | P01687 mus musculus |
| 24 | 43 | 54.4 | 551 | 2 P93370 TOBAC | P01688 mus musculus |
| 25 | 43 | 54.4 | 682 | 1 KIF2 XENLA | P01689 mus musculus |
| 26 | 43 | 54.4 | 686 | 2 Q6PF78 XENLA | P01690 mus musculus |
| 27 | 43 | 54.4 | 1841 | 2 Q7XZF5 ARATH | P01691 mus musculus |
| 28 | 43 | 54.4 | 1868 | 2 Q9LVX3 ARATH | P01692 mus musculus |
| 29 | 42 | 53.2 | 111 | 1 KV3A MOUSE | P01693 mus musculus |
| 30 | 42 | 53.2 | 112 | 1 KV3B MOUSE | P01694 mus musculus |
| 31 | 42 | 53.2 | 153 | 2 Q9AQY5 9CHLO | P01695 mus musculus |

| | | | | | | |
|-----|------|------|------|---|---------------|---------------------|
| 32 | 42 | 53.2 | 193 | 2 | Q8G5W1 BIFLO | Q8G5W1 bifidobacte |
| 33 | 42 | 53.2 | 218 | 2 | Q925S1 MOUSE | Q925S1 mus musculu |
| 34 | 42 | 53.2 | 223 | 2 | Q4Z6L2 PLABE | Q4Z6L2 plasmodium |
| 35 | 42 | 53.2 | 270 | 2 | Q728X5 DESVH | Q728X5 desulfovibr |
| 36 | 42 | 53.2 | 303 | 1 | XERC_BACHD | Q9K4Z5 bacillus ha |
| 37 | 42 | 53.2 | 465 | 2 | Q4Q3M6 LEIMA | Q4Q3M6 leishmania |
| 38 | 42 | 53.2 | 587 | 2 | Q7QWA9 HALMA | Q7QWA9 giardia lam |
| 39 | 42 | 53.2 | 653 | 2 | Q5V072 HALMA | Q5V072 haloarcula |
| 40 | 42 | 53.2 | 724 | 2 | Q54S11 DICDI | Q54S11 dictyosteli |
| 41 | 42 | 53.2 | 4034 | 2 | Q7B5J5 GALA | Q7B5J5 giardia lam |
| 42 | 41 | 51.9 | 108 | 1 | KV3V MOUSE | P01674 mus musculu |
| 43 | 41 | 51.9 | 111 | 1 | KV3H MOUSE | P01660 mus musculu |
| 44 | 41 | 51.9 | 111 | 1 | KV3J MOUSE | P01662 mus musculu |
| 45 | 41 | 51.9 | 111 | 1 | KV3K MOUSE | P01663 mus musculu |
| 46 | 41 | 51.9 | 131 | 1 | KV3I MOUSE | P01661 mus musculu |
| 47 | 41 | 51.9 | 156 | 2 | Q87136 VIBPA | Q87136 vibrio para |
| 48 | 41 | 51.9 | 160 | 2 | Q735Z4 BACC1 | Q735Z4 bacillus ce |
| 49 | 41 | 51.9 | 168 | 1 | NUDT3 MOUSE | Q9J146 mus musculu |
| 50 | 41 | 51.9 | 168 | 1 | NUDT3 RAT | Q565C7 rattus norv |
| 51 | 41 | 51.9 | 172 | 1 | NUDT3 HUMAN | Q95989 homo sapien |
| 52 | 41 | 51.9 | 179 | 2 | Q5AJC2 BRARE | Q5AJC2 brachydanio |
| 53 | 41 | 51.9 | 180 | 2 | Q5IK11 9VIRU | Q5IK11 uncultured |
| 54 | 41 | 51.9 | 195 | 2 | Q5DCX7 SCHJA | Q5DCX7 schistosoma |
| 55 | 41 | 51.9 | 203 | 2 | Q4RIE4 TETNG | Q4RIE4 tetraodon n |
| 56 | 41 | 51.9 | 208 | 2 | Q4TGN3 TETNG | Q4TGN3 tetraodon n |
| 57 | 41 | 51.9 | 210 | 2 | Q6LG66 PHOPR | Q6LG66 photobacter |
| 58 | 41 | 51.9 | 229 | 2 | Q4SSC2 TETNG | Q4SSC2 tetraodon n |
| 59 | 41 | 51.9 | 335 | 2 | Q4ZN79 PSESJ | Q4ZN79 pseudomonas |
| 60 | 41 | 51.9 | 335 | 2 | Q87VW2 PSESJ | Q87VW2 pseudomonas |
| 61 | 41 | 51.9 | 336 | 2 | Q9X6V5 PSEAE | Q9X6V5 pseudomonas |
| 62 | 41 | 51.9 | 336 | 2 | Q4K5G5 PSEAF5 | Q4K5G5 pseudomonas |
| 63 | 41 | 51.9 | 340 | 2 | Q9HX24 PSEAF5 | Q9HX24 pseudomonas |
| 64 | 41 | 51.9 | 348 | 2 | Q88DM0 PSEPK | Q88DM0 pseudomonas |
| 65 | 41 | 51.9 | 357 | 2 | Q822P3 ENTFA | Q822P3 enterococcu |
| 66 | 41 | 51.9 | 459 | 1 | CMWH_HAEIN | P46458 haemophilus |
| 67 | 41 | 51.9 | 575 | 2 | Q7PZK9 ANOGA | Q7PZK9 anopheles g |
| 68 | 41 | 51.9 | 692 | 2 | Q8DVA0 STRMU | Q8DVA0 streptococc |
| 69 | 41 | 51.9 | 877 | 2 | Q6FWJ3 CANGA | Q6FWJ3 candida gla |
| 70 | 41 | 51.9 | 882 | 2 | Q5ZJ70 CHICK | Q5ZJ70 gallus gall |
| 71 | 41 | 51.9 | 1165 | 2 | Q57YB5 9TRYR | Q57YB5 trypanosoma |
| 72 | 41 | 51.9 | 1173 | 2 | Q4N2G1 THEPA | Q4N2G1 theileria p |
| 73 | 41 | 51.9 | 1364 | 2 | Q6SLE1 COCHE | Q6SLE1 cochlidiobol |
| 74 | 41 | 51.9 | 1378 | 2 | Q4N1P0 THEPA | Q4N1P0 theileria p |
| 75 | 41 | 51.9 | 1843 | 2 | Q4QFW2 LEIMA | Q4QFW2 leishmania |
| 76 | 41 | 51.9 | 3300 | 2 | Q4N127 THEPA | Q4N127 theileria p |
| 77 | 40.5 | 51.3 | 1313 | 2 | Q8IKC0 PLAP7 | Q8IKC0 plasmodium |
| 78 | 40 | 50.6 | 112 | 1 | KV3G MOUSE | P01659 mus musculu |
| 79 | 40 | 50.6 | 131 | 1 | CALL2 ARATH | Q9SRP5 arabidopsis |
| 80 | 40 | 50.6 | 137 | 2 | Q9SRP4 ARATH | Q9SRP4 arabidopsis |
| 81 | 40 | 50.6 | 154 | 2 | Q27163 METTH | Q27163 methanobact |
| 82 | 40 | 50.6 | 171 | 1 | ALL8 OLEU | Q9M7R0 olea europa |
| 83 | 40 | 50.6 | 176 | 2 | Q427L1 SCHPO | Q427L1 schizosacch |
| 84 | 40 | 50.6 | 197 | 1 | Y3235_RHIME | Q92150 rhizobium m |
| 85 | 40 | 50.6 | 204 | 2 | Q5BJW1 RAT | Q5BJW1 rattus norv |
| 86 | 40 | 50.6 | 247 | 2 | Q9WV63 RAT | Q9WV63 rattus norv |
| 87 | 40 | 50.6 | 292 | 2 | Q5XG61 XENLA | Q5XG61 xenopus lae |
| 88 | 40 | 50.6 | 311 | 2 | Q86071 PSESX | Q86071 pseudomonas |
| 89 | 40 | 50.6 | 364 | 2 | Q4S8G0 TETNG | Q4S8G0 tetraodon n |
| 90 | 40 | 50.6 | 369 | 2 | Q5V5A5 HALMA | Q5V5A5 haloarcula |
| 91 | 40 | 50.6 | 397 | 2 | Q4NGC1 9MICC | Q4NGC1 arthrobacte |
| 92 | 40 | 50.6 | 408 | 2 | Q514X7 ENTHI | Q514X7 entamoeba h |
| 93 | 40 | 50.6 | 420 | 2 | Q9SIV3 ARATH | Q9SIV3 arabidopsis |
| 94 | 40 | 50.6 | 435 | 1 | VE2 BPV6 | Q9S1F3 bovine papi |
| 95 | 40 | 50.6 | 478 | 2 | Q52GD0 MAGGR | Q52GD0 magnaporthe |
| 96 | 40 | 50.6 | 509 | 2 | Q7Z5I3 HUMAN | Q7Z5I3 homo sapien |
| 97 | 40 | 50.6 | 520 | 2 | Q4I309 GIBBEZ | Q4I309 gibberella |
| 98 | 40 | 50.6 | 547 | 2 | Q82S62 NITEU | Q82S62 nitrosomona |
| 99 | 40 | 50.6 | 568 | 2 | Q524M2 MAGGR | Q524M2 magnaporthe |
| 100 | 40 | 50.6 | 590 | 2 | Q4XQ57 PLACH | Q4XQ57 plasmodium |
| 101 | 40 | 50.6 | 602 | 2 | Q5ZL76 CHICK | Q5ZL76 gallus gall |
| 102 | 40 | 50.6 | 610 | 1 | TIP MOUSE | Q99KW9 mus musculu |
| 103 | 40 | 50.6 | 610 | 1 | TIP RAT | Q8R4E1 rattus norv |
| 104 | 40 | 50.6 | 610 | 2 | Q5U355 RAT | Q5U355 rattus norv |

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| 105 | 40 | 50.6 | 612 | 1 | TIP HUMAN | Q8tb96 homo sapien | 178 | 38 | 48.1 | 102 | 2 | Q5RH17_BRARE | Q5rhi7 brachydanio |
| 106 | 40 | 50.6 | 612 | 2 | Q5R918_PONPY | Q5r918 pongo pygma | 179 | 38 | 48.1 | 102 | 2 | Q5SNV3_BRARE | Q5snv3 brachydanio |
| 107 | 40 | 50.6 | 612 | 2 | Q7RD52_PONPY | Q7rd52 pongo pygma | 180 | 38 | 48.1 | 104 | 2 | Q5O2E5_BRARE | Q5oze5 brachydanio |
| 108 | 40 | 50.6 | 646 | 2 | Q76Y15_9CAUD | Q76y15 bacterioph | 181 | 38 | 48.1 | 108 | 2 | Q8RU21_GLYSO | Q8ru21 glycine bof |
| 109 | 40 | 50.6 | 659 | 2 | Q54744_MOUSE | Q54744 mus musculu | 182 | 38 | 48.1 | 123 | 1 | YI31_CABEL | Q8r196 caenorhabdi |
| 110 | 40 | 50.6 | 662 | 2 | Q6GPC7_XENLA | Q6gpc7 xenopus lae | 183 | 38 | 48.1 | 126 | 1 | Q61A33_CAEBR | Q61a33 caenorhabdi |
| 111 | 40 | 50.6 | 678 | 2 | Q91W03_MOUSE | Q91w03 mus musculu | 184 | 38 | 48.1 | 130 | 2 | Q9M168_DROME | Q9m168 drosophila |
| 112 | 40 | 50.6 | 679 | 1 | K1F2_HUMAN | Q00139 homo sapien | 185 | 38 | 48.1 | 134 | 2 | Q8EJAO_SHEON | Q8eja0 shewanella |
| 113 | 40 | 50.6 | 679 | 2 | Q5ZKV8_CHICK | Q5zkv8 gallus galli | 186 | 38 | 48.1 | 143 | 2 | Q8QJAO_SHEON | Q8qja0 shewanella |
| 114 | 40 | 50.6 | 696 | 2 | Q8X542_ECO57 | Q8x542 escherichia | 187 | 38 | 48.1 | 149 | 2 | Q6S7N3_9PTOT | Q6s7n3 theileria p |
| 115 | 40 | 50.6 | 712 | 1 | K1F2_MOUSE | P28740 mus musculu | 188 | 38 | 48.1 | 165 | 2 | Q4TE92_TETNG | Q4te92 tetraodon n |
| 116 | 40 | 50.6 | 744 | 2 | Q5R9Y9_PONPY | Q5r9y9 pongo pygma | 189 | 38 | 48.1 | 167 | 1 | ATPQ_ARATH | Q8ft52 arabidopsis |
| 117 | 40 | 50.6 | 808 | 2 | Q9SM62_ARATH | Q9sm62 arabidopsis | 190 | 38 | 48.1 | 186 | 2 | Q9FYK2_ARATH | Q9fyk2 arabidopsis |
| 118 | 40 | 50.6 | 910 | 2 | Q8ILN7_PLAF7 | Q8iln7 plasmodium | 191 | 38 | 48.1 | 229 | 2 | Q6ZK11_ORISA | Q6zkl1 oryza sativ |
| 119 | 40 | 50.6 | 921 | 2 | Q9FH44_ARATH | Q9fh44 arabidopsis | 192 | 38 | 48.1 | 230 | 1 | DAG_ANTMA | Q8b732 antirrhinum |
| 120 | 40 | 50.6 | 984 | 2 | Q8QS29_9BETA | Q8qs29 pongine her | 193 | 38 | 48.1 | 232 | 2 | Q8LB30_ARATH | Q8lb30 arabidopsis |
| 121 | 40 | 50.6 | 1338 | 2 | Q4UAU1_THEAN | Q4uau1 theileria a | 194 | 38 | 48.1 | 232 | 2 | Q9LP21_ARATH | Q9lp21 arabidopsis |
| 122 | 40 | 50.6 | 1416 | 2 | Q6BYK5_DEBHA | Q6byk5 debaryomyce | 195 | 38 | 48.1 | 235 | 2 | Q8L704_ARATH | Q8l704 arabidopsis |
| 123 | 40 | 50.6 | 2267 | 2 | Q9VMS2_DROME | Q9vms2 drosophila | 196 | 38 | 48.1 | 243 | 1 | LPS1B_LYTP1 | Q03975 lytechinus |
| 124 | 39.5 | 50.0 | 86 | 2 | Q7Z3Y5_HUMAN | Q7z3y5 homo sapien | 197 | 38 | 48.1 | 260 | 1 | CALBI_BOVIN | P04467 bos taurus |
| 125 | 39.5 | 50.0 | 133 | 1 | KV2F_HUMAN | P03310 homo sapien | 198 | 38 | 48.1 | 264 | 2 | Q9HKKO_PSEAE | Q9hkk0 pseudomonas |
| 126 | 39 | 49.4 | 57 | 2 | Q5UYL4_HALMA | Q5uyl4 haloarcula | 199 | 38 | 48.1 | 272 | 1 | TYPH_MYCHO | P43050 mycoplasma |
| 127 | 39 | 49.4 | 94 | 2 | Q6EH09_9ENTE | Q6eh09 vagococcus | 200 | 38 | 48.1 | 273 | 2 | Q5ACQ4_CANAL | Q5acq4 candida alb |
| 128 | 39 | 49.4 | 103 | 2 | Q9JL80_MOUSE | Q9jl80 mus musculu | 201 | 38 | 48.1 | 291 | 2 | Q20991_CAEL | Q20991 caenorhabdi |
| 129 | 39 | 49.4 | 108 | 2 | Q8ELX9_STRAS | Q8elx9 streptococc | 202 | 38 | 48.1 | 294 | 2 | Q9KY55_STRCO | Q9ky55 streptomyce |
| 130 | 39 | 49.4 | 196 | 2 | Q94MM9_9VIRU | Q94mm9 cyanophage | 203 | 38 | 48.1 | 296 | 2 | Q9MZ46_PIG | Q9mz46 sus scrofa |
| 131 | 39 | 49.4 | 199 | 2 | Q7QUR8_GIALA | Q7qur8 giardia lam | 204 | 38 | 48.1 | 305 | 2 | Q74ZU9_ASHGO | Q74zu9 ashya goos |
| 132 | 39 | 49.4 | 200 | 2 | Q9AER3_SERMA | Q9aer3 serratia ma | 205 | 38 | 48.1 | 305 | 2 | Q569B9_RAT | Q569b9 rattus norv |
| 133 | 39 | 49.4 | 209 | 2 | Q738G6_BACCI | Q738g6 bacillus ce | 206 | 38 | 48.1 | 315 | 1 | CALU_HUMAN | O43852 homo sapien |
| 134 | 39 | 49.4 | 209 | 2 | Q81QM7_BACAN | Q81qm7 bacillus ce | 207 | 38 | 48.1 | 315 | 1 | Q61AW5_HUMAN | Q61aw5 homo sapien |
| 135 | 39 | 49.4 | 262 | 2 | Q05432_BOMMO | Q05432 bombyx mori | 208 | 38 | 48.1 | 315 | 2 | Q5RDD8_PONPY | Q5rdd8 pongo pygma |
| 136 | 39 | 49.4 | 276 | 2 | Q9HRR1_HALSA | Q9hrr1 halobacteri | 209 | 38 | 48.1 | 315 | 2 | Q6XLQ6_RABIT | Q6x1q6 oryctolagus |
| 137 | 39 | 49.4 | 281 | 2 | Q7UFQ7_RHOBA | Q7ufq7 rhodopirell | 210 | 38 | 48.1 | 321 | 2 | Q6XLQ7_RABIT | Q6x1q7 oryctolagus |
| 138 | 39 | 49.4 | 334 | 1 | VE2_BPV4 | P03345 bovine papi | 211 | 38 | 48.1 | 321 | 1 | LPS1A_LYTP1 | P09485 lytechinus |
| 139 | 39 | 49.4 | 345 | 2 | Q5QWP7_IDILO | Q5qwp7 idiomarina | 212 | 38 | 48.1 | 330 | 2 | Q9JUS3_NEIMA | Q9ju53 neisseria m |
| 140 | 39 | 49.4 | 349 | 2 | Q9FNE9_ARATH | Q9fne9 arabidopsis | 213 | 38 | 48.1 | 332 | 2 | Q54CX8_DICDI | Q54cx8 dictyosteli |
| 141 | 39 | 49.4 | 409 | 1 | THI1_PANTH | P45741 paenibacilli | 214 | 38 | 48.1 | 345 | 2 | O4LKV2_BURK | O4lkv2 burkholderi |
| 142 | 39 | 49.4 | 421 | 2 | Q88T48_LACPL | Q88t48 lactobacilli | 215 | 38 | 48.1 | 359 | 2 | O64560_ARATH | O64560 arabidopsis |
| 143 | 39 | 49.4 | 445 | 2 | Q9AMT8_BRAJA | Q9amt8 bradyrhizob | 216 | 38 | 48.1 | 363 | 2 | Q5F8Y3_NEIG1 | Q5f8y3 neisseria g |
| 144 | 39 | 49.4 | 479 | 2 | Q6VAB3_STERE | Q6vab3 stervia reba | 217 | 38 | 48.1 | 368 | 2 | Q9KQP7_VIBCH | Q9kqp7 vibrio chol |
| 145 | 39 | 49.4 | 492 | 2 | Q65D73_BACLD | Q65d73 bacillus li | 218 | 38 | 48.1 | 369 | 1 | VE2_HPV66 | Q90958 human papil |
| 146 | 39 | 49.4 | 494 | 2 | Q27482_CAEL | Q27482 caenorhabdi | 219 | 38 | 48.1 | 369 | 2 | Q9JZ59_NEIMB | Q9jz59 neisseria m |
| 147 | 39 | 49.4 | 502 | 2 | Q7XKG0_ORISA | Q7xkg0 oryza sativ | 220 | 38 | 48.1 | 371 | 2 | Q705H7_HPV43 | Q705h7 human papil |
| 148 | 39 | 49.4 | 503 | 2 | Q9NA84_CAEL | Q9na84 caenorhabdi | 221 | 38 | 48.1 | 374 | 2 | Q8JL46_9CAUD | Q8jl46 virus phich |
| 149 | 39 | 49.4 | 522 | 2 | Q59740_SCHPO | Q59740 schizosacch | 222 | 38 | 48.1 | 379 | 2 | Q9M7R4_PATR | Q9m7r4 phaodactyl |
| 150 | 39 | 49.4 | 576 | 2 | Q6NWX4_MOUSE | Q6nwx4 mus musculu | 223 | 38 | 48.1 | 400 | 2 | Q924A1_92ZZ2 | Q924a1 plasmid col |
| 151 | 39 | 49.4 | 594 | 2 | Q55GP7_DICDI | Q55gp7 dictyosteli | 224 | 38 | 48.1 | 400 | 2 | Q79VS9_SALTY | Q79vs9 salmonella |
| 152 | 39 | 49.4 | 596 | 2 | Q54KT5_DICDI | Q54kt5 dictyosteli | 225 | 38 | 48.1 | 400 | 2 | Q9R2H5_92ZZ2 | Q9r2h5 plasmid t64 |
| 153 | 39 | 49.4 | 638 | 1 | PDI4_MOUSE | P08003 mus musculu | 226 | 38 | 48.1 | 400 | 2 | O4FIG8_9ENTR | O4fig8 salmonella |
| 154 | 39 | 49.4 | 641 | 2 | Q8BMT6_MOUSE | Q8bmt6 mus musculu | 227 | 38 | 48.1 | 402 | 2 | Q5ECH9_9RHOB | Q5ech9 ruergeria sp |
| 155 | 39 | 49.4 | 643 | 1 | PDI4_RAT | P38659 rattus norv | 228 | 38 | 48.1 | 405 | 2 | Q6UYH7_9CAUD | Q6uyh7 burkholderi |
| 156 | 39 | 49.4 | 643 | 2 | Q6P7S5_RAT | Q6p7s5 rattus norv | 229 | 38 | 48.1 | 407 | 1 | YKR5_CAEL | P34311 caenorhabdi |
| 157 | 39 | 49.4 | 744 | 2 | Q7QH84_ANOGA | Q7qh84 anopheles g | 230 | 38 | 48.1 | 411 | 2 | Q8C1F6_MOUSE | Q8c1f6 mus musculu |
| 158 | 39 | 49.4 | 746 | 2 | Q6FTT2_CANGA | Q6ftt2 candida gla | 231 | 38 | 48.1 | 411 | 2 | Q7TST5_MOUSE | Q7tst5 mus musculu |
| 159 | 39 | 49.4 | 784 | 2 | Q9ZT62_CUCSA | Q9zt62 cucumis sat | 232 | 38 | 48.1 | 428 | 2 | Q887K0_PSESM | Q887k0 pseudomonas |
| 160 | 39 | 49.4 | 814 | 2 | Q4TLI5_9SPHN | Q4tli5 erythrobact | 233 | 38 | 48.1 | 430 | 2 | Q4NZR4_9DELT | Q4nizr4 anaeromyxob |
| 161 | 39 | 49.4 | 840 | 2 | Q6FVD3_CANGA | Q6fvd3 candida gla | 234 | 38 | 48.1 | 434 | 2 | Q5R3Y5_CAEL | Q5r3y5 caenorhabdi |
| 162 | 39 | 49.4 | 869 | 2 | Q74527_SYNY3 | P74527 synechocyst | 235 | 38 | 48.1 | 438 | 2 | Q6N5P6_RHOP | Q6n5p6 rhodopseudo |
| 163 | 39 | 49.4 | 918 | 2 | P7PDU3_PLAYO | Q7pdu3 plasmodium | 236 | 38 | 48.1 | 449 | 2 | Q9SK03_ARATH | Q9sk03 arabidopsis |
| 164 | 39 | 49.4 | 1046 | 2 | Q7SB49_NEUCR | Q7sb49 neurospora | 237 | 38 | 48.1 | 452 | 2 | Q6N1K9_RHOP | Q6n1k9 rhodopseudo |
| 165 | 39 | 49.4 | 1475 | 2 | Q8Y8V4_LISMO | Q8y8v4 listeria mo | 238 | 38 | 48.1 | 458 | 2 | P91079_CAEL | P91079 caenorhabdi |
| 166 | 39 | 49.4 | 1476 | 2 | Q722D0_LISMF | Q722d0 listeria mo | 239 | 38 | 48.1 | 474 | 2 | Q9M3F5_ARATH | Q9m3f5 arabidopsis |
| 167 | 39 | 49.4 | 1895 | 2 | Q74BK3_GEOSL | Q74bk3 geobacter s | 240 | 38 | 48.1 | 477 | 2 | Q510J1_RAT | Q510j1 rattus norv |
| 168 | 39 | 49.4 | 2134 | 2 | Q815M6_PLAF7 | Q815m6 plasmodium | 241 | 38 | 48.1 | 481 | 2 | Q9XTQ3_CAEBR | Q9xtq3 caenorhabdi |
| 169 | 39 | 49.4 | 2735 | 2 | Q5A469_CANAL | Q5a469 candida alb | 242 | 38 | 48.1 | 485 | 1 | PD11_CAEL | Q17967 caenorhabdi |
| 170 | 39 | 49.4 | 2735 | 2 | Q5A4C1_CANAL | Q5a4c1 candida alb | 243 | 38 | 48.1 | 485 | 2 | Q8A292_BACTN | Q8a292 bacteroides |
| 171 | 38.5 | 48.7 | 75 | 1 | LSM6_SCHPO | Q9nuil schizosacch | 244 | 38 | 48.1 | 499 | 2 | Q7T1M2_ORYLA | Q7t1m2 oryzias lat |
| 172 | 38 | 48.1 | 83 | 1 | IBBD2_SOYBN | P01064 glycine max | 245 | 38 | 48.1 | 512 | 1 | VC02_RABPU | Q6r283 rabbitpox v |
| 173 | 38 | 48.1 | 87 | 2 | Q1GDD0_NPVEP | Q1gdd0 epiphyas po | 246 | 38 | 48.1 | 512 | 1 | VC02_VACCC | P21037 vaccinia vi |
| 174 | 38 | 48.1 | 87 | 2 | Q6VTK3_NPVCD | Q6vtk3 choristoneu | 247 | 38 | 48.1 | 512 | 1 | VC02_VACCV | Q17f91 vaccinia vi |
| 175 | 38 | 48.1 | 94 | 1 | CH10_TETHA | Q93gt7 tetragenoco | 248 | 38 | 48.1 | 512 | 1 | VC02_VACCV | P17371 vaccinia vi |
| 176 | 38 | 48.1 | 96 | 2 | Q7UT70_RHOBA | Q7ut70 rhodopirell | 249 | 38 | 48.1 | 512 | 2 | Q8QN27_COWPX | Q8qn27 cowpox viru |
| 177 | 38 | 48.1 | 102 | 2 | Q43709_SOYBN | Q43709 glycine max | 250 | 38 | 48.1 | 514 | 2 | Q4YV50_PLABE | Q4yv50 plasmodium |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|--------------|--------------------|-----|----|------|-----|---|--------------|--------------------|
| 835 | 35 | 44.3 | 80 | 2 | Q8D9R3_VIBVU | Q8d9r3 vibrio vuln | 908 | 35 | 44.3 | 203 | 2 | Q7R956_PLAYO | Q7r956 plasmodium |
| 836 | 35 | 44.3 | 87 | 2 | Q63F62_BACCZ | Q63f62 bacillus ce | 909 | 35 | 44.3 | 203 | 2 | Q4X7U6_PLACH | Q4x7u6 plasmodium |
| 837 | 35 | 44.3 | 88 | 2 | Q50956_NEIGO | Q50956 neisseria g | 910 | 35 | 44.3 | 204 | 2 | Q5CUB8_CRYPV | Q5cub8 cryptospori |
| 838 | 35 | 44.3 | 95 | 2 | Q50958_NEIGO | Q50958 neisseria g | 911 | 35 | 44.3 | 207 | 2 | Q9GQ38_HUMAN | Q9gq38 homo sapien |
| 839 | 35 | 44.3 | 95 | 2 | Q5UWU3_HALMA | Q5uwu3 haloarcula | 912 | 35 | 44.3 | 210 | 2 | Q6RZU7_MUSAC | Q6rzu7 mus acumin |
| 840 | 35 | 44.3 | 96 | 2 | Q50953_NEIGO | Q50953 neisseria g | 913 | 35 | 44.3 | 214 | 2 | Q8MTC2_LEUMA | Q8mtc2 leucophaea |
| 841 | 35 | 44.3 | 98 | 2 | Q6N714_RHOFA | Q6n714 rhodopseudo | 914 | 35 | 44.3 | 217 | 1 | B10S_RHIME | B10s rhizobium m |
| 842 | 35 | 44.3 | 100 | 2 | Q5Y518_STRPN | Q5y518 streptococc | 915 | 35 | 44.3 | 217 | 1 | B10S_RHIME | B10s rhizobium m |
| 843 | 35 | 44.3 | 108 | 2 | Q6G726_STAAS | Q6g726 staphylococ | 916 | 35 | 44.3 | 219 | 2 | Q5EAV5_XENLA | Q5eav5 xenopus lae |
| 844 | 35 | 44.3 | 108 | 2 | Q6GED8_STAAS | Q6ged8 staphylococ | 917 | 35 | 44.3 | 220 | 2 | Q5VEL7_DROMI | Q5vel7 xenopus lae |
| 845 | 35 | 44.3 | 108 | 2 | Q5HDR2_STAAC | Q5hdr2 staphylococ | 918 | 35 | 44.3 | 226 | 2 | Q4J8J0_SULAC | Q4j8j0 sulfolobus |
| 846 | 35 | 44.3 | 108 | 2 | Q7A424_STAAN | Q7a424 staphylococ | 919 | 35 | 44.3 | 230 | 1 | H1S4_SULTO | H1s4 sulfolobus |
| 847 | 35 | 44.3 | 108 | 2 | Q8NV86_STAAN | Q8nv86 staphylococ | 920 | 35 | 44.3 | 232 | 2 | Q6W5M8_9BRAD | Q6w5m8 apifia broo |
| 848 | 35 | 44.3 | 108 | 2 | Q99RX7_STAAM | Q99rx7 staphylococ | 921 | 35 | 44.3 | 232 | 2 | Q4J2N1_AZQVI | Q4j2n1 azotobacter |
| 849 | 35 | 44.3 | 112 | 2 | Q8T343_PLAFA | Q8t343 plasmodium | 922 | 35 | 44.3 | 233 | 2 | Q6CK58_KLULA | Q6ck58 kluyveromyc |
| 850 | 35 | 44.3 | 113 | 2 | Q9PIH0_HUMAN | Q9pih0 homo sapien | 923 | 35 | 44.3 | 233 | 2 | Q4FZT3_RAT | Q4fzt3 rattus norv |
| 851 | 35 | 44.3 | 114 | 2 | Q8T511_PLAFA | Q8t511 plasmodium | 924 | 35 | 44.3 | 235 | 1 | ICLN_CANFA | ICln canis famil |
| 852 | 35 | 44.3 | 114 | 2 | Q9MFE4_BETVU | Q9mfe4 beta vulgar | 925 | 35 | 44.3 | 236 | 1 | ICLN_MOUSE | ICln mus musculu |
| 853 | 35 | 44.3 | 118 | 2 | Q5WDJ6_BACSK | Q5wdj6 bacillus cl | 926 | 35 | 44.3 | 236 | 1 | ICLN_MOUSE | ICln mus musculu |
| 854 | 35 | 44.3 | 127 | 2 | Q6NYP2_BRARE | Q6nyp2 brachydanio | 927 | 35 | 44.3 | 236 | 1 | ICLN_MOUSE | ICln mus musculu |
| 855 | 35 | 44.3 | 129 | 1 | HEMTL_CLOB | Q97mx1 clostridium | 928 | 35 | 44.3 | 237 | 1 | ICLN_MOUSE | ICln mus musculu |
| 856 | 35 | 44.3 | 131 | 1 | FABP2_MANG | P31417 manduca sex | 929 | 35 | 44.3 | 237 | 1 | ICLN_MOUSE | ICln mus musculu |
| 857 | 35 | 44.3 | 134 | 2 | Q7PH17_ANOGA | Q7ph17 anopheles g | 930 | 35 | 44.3 | 238 | 1 | ICLN_MOUSE | ICln mus musculu |
| 858 | 35 | 44.3 | 138 | 2 | Q6W6P1_BRARE | Q6w6p1 brachydanio | 931 | 35 | 44.3 | 238 | 1 | ICLN_MOUSE | ICln mus musculu |
| 859 | 35 | 44.3 | 141 | 2 | Q8LM72_BACAN | Q8lm72 bacillus an | 932 | 35 | 44.3 | 238 | 2 | ICLN_MOUSE | ICln mus musculu |
| 860 | 35 | 44.3 | 142 | 2 | Q5R8R8_PONPY | Q5r8r8 pongo pygma | 933 | 35 | 44.3 | 238 | 2 | ICLN_MOUSE | ICln mus musculu |
| 861 | 35 | 44.3 | 144 | 2 | Q682K9_ARATH | Q682k9 arabidopsis | 934 | 35 | 44.3 | 238 | 2 | ICLN_MOUSE | ICln mus musculu |
| 862 | 35 | 44.3 | 144 | 2 | Q9LEZ1_ARATH | Q9lez1 arabidopsis | 935 | 35 | 44.3 | 239 | 2 | ICLN_MOUSE | ICln mus musculu |
| 863 | 35 | 44.3 | 144 | 2 | Q5HWR9_CAMJR | Q5hwr9 campylobact | 936 | 35 | 44.3 | 241 | 1 | ICLN_MOUSE | ICln mus musculu |
| 864 | 35 | 44.3 | 149 | 2 | Q9AU03_CHLRE | Q9au03 campylobact | 937 | 35 | 44.3 | 241 | 1 | ICLN_MOUSE | ICln mus musculu |
| 865 | 35 | 44.3 | 150 | 2 | Q5ENP3_HETTR | Q5enp3 heterocapsa | 938 | 35 | 44.3 | 243 | 2 | ICLN_MOUSE | ICln mus musculu |
| 866 | 35 | 44.3 | 150 | 2 | Q9LNE7_ARATH | Q9lne7 arabidopsis | 939 | 35 | 44.3 | 243 | 2 | ICLN_MOUSE | ICln mus musculu |
| 867 | 35 | 44.3 | 151 | 2 | P72503_STRPN | P72503 streptococc | 940 | 35 | 44.3 | 244 | 1 | ICLN_MOUSE | ICln mus musculu |
| 868 | 35 | 44.3 | 152 | 2 | Q9SU00_ARATH | Q9su00 arabidopsis | 941 | 35 | 44.3 | 244 | 1 | ICLN_MOUSE | ICln mus musculu |
| 869 | 35 | 44.3 | 152 | 2 | Q8GJE0_CAMJE | Q8gje0 campylobact | 942 | 35 | 44.3 | 245 | 2 | ICLN_MOUSE | ICln mus musculu |
| 870 | 35 | 44.3 | 153 | 2 | Q9AYR9_CHLRE | Q9ayr9 campylobact | 943 | 35 | 44.3 | 245 | 2 | ICLN_MOUSE | ICln mus musculu |
| 871 | 35 | 44.3 | 153 | 2 | Q9AU02_CHLRE | Q9au02 campylobact | 944 | 35 | 44.3 | 246 | 1 | ICLN_MOUSE | ICln mus musculu |
| 872 | 35 | 44.3 | 154 | 2 | Q635C8_BACCZ | Q635c8 bacillus ce | 945 | 35 | 44.3 | 248 | 1 | ICLN_MOUSE | ICln mus musculu |
| 873 | 35 | 44.3 | 154 | 2 | Q6HE06_BACHK | Q6he06 bacillus th | 946 | 35 | 44.3 | 250 | 1 | ICLN_MOUSE | ICln mus musculu |
| 874 | 35 | 44.3 | 154 | 2 | Q731D7_BACC1 | Q731d7 bacillus ce | 947 | 35 | 44.3 | 252 | 1 | ICLN_MOUSE | ICln mus musculu |
| 875 | 35 | 44.3 | 155 | 2 | Q88LY3_NOSPU | Q88ly3 nostoc punc | 948 | 35 | 44.3 | 252 | 1 | ICLN_MOUSE | ICln mus musculu |
| 876 | 35 | 44.3 | 156 | 2 | P72527_STRPN | P72527 streptococc | 949 | 35 | 44.3 | 255 | 2 | ICLN_MOUSE | ICln mus musculu |
| 877 | 35 | 44.3 | 161 | 2 | Q4XHR8_PLACH | Q4xhr8 plasmodium | 950 | 35 | 44.3 | 257 | 2 | ICLN_MOUSE | ICln mus musculu |
| 878 | 35 | 44.3 | 163 | 2 | Q4KPE6_VIRU | Q4kpe6 bacterioph | 951 | 35 | 44.3 | 259 | 2 | ICLN_MOUSE | ICln mus musculu |
| 879 | 35 | 44.3 | 167 | 2 | Q6IAZ6_HUMAN | Q6iaz6 homo sapien | 952 | 35 | 44.3 | 259 | 2 | ICLN_MOUSE | ICln mus musculu |
| 880 | 35 | 44.3 | 169 | 2 | Q8XW47_RALSO | Q8xw47 ralstonia s | 953 | 35 | 44.3 | 268 | 2 | ICLN_MOUSE | ICln mus musculu |
| 881 | 35 | 44.3 | 169 | 2 | Q9ULJ0_NPVST | Q9ulj0 spodoptera | 954 | 35 | 44.3 | 270 | 1 | ICLN_MOUSE | ICln mus musculu |
| 882 | 35 | 44.3 | 173 | 1 | RG510_HUMAN | Q43665 homo sapien | 955 | 35 | 44.3 | 271 | 2 | ICLN_MOUSE | ICln mus musculu |
| 883 | 35 | 44.3 | 173 | 2 | Q5T6B0_HUMAN | Q5t6b0 homo sapien | 956 | 35 | 44.3 | 272 | 2 | ICLN_MOUSE | ICln mus musculu |
| 884 | 35 | 44.3 | 173 | 2 | Q8FND4_COREF | Q8fnd4 corynebacte | 957 | 35 | 44.3 | 273 | 2 | ICLN_MOUSE | ICln mus musculu |
| 885 | 35 | 44.3 | 175 | 2 | Q5L6W9_CHLAB | Q5l6w9 chlamydophi | 958 | 35 | 44.3 | 276 | 2 | ICLN_MOUSE | ICln mus musculu |
| 886 | 35 | 44.3 | 176 | 2 | Q91BA3_NPVST | Q91ba3 spodoptera | 959 | 35 | 44.3 | 276 | 2 | ICLN_MOUSE | ICln mus musculu |
| 887 | 35 | 44.3 | 179 | 2 | Q5G2H2_NEIGO | Q5g2h2 neisseria g | 960 | 35 | 44.3 | 277 | 2 | ICLN_MOUSE | ICln mus musculu |
| 888 | 35 | 44.3 | 179 | 2 | Q5G2H9_NEIGO | Q5g2h9 neisseria g | 961 | 35 | 44.3 | 278 | 2 | ICLN_MOUSE | ICln mus musculu |
| 889 | 35 | 44.3 | 179 | 2 | Q5G2K9_NEIGO | Q5g2k9 neisseria g | 962 | 35 | 44.3 | 281 | 2 | ICLN_MOUSE | ICln mus musculu |
| 890 | 35 | 44.3 | 179 | 2 | Q5G2L4_NEIGO | Q5g2l4 neisseria g | 963 | 35 | 44.3 | 282 | 2 | ICLN_MOUSE | ICln mus musculu |
| 891 | 35 | 44.3 | 179 | 2 | Q5G2M3_NEIGO | Q5g2m3 neisseria g | 964 | 35 | 44.3 | 285 | 2 | ICLN_MOUSE | ICln mus musculu |
| 892 | 35 | 44.3 | 179 | 2 | Q5G2M8_NEIGO | Q5g2m8 neisseria g | 965 | 35 | 44.3 | 286 | 2 | ICLN_MOUSE | ICln mus musculu |
| 893 | 35 | 44.3 | 179 | 2 | Q5G2N5_NEIGO | Q5g2n5 neisseria g | 966 | 35 | 44.3 | 288 | 2 | ICLN_MOUSE | ICln mus musculu |
| 894 | 35 | 44.3 | 179 | 2 | Q5F6Z6_BRUAB | Q5f6z6 brucella ab | 967 | 35 | 44.3 | 291 | 2 | ICLN_MOUSE | ICln mus musculu |
| 895 | 35 | 44.3 | 179 | 2 | Q87X12_BRUSU | Q87x12 brucella me | 968 | 35 | 44.3 | 293 | 2 | ICLN_MOUSE | ICln mus musculu |
| 896 | 35 | 44.3 | 179 | 2 | Q8YBD1_BRUME | Q8ybd1 brucella me | 969 | 35 | 44.3 | 295 | 2 | ICLN_MOUSE | ICln mus musculu |
| 897 | 35 | 44.3 | 181 | 1 | IPVR_UREPA | Q9pqb6 ureaplasma | 970 | 35 | 44.3 | 297 | 2 | ICLN_MOUSE | ICln mus musculu |
| 898 | 35 | 44.3 | 181 | 2 | Q9G5N0_HUMAN | Q9g5n0 homo sapien | 971 | 35 | 44.3 | 297 | 2 | ICLN_MOUSE | ICln mus musculu |
| 899 | 35 | 44.3 | 181 | 2 | P79786_CHICK | P79786 gallus gall | 972 | 35 | 44.3 | 297 | 2 | ICLN_MOUSE | ICln mus musculu |
| 900 | 35 | 44.3 | 186 | 2 | Q75K28_DICDI | Q75k28 dictyosteli | 973 | 35 | 44.3 | 297 | 2 | ICLN_MOUSE | ICln mus musculu |
| 901 | 35 | 44.3 | 186 | 2 | Q552Q1_DICDI | Q552q1 dictyosteli | 974 | 35 | 44.3 | 297 | 2 | ICLN_MOUSE | ICln mus musculu |
| 902 | 35 | 44.3 | 190 | 2 | Q9HMA3_HALSA | Q9hma3 haloarcula | 975 | 35 | 44.3 | 300 | 2 | ICLN_MOUSE | ICln mus musculu |
| 903 | 35 | 44.3 | 190 | 2 | Q7VH21_HELHP | Q7vh21 helicobacte | 976 | 35 | 44.3 | 301 | 2 | ICLN_MOUSE | ICln mus musculu |
| 904 | 35 | 44.3 | 195 | 2 | Q97LB4_CLOB | Q97lb4 clostridium | 977 | 35 | 44.3 | 302 | 1 | ICLN_MOUSE | ICln mus musculu |
| 905 | 35 | 44.3 | 196 | 2 | Q6G4P9_BARHE | Q6g4p9 bartonella | 978 | 35 | 44.3 | 303 | 2 | ICLN_MOUSE | ICln mus musculu |
| 906 | 35 | 44.3 | 201 | 2 | Q54920_STRPN | Q54920 streptococc | 979 | 35 | 44.3 | 308 | 2 | ICLN_MOUSE | ICln mus musculu |
| 907 | 35 | 44.3 | 202 | 2 | Q6M0X4_METMP | Q6m0x4 methanococc | 980 | 35 | 44.3 | 310 | 2 | ICLN_MOUSE | ICln mus musculu |

981 35 44.3 310 2 Q8WQ2 CAEL 08wqg2 caenorhabdi
 982 35 44.3 312 2 Q39449 CICAR Q39449 cicer ariet
 983 35 44.3 314 2 Q9BRF8 HUMAN Q9brf8 homo sapien
 984 35 44.3 314 2 Q9H9M9 HUMAN Q9h9m9 homo sapien
 985 35 44.3 314 2 Q9NUT6 HUMAN Q9nut6 homo sapien
 986 35 44.3 314 2 Q5RCR9 PONPY Q5rcr9 pongo pygma
 987 35 44.3 314 2 Q6SFI4 UNACT Q6sfi4 uncultured
 988 35 44.3 315 1 CALU MOUSE O35887 mus musculus
 989 35 44.3 315 1 CALU RAT O35783 rattus norv
 990 35 44.3 315 2 Q8RU03 METGL Q8ru03 methyllobac
 991 35 44.3 315 2 Q6X1Q8 MUS MUSCUL Q6x1q8 mus musculi
 992 35 44.3 315 2 Q4U471 MESAU Q4u471 mesocricetu
 993 35 44.3 315 2 Q6IP82 XENLA Q6ip82 xenopus lae
 994 35 44.3 315 2 Q6NVMS XENIR Q6nvms xenopus tro
 995 35 44.3 318 2 Q4NLG2 9MICC Q4nlg2 arthrobacte
 996 35 44.3 319 2 Q9R2Z6 NEIGO Q9r2z6 neisseria g
 997 35 44.3 319 2 Q9R2Z9 NEIGO Q9r2z9 neisseria g
 998 35 44.3 319 2 Q9RF55 NEIGO Q9rf55 neisseria g
 999 35 44.3 319 2 Q9RF63 NEIGO Q9rf63 neisseria g
 1000 35 44.3 319 2 Q9RF71 NEIGO Q9rf71 neisseria g

ALIGNMENTS

RESULT 1
 KV3M_MOUSE STANDARD; PRT; 111 AA.
 AC P01665;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Ig kappa chain V-III region PC 7043.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_taxid=10090;
 [1]
 RP PROTEIN SEQUENCE.
 RA MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity.";
 RL Nature 276:785-790 (1978).
 [2]
 RP NUCLEOTIDE SEQUENCE OF 10-99.
 RA MEDLINE=94009207; PubMed=7691608;
 RA Mo J.A., Bona C.A., Holmdahl R.;
 RT "Variable region gene selection of immunoglobulin G-expressing B cells
 RT with specificity for a defined epitope on type II collagen.";
 RL Eur. J. Immunol. 23:2503-2510 (1993).
 [3]
 RP STRUCTURE BY NMR OF 1-111.
 RX MEDLINE=20264305; PubMed=10801487; DOI=10.1016/S0969-2126(00)00119-2;
 RA Tugarinov V., Zvi A., Levy R., Hayek Y., Matsushita S., Anglister J.;
 RT "NMR structure of an anti-gp120 antibody complex with a V3 peptide
 RT reveals a surface important for co-receptor binding.";
 RL Structure 8:395-395 (2000).
 CC
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 CC use as long as its content is in no way modified and this statement is not
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 CC
 DR EMBL; 225444; CAAB0931.1; -; mRNA.
 DR EMBL; 225446; CAAB0933.1; -; mRNA.
 DR EMBL; 225448; CAAB0935.1; -; mRNA.
 DR EMBL; 225450; CAAB0937.1; -; mRNA.
 DR EMBL; 225452; CAAB0939.1; -; mRNA.
 DR EMBL; 225454; CAAB0941.1; -; mRNA.
 DR EMBL; 225458; CAAB0945.1; -; mRNA.

PIR; A01937; KVM543.
 PDB; 1QNZ; NMR; L=1-111.
 DR Ensembl; ENSMUSG0000053225; Mus musculus.
 DR InterPro; IPR007110; Ig-like.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW 3D-structure; Direct protein sequencing; Immunoglobulin domain;
 Immunoglobulin V region.
 FT REGION 1 23
 FT REGION 24 38
 FT REGION 39 53
 FT REGION 54 60
 FT REGION 61 92
 FT REGION 93 101
 FT REGION 102 111
 FT DISULFID 23 92
 FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;
 Query Match 100.0%; Score 79; DB 1; Length 111;
 Best Local Similarity 100.0%; Pred. No. 2.3e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KASQSDYDGD SYN 15
 DB 24 KASQSDYDGD SYN 38
 RESULT 2
 KV3N_MOUSE STANDARD; PRT; 111 AA.
 AC P01666;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig kappa chain V-III region PC 7183.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_taxid=10090;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity.";
 RL Nature 276:785-790 (1978).
 CC
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 DR PIR; B01937; KVM583.
 DR HSSP; P01665; 1QNZ.
 DR SMR; P01666; 1-111.
 DR Ensembl; ENSMUSG0000053225; Mus musculus.
 DR InterPro; IPR007110; Ig-like.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin domain;
 Immunoglobulin V region.
 FT REGION 1 23
 FT REGION 24 38
 FT REGION 39 53
 FT REGION 54 60
 FT REGION 61 92
 FT REGION 93 101
 FT REGION 102 111


```
RL Nature 276:785-790 (1978).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR PIR; D01937; KWSL10.
DR HSSP; P01665; 1QNZ.
DR SMR; P01668; 1-110.
DR Ensembl; ENSMUSG0000053225; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 38
FT REGION 39 53
FT REGION 54 60
FT REGION 61 92
FT REGION 93 100
FT REGION 101 110
FT DISULFID 23 92
FT NON_TER 110 110
SQ SEQUENCE 110 AA; 11950 MW; 69F1A5CE886B1249 CRC64;

Query Match 96.2%; Score 76; DB 1; Length 110;
Best Local Similarity 93.3%; Pred. No. 7.4e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVVDYDGSYNN 15
Db 24 KASQSLDYDGSYNN 38
|||||:|||||

RESULT 6
Q811U6 MOUSE PRELIMINARY; PRT; 111 AA.
AC Q811U6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-human Fc gamma receptor Iii 3G8 kappa light chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RX PubMed:15059139; DOI=10.1111/j.1365-2141.2004.04893.x;
RA Bruenke J., Fischer B., Barbin K., Schreiter K., Wachter Y., Mahr K.,
RA Tiegemeier F., Niederweis M., Peipp M., Zunino S.J., Repp R.,
RA Valerius T., Fey G.H.;
RT "A recombinant bispecific single-chain Fv antibody against HLA class
RT II and Fc gammaRIII (CD16) triggers effective lysis of lymphoma
RT cells."
RL Br. J. Haematol. 125:167-179 (2004).
DR EMBL; AY173024; AA018226.1; -; mRNA.
DR HSSP; P01665; 1QNZ.
DR SMR; Q811U6; 1-111.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Receptor.
FT NON_TER 1 1
```

```
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12101 MW; CEDECEE157F2C94A CRC64;

Query Match 89.9%; Score 71; DB 2; Length 111;
Best Local Similarity 86.7%; Pred. No. 0.00053;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVVDYDGSYNN 15
Db 23 KASQSVDFDGSFNN 37
|||||:|||||

RESULT 7
KV3L MOUSE STANDARD; PRT; 111 AA.
ID KV3L MOUSE
AC P01664;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region CBPC 101.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity; multiple genes encode structurally
RT related mouse kappa variable regions."
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917 (1978).
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A01936; KWSCL.
DR HSSP; P01665; 1QNZ.
DR SMR; P01664; 1-111.
DR Ensembl; ENSMUSG0000053225; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 38
FT REGION 39 53
FT REGION 54 60
FT REGION 61 92
FT REGION 93 101
FT REGION 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11964 MW; E2B1AD98AD965962 CRC64;

Query Match 86.1%; Score 68; DB 1; Length 111;
Best Local Similarity 86.7%; Pred. No. 0.0017;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVVDYDGSYNN 15
Db 24 KASQSVDTGESYNN 38
|||||:|||||

RESULT 8
Q57HK0 SALCH PRELIMINARY; PRT; 282 AA.
ID Q57HK0_SALCH PRELIMINARY; PRT; 282 AA.
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AC Q57HK0;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Putative cytoplasmic protein.
GN OrderedLocusNames=SC3906;
OS Salmonella choleraesuis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=591;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SC-B67;
RX PubMed=15781495; DOI=10.1093/nar/gki297;
RA Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
RA Wang H.-S., Lee Y.-S.;
RT "The genome sequence of Salmonella enterica serovar Choleraesuis, a
RT highly invasive and resistant zoonotic pathogen.";
RL Nucleic Acids Res. 33:1690-1698 (2005).
DR EMBL; AB017220; AAX67812.1; -; Genomic_DNA.
DR InterPro; IPR001611; LRR.
DR PRINTS; PR00019; LEURICHRPT.
KW Complete proteome; Repeat.
SQ SEQUENCE 282 AA; 31862 MW; 975753A4590FEB62 CRC64;

Query Match 60.8%; Score 48; DB 2; Length 282;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KASQSVYDGDYNN 15
: : ||||| |||
DB 263 EALEPDDYDGDYNN 277

RESULT 9
ID Q5PKD6_SALPA PRELIMINARY; PRT; 282 AA.
AC Q5PKD6;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=SPA3856;
OS Salmonella paratyphi-a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=54388;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 9150 / SARB42;
RX PubMed=15531882; DOI=10.1038/ngl470;
RA McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,
RA Porwollik S., Sabo A., Meyer R., Bieri T., Ozersky P., McLellan M.,
RA Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G.,
RA Kohlberg S., Strong C., Du F., Carter J., Kremizki C., Layman D.,
RA Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P.,
RA Delehaunty K., Fronick C., Magrini V., Nhan M., Warren W., Florea L.,
RA Spieth J., Wilson R.K.;
RT "Comparison of genome degradation in Paratyphi A and Typhi, human-
RT restricted serovars of Salmonella enterica that cause typhoid.";
RL Nat. Genet. 36:1268-1274 (2004).
DR EMBL; CP000026; AAV79624.1; -; Genomic_DNA.
DR InterPro; IPR001611; LRR.
DR PRINTS; PR00019; LEURICHRPT.
KW Complete proteome; Hypothetical protein; Repeat.
SQ SEQUENCE 282 AA; 31876 MW; 8A188CF20EAB27 CRC64;

Query Match 60.8%; Score 48; DB 2; Length 282;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KASQSVYDGDYNN 15
: : ||||| |||
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DB 263 EALEPDDYDGDYNN 277

RESULT 10
ID Q8Z2S9_SALTY PRELIMINARY; PRT; 282 AA.
AC Q8Z2S9; Q7C6K9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein STY3863.
GN OrderedLocusNames=STY3863; t3606;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth I., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852 (2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RX DOI=10.1128/JB.185.7.2330-2337.2003;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodyanni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RL J. Bacteriol. 185:2330-2337 (2003).
DR EMBL; AL627279; CAD09611.1; -; Genomic DNA.
DR EMBL; AB016846; AAO71108.1; -; Genomic_DNA.
DR InterPro; IPR001611; LRR.
DR PRINTS; PR00019; LEURICHRPT.
KW Complete proteome; Hypothetical protein; Repeat.
SQ SEQUENCE 282 AA; 31930 MW; EBC0808D9D6B877 CRC64;

Query Match 60.8%; Score 48; DB 2; Length 282;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KASQSVYDGDYNN 15
: : ||||| |||
DB 263 EALEPDDYDGDYNN 277

RESULT 11
ID Q8ZKU0_SALTY PRELIMINARY; PRT; 282 AA.
AC Q8ZKU0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative cytoplasmic protein.
GN OrderedLocusNames=STM4015;
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
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RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du J., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RL LT2.";
RL Nature 413:852-856(2001).
DR EMBL; AB008887; AAL28854.1; -; Genomic_DNA.
DR InterPro; IPR001611; LRR.
DR PRINTS; PR00019; LEURICRPT.
KW Complete proteome; Repeat.
SQ SEQUENCE 282 AA; 31896 MW; 192C4AE31679D2C6 CRC64;

Query Match 60.8%; Score 48; DB 2; Length 282;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KASQSDYDGDSDSYN 15
Db 263 EALEPDDYDGDYNN 277

RESULT 12
Q6CWJ5_KLUJLA
ID Q6CWJ5_KLUJLA PRELIMINARY; PRT; 734 AA.
AC Q6CWJ5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Kluveromyces lactis strain NRRL Y-1140 chromosome B of strain NRRL Y-
DE 1140 of Kluveromyces lactis.
GN OrderedLocNames=KLUJLA0803586g;
OS Kluveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluveromyces.
OX NCBI_TaxID=29985;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed1529592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbé V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boisarane A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantave F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Niclaud J.-M., Nikolaki M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
DR EMBL; CR382122; CAH02087.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000008; C2.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00239; C2; 1.

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DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00219; TyKC; 1.
DR PROSITE; PS00004; C2 DOMAIN 2; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Complete proteome.
SQ SEQUENCE 734 AA; 82341 MW; DB9A39CBA2E2B888 CRC64;

Query Match 58.2%; Score 46; DB 2; Length 734;
Best Local Similarity 72.7%; Pred. No. 73;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 SVDYDGDSDSYN 15
Db 714 SVDYDGDHMD 724

RESULT 13
Q81C28_BACCR
ID Q81C28_BACCR PRELIMINARY; PRT; 94 AA.
AC Q81C28;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=BC2956;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=226900;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Hasekorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis";
RL Nature 423:87-91(2003).
DR EMBL; AB017007; AAP09904.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 94 AA; 11075 MW; 36130065840543B1 CRC64;

Query Match 57.0%; Score 45; DB 2; Length 94;
Best Local Similarity 72.7%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 SVDYDGDSDSYN 15
Db 51 SVDYDGLIYN 61

RESULT 14
KV3C_MOUSE
ID KV3C_MOUSE STANDARD; PRT; 111 AA.
AC P01656;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region MOPC 70.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=67056897; PubMed=4162931;
RA Gray W.R., Dreyer W.J., Hood L.E.;

```


RT "Mechanism of antibody synthesis: size differences between mouse kappa chains."

RL Science 155:465-467(1967).

CC -!- MISCELLANEOUS: This is a Bence-Jones protein.

CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----

DR HSSP; P01655; 1QNZ.

DR SMR; P01656; 1-111.

DR Ensembl; ENSMUSG0000053225; Mus musculus.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003596; IG_v.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

KW Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.

FT REGION 1 23

FT REGION 24 38 Framework-1.

FT REGION 39 53 Complementarity-determining-1.

FT REGION 54 60 Framework-2.

FT REGION 61 92 Complementarity-determining-2.

FT REGION 93 101 Framework-3.

FT REGION 102 111 Complementarity-determining-3.

FT REGION 112 120 Framework-4.

FT DISULFID 23 92 By similarity.

FT NON_TER 111 111

FT SEQUENCE 111 AA; 11904 MW; 4FE7ABC9DF0FC125 CRC64;

Query Match 57.0%; Score 45; DB 1; Length 111;

Best Local Similarity 60.0%; Pred. No. 13;

Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KASQSDVDGDSYMN 15

DB 24 RASESVDSGSGIFMN 38

QY 1 KASQSDVDGDSYMN 15

DB 24 RASESVDSGSGIFMN 38

RESULT 15

QATRC9_9SPHN

ID Q4TRC9_9SPHN PRELIMINARY; PRT; 652 AA.

AC Q4TRC9;

DT 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

DE Putative sulfatase.

GN ORFNames=ELI0597;

OS Erythrobacter litoralis HTCC2594.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;

OC Sphingomonadaceae; Erythrobacter.

OX NCBI_TaxID=314225;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=HTCC2594;

RA Giovannoni S.J., Cho J.-C., Ferreira S., Johnson J., Kravitz S.,

RA Halpern A., Remington K., Beeson K., Tran B., Rogers Y.-H.,

RA Friedman R., Venter J.C.;

RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.

CC -!- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

DR EMBL; AAGG0100001; EAL76791.1; -; Genomic DNA.

SQ SEQUENCE 652 AA; 70199 MW; BBDB32736EE382C4 CRC64;

Query Match 57.0%; Score 45; DB 2; Length 652;

Best Local Similarity 58.3%; Pred. No. 94;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASQSDVDGDSY 13

DB 221 AAQATDFDGDGY 232

RESULT 16

Q4PKA4_9BACT

ID Q4PKA4_9BACT PRELIMINARY; PRT; 294 AA.

AC Q4PKA4;

DT 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

DE Predicted membrane-bound lytic transglycosylase.

OS uncultured bacterium MedebAC35C06.

OC Bacteria; environmental samples.

OX NCBI_TaxID=332273;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Sabehi G., Loy A., Jung K.H., Partha R., Spudich J.L., Isaacson T.,

RA Hirschberg J., Wagner M., Beja O.;

RT "New Insights into Metabolic Properties of Marine Bacteria Encoding

RT Proteorhodopsins."

RL PLOS Biol. 3:e273-e273(2005).

DR EMBL; DQ077553; AAY82601.1; -; Genomic_DNA.

DR InterPro; IPR011757; MltB.

DR TIGRFAMs; TIGR02282; MltB; 1.

SQ SEQUENCE 294 AA; 33961 MW; CE4E2219AC008176 CRC64;

Query Match 55.7%; Score 44; DB 2; Length 294;

Best Local Similarity 54.5%; Pred. No. 57;

Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 SVDYDGDGYMN 15

DB 190 AIDYDGDGYD 200

QY 5 SVDYDGDGYMN 15

DB 190 AIDYDGDGYD 200

RESULT 17

Q6Q940_9GAMM

ID Q6Q940_9GAMM PRELIMINARY; PRT; 296 AA.

AC Q6Q940;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Predicted membrane-bound lytic transglycosylase.

GN ORFNames=Red20E09_24;

OS uncultured marine gamma proteobacterium EBAC20E09.

OC Bacteria; Proteobacteria; Gammaproteobacteria; SAR86 cluster;

OC environmental samples.

OX NCBI_TaxID=266134;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX PubMed=15305915; DOI=10.1111/j.1462-2920.2004.00676.x;

RA Sabehi G., Beja O., Suzuki M.T., Preston C.M., DeLong E.F.;

RT "Different SAR86 subgroups harbour divergent proteorhodopsins."

RL Environ. Microbiol. 6:903-910(2004).

DR EMBL; AY552545; AAS73027.1; -; Genomic_DNA.

DR InterPro; IPR011757; MltB.

DR TIGRFAMs; TIGR02282; MltB; 1.

SQ SEQUENCE 296 AA; 34268 MW; F807CDF4AB8698BD CRC64;

Query Match 55.7%; Score 44; DB 2; Length 296;

Best Local Similarity 54.5%; Pred. No. 58;

Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 SVDYDGDGYMN 15

DB 192 AIDYDGDGYD 202

RESULT 18

Q9NJD9_ONCVO

ID Q9NJD9_ONCVO PRELIMINARY; PRT; 542 AA.

AC Q9NJD9;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

| | | |
|-----------|---|--|
| DT | 01-WAR-2004 (TReMBLrel. 26, Last annotation update) | |
| DE | Calcium-binding protein CBP-1. | |
| GN | Name=cbp-1; | |
| OS | Onchocerca volvulus. | |
| OC | Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; | |
| OC | Onchocercidae; Onchocerca. | |
| OX | NCBI_TaxID=6282; | |
| LN | [1] | |
| RN | NCLEOTIDE SEQUENCE. | |
| RP | MEDLINE=20278137; PubMed=10816503; | |
| RX | DOI=10.1128/TAI.68.6.3491-3501.2000; | |
| RA | Lizotte-Waniewski M., Tawe W., Guiliano D.B., Lu W., Liu J., | |
| RA | Williams S.A., Lustigman S.; | |
| RT | "Identification of potential vaccine and drug target candidates by | |
| RT | expressed sequence tag analysis and immunoscreening of Onchocerca | |
| RT | volvulus larval cDNA libraries."; | |
| RL | Infect. Immun. 68:3491-3501(2000). | |
| DR | EMBL; AF153720; AAF64251.1; -; mRNA. | |
| DR | GO; GO:0005509; F:calcium ion binding; IEA. | |
| DR | InterPro; IPR011992; EF-Hand type. | |
| DR | InterPro; IPR002048; EF-hand_Ca_bd. | |
| DR | Pfam; PF00036; ehand; 5. | |
| DR | SMART; SM00054; EFh; 10. | |
| DR | PROSITE; PS00018; EF_HAND; UNKNOWN_7. | |
| KW | Calcium; Repeat. | |
| SQ | SEQUENCE 542 AA; 61270 MW; 94E3D57FB72D805B CRC64; | |
| | Query Match 55.7%; Score 44; DB 2; Length 542; | |
| | Best Local Similarity 58.3%; Pred. No. 1.1e+02; | |
| | Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps | |
| QY | 4 QSDYDGDGSYNN 15 | |
| | :-: : : : | |
| DB | 380 QEIDSDDGYIN 391 | |
| | | |
| RESULT 19 | | |
| ID | Q6LYG7 METMP PRELIMINARY; PRT; 710 AA. | |
| QI | Q6LYG7 | |
| AC | Q6LYG7 | |
| DT | 05-JUL-2004 (TReMBLrel. 27, Created) | |
| DT | 05-JUL-2004 (TReMBLrel. 27, Last sequence update) | |
| DT | 05-JUL-2004 (TReMBLrel. 27, Last annotation update) | |
| DE | MCM family related protein. | |
| DE | OrderedLocusNames=MMP1024. | |
| GN | Onchococcus maripaludis. | |
| OS | Archaea; Euryarchaeota; Methanococci; Methanococcales; | |
| OC | Methanococcaceae; Methanococcus. | |
| OX | NCBI_TaxID=39152; | |
| LN | [1] | |
| RN | NCLEOTIDE SEQUENCE. | |
| RP | STRAIN=S2 / L1; | |
| RC | PubMed=15466049; DOI=10.1128/JB.186.20.6956-6969.2004; | |
| RA | Hendrickson E.L., Kaul R., Zhou Y., Bovee D., Chapman P., Chung J., | |
| RA | Conway de Macario E., Dodsworth J.A., Gillett W., Graham D.E., | |
| RA | Hackett M., Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J., | |
| RA | Major T.A., Moore B.C., Porat I., Palmeiri A., Rouse G., | |
| RA | Saenphimmachak C., Soell D., Van Dien S., Wang T., Whitman W.B., | |
| RA | Xia Q., Zhang Y., Jarmer F.W., Olson M.V., Leigh J.A.; | |
| RT | "Complete genome sequence of the genetically tractable | |
| RT | hydrogenotrophic methanogen Methanococcus maripaludis."; | |
| RL | J. Bacteriol. 186:6956-6969(2004). | |
| DR | EMBL; BX957221; CAP30580.1; -; Genomic_DNA. | |
| DR | GO; GO:0005524; F:ATP binding; IEA. | |
| DR | GO; GO:0003677; F:DNA binding; IEA. | |
| DR | GO; GO:0008094; F:DNA-dependent ATPase activity; IEA. | |
| DR | GO; GO:0006270; P:DNA replication initiation; IEA. | |
| DR | InterPro; IPR001208; MCM. | |
| DR | Pfam; PF00493; MCM; 1. | |
| DR | PRINTS; PR01657; MCMFAMILY. | |
| DR | Prodom; PD001041; MCM; 1. | |
| DR | SMART; SM00350; MCM; 1. | |
| DR | PROSITE; PS00847; MCM 1; UNKNOWN 1. | |

DR PROSITE; PS50051; MCM_2; 1.
KW Complete proteome.
SQ SEQUENCE 710 AA; 80486 MW; 6BA543F5C2DBDF6D CRC64;

Query Match 55.7%; Score 44; DB 2; Length 710;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 KASQSVDYDGDSYNN 15
::|:|::|:|
Db 168 RSEMSIDYDSSAYVN 182

RESULT 20
MCL1 SCHPO
ID_MCL1 SCHPO STANDARD; PRT; 815 AA.
AC Q9C107;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Minichromosome loss protein 1.
GN Names=mcl1; ORFNames=SPAB1E7.02c;
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
[1]
RP NUCLEOTIDE SEQUENCE, FUNCTION, AND SUBCELLULAR LOCATION.
RX MEDLINE=22343090; PubMed=12455694; DOI=10.1128/EC.1.5.758-773.2002;
RA Williams D.R., McIntosh J.R.;
RT "mcl1", the Schizosaccharomyces pombe homologue of CTF4, is important
RT for chromosome replication, cohesion, and segregation.";
RL Eukaryot. Cell 1:758-773(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=972;
RC MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M.H., Lyne R., Stewart A.,
RA Sgouras J.G., Peat N., Hayes J., Baker S.G., Baaham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltham T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D.E., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K.D., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moulé S., Mungall K.L., Murphy L.D., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K.M., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M.N., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J.R., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Duesterhoeft A., Fritzc C., Holzer E., Moestl D.,
RA Hilbert H., Borzym K., Langer I., Beck A., Leirach H., Reinhardt R.,
RA Pohl T.M., Eger P., Zimmermann W., Wedler H., Wamburt R., Fournelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.B., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shipakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -!- FUNCTION: Has a role in regulating DNA replication complexes. Acts
CC as a regulator of post DNA replication initiation. Associates with
CC chromatin during G1 and S phases of mitosis.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Contains 6 WD repeats.
CC -----
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CC use.

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EMBL: AL590605; CAP36919.1; -: Genomic_DNA.
GeneDB: Spombe; SPAPB1E7.02c; -
GO: GO:0006260; P:DNA replication; TAS.
GO: GO:0007062; P:sister chromatid cohesion; TAS.
GO: GO:0000723; P:telomere maintenance; IMP.
InterPro: IPR001680; WD40.
Pfam: PF00400; WD40; 6.

SMART: SM00320; WD40; 6.
PROSITE: PS00678; WD_REPEATS_1; FALSE_NEG.
PROSITE: PS00882; WD_REPEATS_2; 1.

PROSITE: PS50082; WD_REPEATS_2; 1.
KW Complete proteome; DNA replication; Nuclear protein; Repeat;
WD repeat.

REPEAT 11 50 WD 1.
REPEAT 53 90 WD 2.
REPEAT 93 132 WD 3.
REPEAT 135 174 WD 4.
REPEAT 228 267 WD 5.
REPEAT 517 553 WD 6.
SEQUENCE 815 AA; 90986 MW; D3AD3EP2D7997C54 CRC64;

Query Match 55.7%; Score 44; DB 1; Length 815;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 SVDYDGDSDYM 14
DB 366 SLDLGDSDYM 375

RESULT 21

P97596 RAT PRELIMINARY; PRT; 137 AA.
AC P97596;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mast cell protease 10 (Fragment).
GN Names=Mcp10; Synonyms=RMCP-10;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

[1] NUCLEOTIDE SEQUENCE.

RC STRAIN=Wistar;
RX MEDLINE=97149430; PubMed=8996238; DOI=10.1084/jem.185.1.13;
RA Lutzelshwab C., Pejler G., Avekogh M., Hellman L.;
RT "Secretory granule proteases in rat mast cells. Cloning of 10
RT different serine proteases and a carboxypeptidase A from various rat
RT mast cell populations.";
RL J. Exp. Med. 185:13-29(1997).
DR EMBL: U67913; AAB48266.1; -: mRNA.
DR HSSP: P80219; LEUF.
DR RGD: 3063; Mcp10.

DR GO: GO:0008233; F:peptidase activity; IEA.
DR GO: GO:0004295; F:trypsin activity; IEA.
DR GO: GO:0030195; P:negative regulation of blood coagulation; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001254; Peptidase_S1_S6.
DR Pfam: PF00089; Trypsin; 1.
DR SMART: SM00020; Tryp_SPC; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.

KW Protease.
FT NON_TER 1 1
FT NON_TER 137 137

SQ SEQUENCE 137 AA; 15019 MW; 83632B52786085BF CRC64;
Query Match 54.4%; Score 43; DB 2; Length 137;

Best Local Similarity 53.3%; Pred. No. 36;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 KASQSDVDYDGDSDYM 15
DB 29 KAKPHENYDGDSDYM 43

RESULT 22

Q9W2L0 DROME PRELIMINARY; PRT; 186 AA.
AC Q9W2L0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG9406-PA.

GN Name=CG9406; ORFNames=CG9406;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;
RN [1] NUCLEOTIDE SEQUENCE.

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadiot E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hoston D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reiner B.C., Remington K., Saunders R.D.C., Scheeler F., Smith T.,
RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
RN [2] NUCLEOTIDE SEQUENCE.

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;

RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila

```
RT melanogaster euchromatic genome sequence." ;
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
RN [3]
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirekas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomes perspective." ;
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review." ;
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirekas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence." ;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL, AE003453; RAP46680.1; -; Genomic_DNA.
DR HSSP; P02588; IPON.
DR Ensembl; CG9406; Drosophila melanogaster.
DR FlyBase; FBgn0034592; CG9406.
DR GO; GO:0005509; P:calcium ion binding; IEA.
DR InterPro; IPR011992; EF-Hand type.
DR InterPro; IPR002048; EF_hand_Ca_bd.
DR Pfam; PF00036; ethand; 2.
DR SMART; SM00054; EFh; 2.
KW Repeat.
SQ SEQUENCE 186 AA; 21301 MW; 7B8A6AA5A87AFAFE CRC64;

Query Match 54.4%; Score 43; DB 2; Length 186;
Best Local Similarity 50.0%; Pred. No. 51;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASQSVVDYDGSYM 14
||:|||||:|:|:|
Db 56 KATDSVDIPGEAHL 69

RESULT 23
Q4SMD4_TETNG
ID Q4SMD4_TETNG PRELIMINARY; PRT; 380 AA.
AC Q4SMD4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 3 SCAP14553, whole genome shotgun sequence.
GN ORFNames=GSTENG00015822001;
OS Tetradon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
```

```
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype." ;
RL Nature 431:946-957 (2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL, CAAE01014553; CAF98198.1; -; Genomic DNA.
SQ SEQUENCE 380 AA; 41957 MW; C3E19B5FADBE6A673 CRC64;

Query Match 54.4%; Score 43; DB 2; Length 380;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 KASQSVVDYDGSYNN 15
||:|||||:|:|:|
Db 32 KSESDDDFDGSESTWN 46

RESULT 24
P93370_TOBAC
ID P93370_TOBAC PRELIMINARY; PRT; 551 AA.
AC P93370;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Calmodulin-binding protein.
GN Name=rcB60;
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Wisconsin 38;
RA Dash S., Lu Y., Harrington H.M.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U58971; AAB37246.1; -; mRNA.
DR PIR; T03793; T03793.
SQ SEQUENCE 551 AA; 61598 MW; 813879E25125C374 CRC64;

Query Match 54.4%; Score 43; DB 2; Length 551;
Best Local Similarity 53.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 SQSVVDYDGSYNN 15
||:|||||:|:|:|
Db 292 NQVVEYDGKSFNL 304

RESULT 25
KIF2_XENLA
ID KIF2_XENLA STANDARD; PRT; 682 AA.
AC Q91637;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
```

DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Kinesin-like protein KIF2 (Kinesin-related protein XKIF2).
 GN Name=KIF2;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE, AND SEQUENCE REVISION.
 RC TISSUE=Ovary;
 RA Walczak C.E.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RP NUCLEOTIDE SEQUENCE OF 124-682.
 RC TISSUE=Ovary;
 RX MEDLINE=96140638; PubMed=8548824; DOI=10.1016/S0092-8674(00)80991-5;
 RA Walczak C.E., Mitchison T.J., Desai A.;
 RT "XKIM1: a Xenopus kinesin-related protein that regulates microtubule
 dynamics during mitotic spindle assembly.";
 RL Cell 84:37-47(1996).
 CC -1- SIMILARITY: Belongs to the kinesin-like protein family. MCAK/KIF2
 subfamily.
 CC -1- SIMILARITY: Contains 1 kinesin-motor domain.
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 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC -----
 CC EMBL; U36486; AAC59744.2; ALT_INIT; mRNA.
 DR HSSP; P33173; 1155.
 DR SMR; Q91637; 168-528.
 DR InterPro; IPR001752; kinesin_motor.
 DR Pfam; PF00225; Kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
 DR PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
 KW ATP-binding; Coiled coil; Microtubule; Motor protein;
 KW Nucleotide-binding.
 FT DOMAIN 193 542 Kinesin-motor.
 FT NP BIND 288 295 ATP (By similarity).
 FT REGION 1 192 Globular (Potential).
 FT COILED 543 682 Potential.
 FT SEQUENCE 682 AA; 77414 MW; 3DA295BB319063F8 CRC64;
 SQ
 Query Match 54.4%; Score 43; DB 1; Length 682;
 Best Local Similarity 63.6%; Pred. No. 2.2e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 3 SQSVYDGDYSY 13
 Db 625 TEEVDYDADSY 635
 RESULT 26
 Q6PF78_XENLA PRELIMINARY; PRT; 686 AA.
 AC Q6PF78;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Kif2-A-prov protein.
 GN Name=kif2-A-prov;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S.G., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC057698; AAH57698.1; -; mRNA.
 DR SMR; Q6PF78; 175-535.
 DR GO; GO:0005874; C-microtubule; IEA.
 DR GO; GO:0005875; C-microtubule associated complex; IEA.
 DR GO; GO:0005524; F-ATP binding; IEA.
 DR GO; GO:0003777; F-microtubule motor activity; IEA.
 DR GO; GO:0007018; P-microtubule-based movement; IEA.
 DR InterPro; IPR001752; Kinesin_motor.
 DR Pfam; PF00225; Kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
 DR PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
 KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
 SQ SEQUENCE 686 AA; 77854 MW; 20997A76672471D5 CRC64;
 Query Match 54.4%; Score 43; DB 2; Length 686;
 Best Local Similarity 63.6%; Pred. No. 2.2e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 3 SQSVYDGDYSY 13
 Db 629 TEEVDYDADSY 639
 RESULT 27
 Q7XZF5_ARATH PRELIMINARY; PRT; 1841 AA.
 ID Q7XZF5_ARATH PRELIMINARY;
 AC Q7XZF5;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE RST1.
 GN Name=RST1;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

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OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Chen X., Goodwin S.M., Liu X., Jenks M.A.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY307371; RAY4222.1; -; mRNA.
DR InterPro; IPR001395; Altdo/Ket_red.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR PROSITE; PS00063; ALDO-KETO REDUCTASE 3; UNKNOWN 1.
DR PROSITE; PS00237; G PROTEIN RECEPTOR 1; UNKNOWN 1.
SQ SEQUENCE 1841 AA; 203599 MW; 0AAD658B64BEA12F CRC64;

Query Match 54.4%; Score 43; DB 2; Length 1841;
Best Local Similarity 60.0%; Pred. No. 6.5e-02;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 KASQSDVDGDSYMN 15
DB 1047 EASASDIDSYSYN 1061
:|||||

RESULT 28
Q9LVX3 ARATH PRELIMINARY; PRT; 1868 AA.
AC Q9LVX3 ARATH PRELIMINARY; PRT; 1868 AA.
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGF10.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20277480; PubMed=10819329;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:131-135(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AB018114; BAB02691.1; -; Genomic_DNA.
DR InterPro; IPR001395; Altdo/Ket_red.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR PROSITE; PS00063; ALDO-KETO REDUCTASE 3; UNKNOWN 1.
DR PROSITE; PS00237; G PROTEIN RECEPTOR 1; UNKNOWN 1.
SQ SEQUENCE 1868 AA; 206711 MW; 0799ADC38CC0C5F0 CRC64;

Query Match 54.4%; Score 43; DB 2; Length 1868;
Best Local Similarity 60.0%; Pred. No. 6.6e-02;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 KASQSDVDGDSYMN 15
DB 1074 EASASDIDSYSYN 1088
:|||||

RESULT 29
KV3A MOUSE
ID KV3A MOUSE STANDARD; PRT; 111 AA.
AC P01654;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region PC 2880/PC 1229.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
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CC use as long as its content is in no way modified and this statement is not
CC removed.
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OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
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DR PIR; B93204; KWS80.
DR HSSP; P01665; 1QNZ.
DR SMR; P01654; 1-111.
DR Ensembl; ENSMUSG00000053225; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 38 Complementarity-determining-1.
FT REGION 39 53 Framework-2.
FT REGION 54 60 Complementarity-determining-2.
FT REGION 61 92 Framework-3.
FT REGION 93 101 Complementarity-determining-3.
FT REGION 102 111 Framework-4.
FT DISULFID 23 92 By similarity.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11980 MW; AFEAC6A9D26FC12D CRC64;

Query Match 53.2%; Score 42; DB 1; Length 111;
Best Local Similarity 60.0%; Pred. No. 42;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KASQSDVDGDSYMN 15
DB 24 RASESDVNYGIFSN 38
:|||||

RESULT 30
KV3B MOUSE
ID KV3B MOUSE STANDARD; PRT; 112 AA.
AC P01655;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region PC 7132.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
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CC removed.
 CC -----
 DR HSP; P01665; 1QNZ.
 DR SMR; P01655; 1-112.
 DR Ensembl; ENSMUSG00000053225; Mus musculus.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin domain;
 KW Immunoglobulin v region.
 FT REGION 1 23
 FT REGION 24 38
 FT REGION 39 53
 FT REGION 54 60
 FT REGION 61 92
 FT REGION 93 102
 FT REGION 103 112
 FT DISULFID 23 92
 FT NON_TER 112 112
 SQ SEQUENCE 112 AA; 12054 MW; 5F0DD25EE20BE611 CRC64;
 Query Match 53.2%; Score 42; DB 1; Length 112;
 Best Local Similarity 60.0%; Pred. No. 43;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 KASQSVVDYDGDSTVN 15
 DB 24 RASESDVNGISFMN 38
 RESULT 31
 Q9A0Y5_9CHLO PRELIMINARY; PRT; 153 AA.
 AC Q9A0Y5_9CHLO PRELIMINARY; PRT; 153 AA.
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Cytochrome c oxidase subunit II (EC 1.9.3.1).
 GN Name=cox2b;
 OS Polytomella sp. Pringsheim 198.80.
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
 OC Chlamydomonadales; Chlamydomonadaceae; Polytomella.
 OX NCBI_TaxID=37502;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Pringsheim 198.80;
 RX MEDLINE=21179187; PubMed=11094061; DOI=10.1074/jbc.M010244200;
 RA Perez-Martinez X., Antaramian A., Vazquez-Acevedo M., Funes S.,
 RA Tokunova E., d'Alayer J., Claros M.G., Davidson E., King M.P.,
 RA Gonzalez-Halphen D.;
 RT "Subunit II of cytochrome c oxidase in Chlamydomonas algae is a
 RT heterodimer encoded by two independent nuclear genes."
 RL J. Biol. Chem. 276:11302-11309(2001).
 DR EMBL; AF305542; AAK32116.1; -; Genomic DNA.
 DR EMBL; AF305079; AAK30366.1; -; mRNA.
 DR HSP; P18400; 1CYX.
 DR GO; GO:0016020; C.membrane; IEA.
 DR GO; GO:000507; F.copper ion binding; IEA.
 DR GO; GO:0004129; F.cytochrome-c oxidase activity; IEA.
 DR GO; GO:0016491; F.oxidoreductase activity; IEA.
 DR GO; GO:0006118; P.electron transport; IEA.
 DR InterPro; IPR001505; Copper_CuA.
 DR InterPro; IPR002429; Cyt_c-ox_2.
 DR Pfam; PF00116; COX2; 1.
 DR PRINTS; PR01166; CYCOXIDASEII.
 DR ProDom; PD000131; Copper_CuA; 1.
 DR PROSITE; PS00078; COX2; 1.
 DR PROSITE; PS00857; COX2_CUA; 1.
 KW Oxidoreductase.
 SQ SEQUENCE 153 AA; 17219 MW; A69030F3E4746238 CRC64;
 Query Match 53.2%; Score 42; DB 2; Length 153;

Best Local Similarity 61.5%; Pred. No. 60;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 2 ASQSVVDYDGDSTVN 14
 DB 36 ASQIQYNFDSYM 48
 RESULT 32
 Q8GSW1_BIFLO PRELIMINARY; PRT; 193 AA.
 ID Q8GSW1_BIFLO PRELIMINARY; PRT; 193 AA.
 AC Q8GSW1; DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Xanthine phosphoribosyltransferase.
 GN Name=xpt; OrderedLocusNames=BL0891;
 OS Bifidobacterium longum.
 OC Bacteria; Actinobacteria; Actinobacteriales; Bifidobacteriales;
 OC Bifidobacteriaceae; Bifidobacterium.
 OX NCBI_TaxID=216816;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=NCC 2705;
 RX MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.212527599;
 RA Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
 RA Pessi G., Zwaalen M.-C., Desiere F., Bork P., Delley M.,
 RA Pridmore R.D., Arigoni F.;
 RT "The genome sequence of Bifidobacterium longum reflects its adaptation
 RT to the human gastrointestinal tract."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
 CC -!- SUBUNIT: Homodimer (By similarity).
 DR EMBL; AE014295; AAN24704.1; -; Genomic DNA.
 DR GO; GO:0000287; P.magnesium ion binding; IEA.
 DR GO; GO:0016763; P.transferase activity; transferring pentosyl. . . ; IEA.
 DR GO; GO:0009116; P.nucleoside metabolism; IEA.
 DR GO; GO:0043101; P.purine salvage; IEA.
 DR GO; GO:0046110; P.xanthine metabolism; IEA.
 DR InterPro; IPR000836; PRTtransferase.
 DR InterPro; IPR010079; XPR trans.
 DR Pfam; PF00156; PribosylTran; 1.
 DR TIGRfams; TIGR01744; XPRase; 1.
 KW Complete proteome; Glycosyltransferase; Magnesium; Transferase.
 SQ SEQUENCE 193 AA; 20769 MW; 1480E1D885AF6B75 CRC64;
 Query Match 53.2%; Score 42; DB 2; Length 193;
 Best Local Similarity 53.8%; Pred. No. 78;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 KASQSVVDYDGDSTVN 13
 DB 81 KKAQSLNLDGQY 93
 RESULT 33
 Q925S1_MOUSE PRELIMINARY; PRT; 218 AA.
 ID Q925S1_MOUSE PRELIMINARY; PRT; 218 AA.
 AC Q925S1; DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE MRP5 (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/c;
 RX PubMed=11819679;
 RA Cui D.X., Zeng G.Y., Wang F., Xu J.R., Ren D.Q., Guo Y.H., Tian F.R.,
 RA Yan X.J., Hou Y., Su C.Z.;

CC molecules of xerC and two molecules of xerD (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the "phage" integrase family. XerC type 1
CC subfamily.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: BA000004; BAB06184.1; -; Genomic_DNA.
CC F1R; A83958; A83958.
CC DR HSP; P21891; 1AOP.
CC DR HAMAP; MF_01808; -; 1.
CC DR InterPro; IPR004107; Phage_integrase.
CC DR InterPro; IPR002104; Phage_integrase.
CC DR InterPro; IPR011931; Recomb_XerC.
CC DR Pfam; PF02899; Phage_integr_N; 1.
CC DR Pfam; PF00589; Phage_integrase; 1.
CC DR TIGRFAMs; TIGR02224; recomb_XerC; 1.
CC KW Cell cycle; Cell division; Chromosome partition; Complete proteome;
CC DNA integration; DNA recombination; DNA-binding.
CC FT ACT_SITE 150 150 By similarity.
CC FT ACT_SITE 174 174 By similarity.
CC FT ACT_SITE 249 249 By similarity.
CC FT ACT_SITE 252 252 By similarity.
CC FT ACT_SITE 275 275 By similarity.
CC FT ACT_SITE 284 284 O-(3'-phospho-DNA)-tyrosine intermediate
CC (By similarity).
CC SQ SEQUENCE 303 AA; 35035 MW; D10E8AAFE1D6705 CRC64;
Query Match 53.2%; Score 42; DB 1; Length 303;
Best Local Similarity 53.3%; Pred. No. 1.3e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 KASQSVVDYDGD SYMN 15
DB 204 KKSKSVLDPLGDLFLN 218

RESULT 37
Q4Q3M6 LEIMA
ID Q4Q3M6 LEIMA PRELIMINARY; PRT; 465 AA.
AC Q4Q3M6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=LmjF33.3100;
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Friedlin;
RA Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,
RA Smith D., Collins M., Foster N., Harris D., Oliver K., O'Neil S.,
RA Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; C7005270; CAJ06862.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51898 MW; F5429A02B0F03301 CRC64;
Query Match 53.2%; Score 42; DB 2; Length 465;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 4 QSVVDYDGD SYMN 15
DB 415 KSMVDYDGTAFLN 426

RESULT 38
Q7QWA9 GIALA
ID Q7QWA9 GIALA PRELIMINARY; PRT; 587 AA.
AC Q7QWA9;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GLP 177 18980 17217.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AACB01000072; EAA39336.1; -; Genomic_DNA.
CC GO; GO:0005509; F:calcium ion binding; IEA.
CC InterPro; IPR011992; EF-Hand type.
CC InterPro; IPR002048; EF_Hand_Ca_bd.
CC Pfam; PF00036; ehand; 1.
CC PROSITE; PS00018; EF_HAND; UNKNOWN_1.
CC Calcium; Repeat.
CC SQ SEQUENCE 587 AA; 66458 MW; A3C5FC5DEF358A09 CRC64;
Query Match 53.2%; Score 42; DB 2; Length 587;
Best Local Similarity 58.3%; Pred. No. 2.7e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 4 QSVVDYDGD SYMN 15
DB 27 QAVDMVDGSGYVS 38

RESULT 39
QSV072 HALMA
ID QSV072 HALMA PRELIMINARY; PRT; 653 AA.
AC QSV072;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=rrnAC2250;
OS Haloarcula marismortui (Halo bacterium marismortui).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Haloarcula.
OX NCBI_TaxID=2238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 43049;
RX PubMed=15520287; DOI=10.1101/gr.2700304;
RA Baliga N.S., Bonneau R., Facciotti M.T., Pan M., Glusman G.,
RA Deutsch E.W., Shannon P., Chiu Y., Weng R.S., Gan R.R., Hung P.,
RA Date S.V., Marcotte E., Hood L., Ng W.V.;
RT "Genome sequence of Haloarcula marismortui: a halophilic archaeon from
RT The Dead Sea."
RL Genome Res. 14:2221-2234(2004).
DR EMBL; AY596297; AAV47081.1; -; Genomic_DNA.
DR GO; GO:0005856; C:cytoskeleton; IEA.
DR InterPro; IPR002017; Spectrin.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 653 AA; 74990 MW; 772A3303B13EC236 CRC64;
Query Match 53.2%; Score 42; DB 2; Length 653;
Best Local Similarity 40.0%; Pred. No. 3e+02;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 1 KASQSVVDYDGD SYMN 15


```
DE Ig kappa chain V-III region ABPC 22/PC 9245.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE (ABPC 22).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
RN [2]
RP PROTEIN SEQUENCE (PC 9245).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Garmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
CC -1- MISCELLANEOUS; The ABPC22 and PC9241 sequences are identical.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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-----
DR HSSP; P01665; 1QNZ.
DR SNR; P01662; 1-111.
DR ENSEMBL; ENSMUSG00000060064; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 38
FT REGION 39 53
FT REGION 54 60
FT REGION 61 92
FT REGION 93 101
FT REGION 102 111
FT DISULFID 23 92
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;

Query Match 51.9%; Score 41; DB 1; Length 111;
Best Local Similarity 53.3%; Pred. No. 62;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASQSVDYDGSVMN 15
   :||| | |:|:
DB 24 RASESVDSYGNSFMH 38

RESULT 45
KV3K_MOUSE
ID KV3K_MOUSE STANDARD; PRT; 111 AA.
AC P01663;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region PC 4050.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
```

```
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
RT "Rearrangement of genetic information may produce immunoglobulin  
RL diversity."; Nature 276:785-790(1978).  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC -----  
DR HSSP; P01665; 1QNZ.  
DR SMR; P01663; 1-111.  
DR Ensembl; ENSMUSG00000060064; Mus musculus.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
KW Direct protein sequencing; Immunoglobulin domain;  
KW Immunoglobulin V region.  
KW Immunoglobulin V region; Signal.  
FT REGION 1 23  
FT REGION 24 38 Framework-1.  
FT REGION 39 53 Complementarity-determining-1.  
FT REGION 54 60 Framework-2.  
FT REGION 61 92 Complementarity-determining-2.  
FT REGION 93 101 Framework-3.  
FT REGION 102 111 Complementarity-determining-3.  
FT DISULFID 23 92 Framework-4.  
FT NON_TER 111 111 By similarity.  
SQ SEQUENCE 111 AA; 12005 MW; 39D8761913453CB CRC64;  
  
Query Match 51.9%; Score 41; DB 1; Length 111;  
Best Local Similarity 53.3%; Pred. No. 62;  
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 KASQSVVDYDGSVMN 15  
Db :||:|||||:|:|:  
24 RASESVDSYGNFSFMH 38  
  
RESULT 46  
KV31_MOUSE  
ID KV31_MOUSE STANDARD; PRT; 131 AA.  
AC P01661;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ig kappa chain V-III region MOPC 63 precursor.  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP PROTEIN SEQUENCE OF 1-35.  
RX MEDLINE=78235887; PubMed=98179;  
RA Burestein Y., Schechter I.;  
RT "Primary structures of N-terminal extra peptide segments linked to the  
RT variable and constant regions of immunoglobulin light chain  
RT precursors; implications on the organization and controlled expression  
RT of immunoglobulin genes."; Biochemistry 17:2392-2400(1978).  
RL Biochemistry 17:2392-2400(1978).  
RN [2]  
RP PROTEIN SEQUENCE OF 21-131.  
RX MEDLINE=73140225; PubMed=4691517;  
RA McKean D.J., Potter M., Hood L.E.;  
RT "Mouse immunoglobulin chains. Pattern of sequence variation among  
RT kappa chains with limited sequence differences."; Biochemistry 12:760-771(1973).  
RN [3]  
RP SEQUENCE REVISION.  
RX MEDLINE=79012520; PubMed=99744;  
RA McKean D.J., Bell M., Potter M.;  
  
"Mechanisms of antibody diversity: multiple genes encode structurally  
related mouse kappa variable regions."; Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).  
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CC -----  
DR PIR; B90412; KVM5M6.  
DR HSSP; P01665; 1QNZ.  
DR SMR; P01661; 21-131.  
DR Ensembl; ENSMUSG00000060064; Mus musculus.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
KW Direct protein sequencing; Immunoglobulin domain;  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 20  
FT CHAIN 21 131 Ig kappa chain V-III region MOPC 63.  
FT REGION 21 43 Framework-1.  
FT REGION 44 58 Complementarity-determining-1.  
FT REGION 59 73 Framework-2.  
FT REGION 74 80 Complementarity-determining-2.  
FT REGION 81 112 Framework-3.  
FT REGION 113 121 Complementarity-determining-3.  
FT REGION 122 131 Framework-4.  
FT DISULFID 43 112 By similarity.  
FT NON_TER 131 131  
SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;  
  
Query Match 51.9%; Score 41; DB 1; Length 131;  
Best Local Similarity 53.3%; Pred. No. 75;  
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 KASQSVVDYDGSVMN 15  
Db :||:|||||:|:|:  
44 RASESVDSYGNFSFMH 58  
  
RESULT 47  
Q87I36_VIBPA  
ID Q87I36_VIBPA PRELIMINARY; PRT; 156 AA.  
AC Q87I36;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein VPA0770.  
GN OrderedLocustNames=VPA0770;  
OS Vibrio parahaemolyticus.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrio.  
OX NCBI_TaxID=670;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RX STRAIN=RIMD 2210633 / Serotype O3:K6;  
RC MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;  
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,  
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,  
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;  
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism  
RT distinct from that of V. cholerae."; Lancet 361:743-749(2003).  
RL Lancet 361:743-749(2003).  
DR EMBL; BA000032; BAC62113.1; -: Genomic DNA.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 156 AA; 17946 MW; D57A8B5CAEFD991F CRC64;  
  
Query Match 51.9%; Score 41; DB 2; Length 156;  
Best Local Similarity 50.0%; Pred. No. 91;  
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

QY 2 ASQVDYDGSYNV 15
 DB 92 ASESTQYIGDQFLN 105

RESULT 48
 Q735Z4_BACCI PRELIMINARY; PRT; 160 AA.
 AC Q735Z4; (Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DE Hypochemical protein.
 GN OrderedLocusNames=BCE31007;
 OS Bacillus cereus (strain ATCC 10987).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OX NCBI_TaxID=222523;
 RN [1]

NUCLEOTIDE SEQUENCE
 RP PubMed=14960714; DOI=10.1093/nar/ghk258;
 RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
 RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
 RA Nelson W.C., Kolscoe A.-B., Fraser C.M., Read T.D.;
 RT "The genome sequence of *Bacillus cereus* ATCC 10987 reveals metabolic
 RT adaptations and a large plasmid related to *Bacillus anthracis* pXO1.";
 RL Nucleic Acids Res. 32:977-988(2004).
 DR EMBL; AS017273; AAS41918.1; -; Genomic_DNA.
 DR TIGR; BCE31007; -;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 160 AA; 18815 MW; 547CAD0CC78F8E93 CRC64;

Query Match 51.9%; Score 41; DB 2; Length 160;
 Best Local Similarity 70.0%; Pred. No. 93;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 VYDGDGSYNV 15
 DB 45 VYDGDQLYIN 54

RESULT 49
 ID NUDT3_MOUSE STANDARD; PRT; 168 AA.
 AC Q9J146; Q6PG02; Q8BV71;
 DT 13-SEP-2005 (Rel. 48, Created)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Diphosphoinositol polyphosphate phosphohydrolase 1 (EC 3.6.1.52)
 DE (DIPP-1) (muDIPP1) (biadenosine 5',5',-P1,P6-hexaphosphate hydrolase
 DE 1) (EC 3.6.1.-) (Nucleoside diphosphate-linked moiety X motif 3)
 DE (Nudix motif 3).
 GN Name=Nudt3; Synonyms=Dipp1;
 OS Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

NUCLEOTIDE SEQUENCE [MRNA], TISSUE SPECIFICITY, AND MUTAGENESIS OF
 GLU-70.
 RP PubMed=15212765; DOI=10.1016/j.cellsig.2004.02.009;
 RX Chu C., Alapat D., Wen X., Timo K., Burstein D., Lisanti M.,
 RA Shears S., Kohtz D.S.;
 RT "Ectopic expression of murine diphosphoinositol polyphosphate
 RT phosphohydrolase 1 attenuates signaling through the ERK1/2 pathway.";
 RL Cell. Signal. 16:1045-1059(2004).
 RN [2]

NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP STRAIN=C57BL/6, and FVB/N; TISSUE=Brain, and Mammary tumor;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Maman A., Rodrigues S., Sanchez A.,
 RA Whiting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]

NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 81-168.
 RP STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RX Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kiyosawa H.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanagaya A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Perle G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).

-|- FUNCTION: Cleaves a beta-phosphate from the diphosphate groups in
 CC PP-insP5 (diphosphoinositol pentakisphosphate) and [PP]2-InsP4
 CC (bisdiphosphoinositol tetrakisphosphate), suggesting that it may
 CC play a role in signal transduction. InsP6 (inositol
 CC hexakisphosphate) is not a substrate. Also able to catalyze the
 CC hydrolysis of dinucleoside oligophosphates, with Ap6A and Ap5A
 CC being the preferred substrates. The major reaction products are
 CC ADP and p6a from Ap6A and ADP and ATP from Ap5A. Also able to
 CC hydrolyze PRPP (5-phosphoribosyl 1-pyrophosphate) (By similarity).
 CC Acts as a negative regulator of the ERK1/2 pathway.
 CC -|- CATALYTIC ACTIVITY: Diphospho-myo-inositol polyphosphate + H(2)O =
 CC myo-inositol polyphosphate + phosphate.
 CC -|- COFACTOR: Magnesium (By similarity).
 CC -|- ENZYME REGULATION: Inhibited by fluoride and InsP6 (By
 CC similarity).
 CC -|- SUBUNIT: Monomer (By similarity).
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -|- TISSUE SPECIFICITY: Present in heart, lung, liver and spleen (at
 CC protein level). Widely expressed.
 CC -|- SIMILARITY: Belongs to the Nudix hydrolase family. DIPP subfamily.
 CC -|- CAUTION: Ref.2 (AAH57331) sequence differs from that shown because

```

CC      it is chimeric at the C-terminus.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
DR      EMBL; AF264064; AAF74761.1; -; mRNA.
DR      EMBL; BC016534; AAH16534.1; -; mRNA.
DR      EMBL; BC046805; AAH46805.1; -; mRNA.
DR      EMBL; BC057331; AAH57331.1; ALT SEQ; mRNA.
DR      EMBL; AK079658; BAC37717.1; -; mRNA.
DR      Ensemble; ENSMUSG00000042113; Mus musculus.
DR      MGI; MGI:1928484; Nudt3.
DR      GO; GO:0005622; C:intracellular; ISS.
DR      GO; GO:0008486; P:diphosphoinositol-polyposphatase diphosphata. . .; ISS.
DR      GO; GO:0019722; P:calcium-mediated signaling; ISS.
DR      GO; GO:0019935; P:cyclic-nucleotide-mediated signaling; ISS.
DR      GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR      GO; GO:0046907; P:intracellular transport; ISS.
DR      GO; GO:0046831; P:regulation of RNA-nucleus export; ISS.
DR      InterPro; IPR000086; NUDIX_hydrolase.
DR      Pfam; PF00293; NUDIX; 1.
DR      PRINTS; PR00502; NUDIXFAMILY.
DR      PROSITE; PS00893; NUDIX; 1.
KW      Hydrolase; Magnesium; Metal-binding.
FT      MOTIF 51 72 NUDIX box.
FT      METAL 66 66 Magnesium (By similarity).
FT      METAL 70 70 Magnesium (Probable).
FT      SITE 84 84 Important for substrate recognition (By
FT      SITE 91 91 similarity).
FT      SITE 91 91 Important for substrate recognition (By
FT      MUTAGEN 70 70 E->Q: Loss of enzyme activity, but
FT      pathway.
FT      SEQUENCE 168 AA; 19030 MW; E543B5CB5E20910 CRC64;

Query Match 51.9%; Score 41; DB 1; Length 168;
Best Local Similarity 53.8%; Pred. No. 99;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KASQSVVDGDSY 13
Db |:::|||||
5 KSNQRTYDGDGY 17

RESULT 50
NUDT3 RAT STANDARD; PRT; 168 AA.
AC Q566C7;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Diphosphoinositol polyposphatase phosphohydrolase 1 (EC 3.6.1.52)
DE (DIPP-1) (Diadenosine 5',5''-P1,P6-hexaphosphate hydrolase 1)
DE (EC 3.6.1.-) (Nucleoside diphosphate-linked moiety X motif 3) (Nudix
DE motif 3).
GN Name=Nudt3; Synonyms=Dipp, Dipp1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Brain;
RG NIH - Mammalian Gene Collection (MGC) project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
[2]
RP PROTEIN SEQUENCE OF 3-17; 20-115 AND 117-121, FUNCTION, ENZYME
RP ACTIVITY, COFACTOR, ENZYME REGULATION, AND SUBUNIT.

```

```

RX MEDLINE=99043866; PubMed=9822604; DOI=10.1093/emboj/17.22.6599;
RA Saffary S.T., Caffrey J.J., Tang X., Benbenek M.E., Moyer M.B.,
RA Burkhardt W.A., Shears S.B.;
RT "A novel context for the 'MutT' module, a guardian of cell integrity,
RT in a diphosphoinositol polyphosphate phosphohydrolase.";
RL EMBO J. 17:6599-6607(1998).
CC -!- FUNCTION: Cleaves a beta-phosphate from the diphosphate groups in
CC PP-insP5 (diphosphoinositol pentakisphosphate) and [PP]2-insP4
CC (bisdiphosphoinositol tetrakisphosphate), suggesting that it may
CC play a role in signal transduction. InsP6 (inositol
CC hexakisphosphate) is not a substrate. Acts as a negative regulator
CC of the ERK1/2 pathway. Also able to catalyzes the hydrolysis of
CC dinucleoside oligophosphates, with Ap6A and Ap5A being the
CC preferred substrates. The major reaction products are ADP and p4a
CC from Ap6A and ADP and ATP from Ap5A. Also able to hydrolyze PRPP
CC (5-phosphoribosyl 1-pyrophosphate).
CC -!- CATALYTIC ACTIVITY: Diphospho-myo-inositol polyphosphate + H(2)O =
CC myo-inositol polyphosphate + phosphate.
CC -!- COFACTOR: Magnesium.
CC -!- ENZYME REGULATION: Inhibited by fluoride and InsP6.
CC -!- BIOPHYSICOCHEMICAL PROPERTIES:
CC Kinetic parameters:
CC KM=340 nM for PP-InsP5;
CC KM=34 nM for [PP]2-InsP4;
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the Nudix hydrolase family. DIPP subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR      EMBL; BC093618; AAH93618.1; -; mRNA.
DR      RGD; 1310183; Nudt3.
DR      InterPro; IPR000086; NUDIX_hydrolase.
DR      Pfam; PF00293; NUDIX; 1.
DR      PRINTS; PR00502; NUDIXFAMILY.
DR      PROSITE; PS00893; NUDIX; 1.
KW      Direct protein sequencing; Hydrolase; Magnesium; Metal-binding.
FT      MOTIF 51 72 NUDIX box.
FT      METAL 66 66 Magnesium (By similarity).
FT      METAL 70 70 Magnesium (By similarity).
FT      SITE 84 84 Important for substrate recognition (By
FT      SITE 91 91 similarity).
FT      SITE 91 91 Important for substrate recognition (By
FT      SEQUENCE 168 AA; 19096 MW; 6743B325524B634E CRC64;

Query Match 51.9%; Score 41; DB 1; Length 168;
Best Local Similarity 53.8%; Pred. No. 99;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KASQSVVDGDSY 13
Db |:::|||||
5 KSNQRTYDGDGY 17

Search completed: February 23, 2006, 09:49:26
Job time : 185.231 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 09:29:34 ; Search time 77.5385 seconds
(without alignments)
50.999 Million cell updates/sec

Title: US-10-723-872-20

Perfect score: 50
Sequence: 1 QQSNEDPPT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query % | Match | Length | DB ID | Description |
|------------|-------|---------|-------|--------|----------|-------------|
| 1 | 50 | 100.0 | 9 | 2 | AAR70197 | Mab 3B9 1 |
| 2 | 50 | 100.0 | 9 | 2 | AAY23774 | CDR of th |
| 3 | 50 | 100.0 | 9 | 2 | AAY18116 | Light cha |
| 4 | 50 | 100.0 | 52 | 6 | ABU56909 | Bon7/A Hc |
| 5 | 50 | 100.0 | 107 | 8 | ADR38683 | Mouse lig |
| 6 | 50 | 100.0 | 111 | 2 | AAY23781 | Light cha |
| 7 | 50 | 100.0 | 111 | 2 | AAY18123 | Light cha |
| 8 | 50 | 100.0 | 111 | 8 | ADR15140 | Mouse ant |
| 9 | 50 | 100.0 | 112 | 8 | ADR38675 | Mouse lig |
| 10 | 50 | 100.0 | 131 | 2 | AAR29008 | p64-K4 pr |
| 11 | 50 | 100.0 | 131 | 2 | AAR70202 | Humanized |
| 12 | 50 | 100.0 | 131 | 2 | AAW30278 | Light cha |
| 13 | 50 | 100.0 | 131 | 2 | AAW30274 | Light cha |
| 14 | 50 | 100.0 | 131 | 2 | AAY23779 | Light cha |
| 15 | 50 | 100.0 | 131 | 2 | AAY18126 | Light cha |
| 16 | 50 | 100.0 | 132 | 2 | AAR70189 | Mouse Mab |
| 17 | 50 | 100.0 | 132 | 2 | AAY23767 | Light cha |
| 18 | 50 | 100.0 | 132 | 2 | AAY18120 | Light cha |
| 19 | 47 | 94.0 | 9 | 8 | ADT75077 | Murine li |
| 20 | 47 | 94.0 | 113 | 8 | ADT75056 | Light cha |
| 21 | 45 | 90.0 | 9 | 2 | AAR70201 | Humanized |
| 22 | 45 | 90.0 | 9 | 2 | AAY23778 | CDR of th |
| 23 | 45 | 90.0 | 9 | 2 | AAY18119 | Light cha |
| 24 | 45 | 90.0 | 9 | 3 | AAY51138 | Murine CD |

| | | | | | | |
|----|----|------|-----|---|----------|------------|
| 25 | 45 | 90.0 | 9 | 3 | AAY59261 | Antibody |
| 26 | 45 | 90.0 | 10 | 5 | AAU70354 | Mouse Kap |
| 27 | 45 | 90.0 | 103 | 3 | AAY51140 | Murine de |
| 28 | 45 | 90.0 | 103 | 3 | AAY59263 | Antibody |
| 29 | 45 | 90.0 | 111 | 3 | AAY51146 | Murine de |
| 30 | 45 | 90.0 | 111 | 3 | AAY51144 | Murine de |
| 31 | 45 | 90.0 | 111 | 3 | AAY59267 | Antibody |
| 32 | 45 | 90.0 | 112 | 6 | ABO10750 | Variable |
| 33 | 45 | 90.0 | 112 | 6 | ABR44694 | Murine Mu |
| 34 | 45 | 90.0 | 112 | 8 | ADU67960 | Mouse Kab |
| 35 | 45 | 90.0 | 113 | 8 | ADQ90832 | Kabat sub |
| 36 | 45 | 90.0 | 131 | 2 | AAR32123 | Anti-CD4 |
| 37 | 45 | 90.0 | 131 | 2 | AAR75355 | Humanized |
| 38 | 45 | 90.0 | 131 | 2 | AAY23771 | Light cha |
| 39 | 45 | 90.0 | 131 | 2 | AAY18118 | Light cha |
| 40 | 45 | 90.0 | 305 | 3 | AAY51142 | Murine de |
| 41 | 45 | 90.0 | 305 | 3 | AAY51141 | Murine de |
| 42 | 45 | 90.0 | 305 | 3 | AAY59264 | Antibody |
| 43 | 45 | 90.0 | 305 | 3 | AAY59265 | Antibody |
| 44 | 42 | 84.0 | 17 | 2 | AAR66145 | CD-4 anti |
| 45 | 42 | 84.0 | 115 | 2 | AAR04134 | Anti-Leu |
| 46 | 42 | 84.0 | 131 | 2 | AAR04132 | Anti-Leu |
| 47 | 42 | 84.0 | 215 | 2 | AAR64202 | Monoclonal |
| 48 | 41 | 82.0 | 9 | 2 | AAW83029 | Anti-Fas |
| 49 | 41 | 82.0 | 9 | 3 | AAE14746 | Mouse ant |
| 50 | 41 | 82.0 | 9 | 5 | AAW90896 | Murine an |
| 51 | 41 | 82.0 | 9 | 5 | ABY74911 | Humanised |
| 52 | 41 | 82.0 | 9 | 5 | ABY74865 | Humanised |
| 53 | 41 | 82.0 | 9 | 8 | ADT75014 | Murine li |
| 54 | 41 | 82.0 | 103 | 2 | AAR47933 | Light cha |
| 55 | 41 | 82.0 | 103 | 2 | AAW89349 | Mouse 23F |
| 56 | 41 | 82.0 | 109 | 8 | ADT74994 | Light cha |
| 57 | 41 | 82.0 | 111 | 2 | AAR47494 | Murine an |
| 58 | 41 | 82.0 | 111 | 2 | AAR47492 | Humanised |
| 59 | 41 | 82.0 | 111 | 2 | AAR47935 | Humanised |
| 60 | 41 | 82.0 | 111 | 2 | AAW89351 | Humanised |
| 61 | 41 | 82.0 | 112 | 8 | ADG25827 | Anti-CD30 |
| 62 | 41 | 82.0 | 134 | 5 | ABY79725 | Anti-Stre |
| 63 | 41 | 82.0 | 238 | 2 | AAW83035 | Anti-Fas |
| 64 | 41 | 82.0 | 238 | 2 | AAW83042 | Anti-Fas |
| 65 | 41 | 82.0 | 238 | 2 | AAW83034 | Anti-Fas |
| 66 | 41 | 82.0 | 238 | 2 | AAW83033 | Anti-Fas |
| 67 | 41 | 82.0 | 238 | 2 | AAW83032 | Anti-Fas |
| 68 | 41 | 82.0 | 238 | 2 | AAW83031 | Anti-Fas |
| 69 | 41 | 82.0 | 238 | 3 | ABE14748 | Mouse ant |
| 70 | 41 | 82.0 | 238 | 3 | ABE14774 | Humanised |
| 71 | 41 | 82.0 | 238 | 3 | ABE14773 | Humanised |
| 72 | 41 | 82.0 | 238 | 3 | ABE14777 | Humanised |
| 73 | 41 | 82.0 | 238 | 3 | ABE14778 | Humanised |
| 74 | 41 | 82.0 | 238 | 3 | ABE14772 | Humanised |
| 75 | 41 | 82.0 | 238 | 3 | AAW90931 | Humanised |
| 76 | 41 | 82.0 | 238 | 3 | AAW90927 | Humanised |
| 77 | 41 | 82.0 | 238 | 3 | AAW90932 | Humanised |
| 78 | 41 | 82.0 | 238 | 3 | AAW90924 | Humanised |
| 79 | 41 | 82.0 | 238 | 3 | AAW90898 | Murine an |
| 80 | 41 | 82.0 | 238 | 3 | AAW90928 | Humanised |
| 81 | 41 | 82.0 | 238 | 3 | AAW90923 | Humanised |
| 82 | 41 | 82.0 | 238 | 3 | AAW90922 | Humanised |
| 83 | 41 | 82.0 | 238 | 3 | AAW90930 | Humanised |
| 84 | 41 | 82.0 | 238 | 5 | ABE74937 | Humanised |
| 85 | 41 | 82.0 | 238 | 5 | ABE74938 | Humanised |
| 86 | 41 | 82.0 | 238 | 5 | ABE74939 | Humanised |
| 87 | 41 | 82.0 | 238 | 5 | ABE74942 | Humanised |
| 88 | 41 | 82.0 | 238 | 5 | ABE74943 | Humanised |
| 89 | 41 | 82.0 | 238 | 5 | ABE74913 | Humanised |
| 90 | 41 | 82.0 | 238 | 5 | ABE74897 | Humanised |
| 91 | 41 | 82.0 | 238 | 5 | ABE74899 | Humanised |
| 92 | 41 | 82.0 | 238 | 5 | ABE74867 | Humanised |
| 93 | 41 | 82.0 | 238 | 5 | ABE74900 | Humanised |
| 94 | 41 | 82.0 | 238 | 5 | ABE74892 | Humanised |
| 95 | 41 | 82.0 | 238 | 5 | ABE74893 | Humanised |
| 96 | 41 | 82.0 | 238 | 5 | ABE74891 | Humanised |
| 97 | 41 | 82.0 | 238 | 5 | ABE74896 | Humanised |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|-----------|---------------------|-----|----|------|-----|---|----------|---------------------|
| 98 | 41 | 82.0 | 238 | 5 | ABB74901 | Abb74901 Humanised | 171 | 38 | 76.0 | 110 | 5 | AAO18536 | Aao18536 Murine Ma |
| 99 | 40 | 80.0 | 7 | 8 | ADRI5167 | Adri5167 Mouse ant | 172 | 38 | 76.0 | 112 | 9 | ABE21446 | Aeb21446 Anti-IL13 |
| 100 | 40 | 80.0 | 9 | 2 | AAR75477 | Aar75477 Mouse ant | 173 | 38 | 76.0 | 112 | 9 | ABE21493 | Aeb21493 Anti-IL13 |
| 101 | 40 | 80.0 | 52 | 6 | ABU56910 | Abu56910 BoNT/A Hc | 174 | 38 | 76.0 | 112 | 9 | ABE21495 | Aeb21495 Anti-IL13 |
| 102 | 40 | 80.0 | 111 | 8 | ADF71897 | Adf71897 Hu3G8VL-1 | 175 | 38 | 76.0 | 112 | 9 | ABE21501 | Aeb21501 Anti-IL13 |
| 103 | 40 | 80.0 | 112 | 2 | ARL13089 | Aar13089 Murine 1B | 176 | 38 | 76.0 | 112 | 9 | ABE31253 | Aeb31253 Antibody |
| 104 | 40 | 80.0 | 112 | 5 | ABB77332 | Abb77332 Mouse 1B4 | 177 | 38 | 76.0 | 112 | 9 | ABE31259 | Aeb31259 Antibody |
| 105 | 40 | 80.0 | 112 | 5 | ABB77331 | Abb77331 Veneered | 178 | 38 | 76.0 | 112 | 9 | ABE31204 | Aeb31204 Antibody |
| 106 | 40 | 80.0 | 112 | 6 | ABO27167 | AbO27167 Humanised | 179 | 38 | 76.0 | 112 | 9 | ABE31251 | Aeb31251 Antibody |
| 107 | 40 | 80.0 | 112 | 6 | ABO27166 | AbO27166 Mouse ant | 180 | 38 | 76.0 | 113 | 9 | ABE21354 | Aeb21354 Mouse ant |
| 108 | 40 | 80.0 | 112 | 8 | ADR38676 | Adr38676 Mouse lig | 181 | 38 | 76.0 | 113 | 9 | ABE31112 | Aeb31112 Antibody |
| 109 | 40 | 80.0 | 112 | 8 | ADR38684 | Adr38684 Mouse lig | 182 | 38 | 76.0 | 132 | 2 | AA37716 | Aar37716 Mouse 4C1 |
| 110 | 40 | 80.0 | 112 | 9 | ADV77267 | Adv77267 Murine an | 183 | 38 | 76.0 | 215 | 2 | AA37716 | Aar37716 Light cha |
| 111 | 40 | 80.0 | 112 | 9 | ADV77266 | Adv77266 Veneered | 184 | 38 | 76.0 | 218 | 8 | ADP88435 | Adp88435 Antibody |
| 112 | 40 | 80.0 | 112 | 8 | ADX72851 | Adx72851 Plant ful | 185 | 38 | 76.0 | 218 | 8 | ADP88427 | Adp88427 Antibody |
| 113 | 40 | 80.0 | 112 | 8 | ADF71899 | Adf71899 Hu3G8VL-1 | 186 | 38 | 76.0 | 218 | 8 | ADP88451 | Adp88451 Antibody |
| 114 | 40 | 80.0 | 249 | 4 | ABAB20436 | Abab20436 Anti-FIX/ | 187 | 38 | 76.0 | 218 | 8 | ADP88443 | Adp88443 Antibody |
| 115 | 40 | 80.0 | 249 | 4 | ABAB20435 | Abab20435 Anti-FIX/ | 188 | 38 | 76.0 | 238 | 6 | ADA47339 | Ada47339 TRX1 lig |
| 116 | 40 | 80.0 | 294 | 4 | ABAB20442 | Abab20442 Anti-FIX/ | 189 | 38 | 76.0 | 238 | 6 | ADA47330 | Ada47330 TRX1 lig |
| 117 | 40 | 80.0 | 325 | 4 | ABAB20438 | Abab20438 Anti-FIX/ | 190 | 38 | 76.0 | 238 | 6 | ADA47338 | Ada47338 TRX1 lig |
| 118 | 40 | 80.0 | 325 | 4 | ABAB20437 | Abab20437 Anti-FIX/ | 191 | 38 | 76.0 | 238 | 6 | ADA47332 | Ada47332 TRX1 lig |
| 119 | 39 | 78.0 | 9 | 2 | AAW01149 | Aaw01149 Mab 1.4 1 | 193 | 38 | 76.0 | 238 | 8 | ADP88442 | Adp88442 Antibody |
| 120 | 39 | 78.0 | 9 | 2 | AAW01149 | Aaw01149 Mab 1.4 1 | 193 | 38 | 76.0 | 238 | 8 | ADP88450 | Adp88450 Antibody |
| 121 | 39 | 78.0 | 9 | 2 | AAW44172 | Aaw44172 Monoclonal | 194 | 38 | 76.0 | 238 | 8 | ADP88426 | Adp88426 Antibody |
| 122 | 39 | 78.0 | 9 | 4 | AAU07462 | Aau07462 Synthetic | 195 | 38 | 76.0 | 238 | 8 | ADQ87972 | Adq87972 Light cha |
| 123 | 39 | 78.0 | 9 | 5 | AAU99855 | Aau99855 Mouse AC1 | 196 | 38 | 76.0 | 238 | 8 | ADQ87976 | Adq87976 Light cha |
| 124 | 39 | 78.0 | 9 | 7 | AAO29929 | Aao29929 Mouse ant | 197 | 38 | 76.0 | 238 | 8 | ADQ87964 | Adq87964 Light cha |
| 125 | 39 | 78.0 | 9 | 8 | ADJ87918 | Adj87918 Mouse AC1 | 198 | 38 | 76.0 | 238 | 8 | ADQ87968 | Adq87968 Light cha |
| 126 | 39 | 78.0 | 9 | 8 | ADP38847 | Adp38847 Mouse lig | 199 | 38 | 76.0 | 238 | 8 | ADQ87968 | Adq87968 Light cha |
| 127 | 39 | 78.0 | 52 | 6 | ABU56912 | Abu56912 BoNT/A Hc | 200 | 38 | 76.0 | 248 | 9 | ABE21503 | Aeb21503 Anti-IL13 |
| 128 | 39 | 78.0 | 106 | 2 | AA33309 | Aar33309 MaB15 lig | 201 | 38 | 76.0 | 248 | 9 | ABE31261 | Aeb31261 Monoclonal |
| 129 | 39 | 78.0 | 106 | 3 | AA85197 | Aay85197 Light cha | 202 | 38 | 76.0 | 291 | 6 | ABR42054 | Abr42054 CDR3 from |
| 130 | 39 | 78.0 | 107 | 8 | ADQ06815 | Ado06815 Virucidal | 203 | 37 | 74.0 | 9 | 2 | AAW27346 | Aaw27346 CDR3 from |
| 131 | 39 | 78.0 | 107 | 8 | ADQ06843 | Ado06843 Virucidal | 204 | 37 | 74.0 | 9 | 8 | ADT75081 | Adt75081 Murine li |
| 132 | 39 | 78.0 | 107 | 8 | ADQ06816 | Ado06816 Virucidal | 205 | 37 | 74.0 | 9 | 8 | ADT75144 | Adt75144 Murine li |
| 133 | 39 | 78.0 | 107 | 8 | ADQ06814 | Ado06814 Virucidal | 206 | 37 | 74.0 | 9 | 8 | ADT75015 | Adt75015 Murine li |
| 134 | 39 | 78.0 | 111 | 1 | AAFP90841 | Aap90841 Immunoglo | 207 | 37 | 74.0 | 52 | 6 | ABU56917 | Abu56917 BoNT/A Hc |
| 135 | 39 | 78.0 | 111 | 2 | AA85123 | Aay85123 Mouse ant | 208 | 37 | 74.0 | 53 | 6 | ABU56848 | Abu56848 BoNT/A Hc |
| 136 | 39 | 78.0 | 111 | 2 | AA85127 | Aay85127 Mouse-hum | 209 | 37 | 74.0 | 107 | 2 | AAW27353 | Aaw27353 Light cha |
| 137 | 39 | 78.0 | 111 | 2 | AA85127 | Aay85127 Mouse-hum | 210 | 37 | 74.0 | 109 | 8 | ADT75009 | Adt75009 Light cha |
| 138 | 39 | 78.0 | 111 | 2 | AA85127 | Aay85127 Mouse-hum | 211 | 37 | 74.0 | 109 | 8 | ADT74995 | Adt74995 Light cha |
| 139 | 39 | 78.0 | 111 | 5 | AAU99852 | Aau99852 Chimeric | 212 | 37 | 74.0 | 109 | 8 | ADT75003 | Adt75003 Light cha |
| 140 | 39 | 78.0 | 111 | 7 | AAO29926 | Aao29926 Mouse AC1 | 213 | 37 | 74.0 | 111 | 2 | AA48622 | Aar48622 Sequence |
| 141 | 39 | 78.0 | 111 | 8 | ADJ87912 | Adj87912 Mouse AC1 | 214 | 37 | 74.0 | 111 | 2 | AA48623 | Aar48623 Sequence |
| 142 | 39 | 78.0 | 111 | 9 | ADY85020 | Ady85020 Human HMG | 215 | 37 | 74.0 | 111 | 2 | AA65172 | Aar65172 Murine NM |
| 143 | 39 | 78.0 | 111 | 9 | ABE13680 | Aeb13680 Human vlc | 216 | 37 | 74.0 | 111 | 8 | ADT75059 | Adt75059 Region pr |
| 144 | 39 | 78.0 | 111 | 9 | ABE13688 | Aeb13688 Human ant | 217 | 37 | 74.0 | 111 | 8 | ADT75059 | Adt75059 Light cha |
| 145 | 39 | 78.0 | 111 | 9 | ABE13684 | Aeb13684 Human ant | 218 | 37 | 74.0 | 112 | 2 | AA10539 | Aar10539 Chimeric |
| 146 | 39 | 78.0 | 111 | 9 | ABE13678 | Aeb13678 Human lig | 219 | 37 | 74.0 | 112 | 2 | AA79156 | Aar79156 Human Igs |
| 147 | 39 | 78.0 | 111 | 9 | ABE13682 | Aeb13682 Human ant | 220 | 37 | 74.0 | 112 | 2 | AA79158 | Aar79158 Human Igs |
| 148 | 39 | 78.0 | 111 | 9 | ABE13689 | Aeb13689 Human ant | 221 | 37 | 74.0 | 112 | 2 | AAW27527 | Aaw27527 Light cha |
| 149 | 39 | 78.0 | 111 | 9 | ABE13683 | Aeb13683 Human ant | 222 | 37 | 74.0 | 112 | 2 | AAW27358 | Aaw27358 Light cha |
| 150 | 39 | 78.0 | 112 | 2 | AA24575 | Aar24575 Human x m | 223 | 37 | 74.0 | 112 | 8 | ADR38689 | Adr38689 Mouse lig |
| 151 | 39 | 78.0 | 112 | 4 | AAU07516 | Aau07516 Antibody | 224 | 37 | 74.0 | 112 | 8 | ADT75130 | Adt75130 Light cha |
| 152 | 39 | 78.0 | 112 | 4 | AAU07480 | Aau07480 Synthetic | 225 | 37 | 74.0 | 112 | 8 | ADT75123 | Adt75123 Light cha |
| 153 | 39 | 78.0 | 113 | 4 | AA871895 | Aab71895 Monoclonal | 226 | 37 | 74.0 | 112 | 8 | ADT75137 | Adt75137 Light cha |
| 154 | 39 | 78.0 | 113 | 8 | ADQ06847 | Ado06847 Virucidal | 227 | 37 | 74.0 | 112 | 8 | ADT75136 | Adt75136 Light cha |
| 155 | 39 | 78.0 | 113 | 8 | ADQ06796 | Ado06796 Virucidal | 228 | 37 | 74.0 | 113 | 8 | ADT75124 | Adt75124 Light cha |
| 156 | 39 | 78.0 | 113 | 8 | ADQ06849 | Ado06849 Virucidal | 229 | 37 | 74.0 | 113 | 8 | ADT75131 | Adt75131 Light cha |
| 157 | 39 | 78.0 | 113 | 8 | ADQ06851 | Ado06851 Virucidal | 230 | 37 | 74.0 | 113 | 8 | ADT75127 | Adt75127 Light cha |
| 158 | 39 | 78.0 | 131 | 1 | AA90543 | Aap90543 Amino aci | 231 | 37 | 74.0 | 113 | 8 | ADT75135 | Adt75135 Light cha |
| 159 | 39 | 78.0 | 131 | 2 | AAW01143 | Aaw01143 Mab 1.4 1 | 232 | 37 | 74.0 | 121 | 2 | AA48616 | Aar48616 Sequence |
| 160 | 39 | 78.0 | 131 | 2 | AAW44168 | Aaw44168 Monoclonal | 233 | 37 | 74.0 | 121 | 2 | AAW09259 | Aaw09259 Monoclonal |
| 161 | 39 | 78.0 | 218 | 2 | AAW13563 | Aaw13563 Humanised | 234 | 37 | 74.0 | 132 | 2 | AA10920 | Aar10920 kappa lig |
| 162 | 39 | 78.0 | 218 | 9 | ABE13693 | Aeb13693 Human ant | 235 | 37 | 74.0 | 179 | 8 | ADS17745 | Adsl7745 Anti-CEA |
| 163 | 39 | 78.0 | 220 | 8 | ADQ06858 | Ado06858 Virucidal | 236 | 37 | 74.0 | 223 | 8 | ADS17434 | Adsl7434 Amino aci |
| 164 | 39 | 78.0 | 220 | 8 | ADQ06856 | Ado06856 Virucidal | 237 | 37 | 74.0 | 237 | 2 | AAW73873 | Aaw73873 Human ant |
| 165 | 39 | 78.0 | 252 | 2 | AAW01751 | Aaw01751 MHI monoc | 238 | 37 | 74.0 | 240 | 2 | ADD12876 | Add12876 C2D8/meta |
| 166 | 39 | 78.0 | 252 | 4 | AAU07497 | Aau07497 Synthetic | 239 | 37 | 74.0 | 543 | 7 | ADD12876 | Add12876 C2D8/meta |
| 167 | 38 | 76.0 | 9 | 5 | AAO18542 | Aao18542 Murine Ma | 240 | 37 | 74.0 | 622 | 6 | ABR52917 | Abr52917 Protein s |
| 168 | 38 | 76.0 | 9 | 5 | ABE21466 | Aeb21466 Mouse ant | 241 | 37 | 74.0 | 692 | 6 | ABR52917 | Abr52917 Protein s |
| 169 | 38 | 76.0 | 9 | 9 | ABE31224 | Aeb31224 Antibody | 242 | 37 | 74.0 | 692 | 7 | ADK62484 | Adk62484 Disease t |
| 170 | 38 | 76.0 | 28 | 3 | AA91016 | Aay91016 1F7 antib | 243 | 37 | 74.0 | 692 | 8 | ADK62484 | Adk62484 Disease t |

| | | | | | | | | | | | | | |
|-----|----|------|------|---|-----------|---------------------|-----|----|------|------|---|----------|---------------------|
| 244 | 37 | 74.0 | 1040 | 8 | ADSI17749 | Adsi17749 Rat major | 317 | 35 | 70.0 | 218 | 3 | AAB07472 | Aab07472 Amino aci |
| 245 | 37 | 74.0 | 1072 | 8 | ADSI17747 | Adsi17747 Human maj | 318 | 35 | 70.0 | 218 | 4 | AAB47087 | Aab47087 Anti-IgE |
| 246 | 37 | 74.0 | 1127 | 8 | ADSI17789 | Adsi17789 Polylysin | 319 | 35 | 70.0 | 218 | 4 | AAB76947 | Aab76947 Full vari |
| 247 | 37 | 74.0 | 1159 | 8 | ADSI17787 | Adsi17787 Polylysin | 320 | 35 | 70.0 | 218 | 4 | AAB76949 | Aab76949 Full leng |
| 248 | 37 | 74.0 | 1206 | 8 | ADSI17763 | Adsi17763 GAL4 + ra | 321 | 35 | 70.0 | 218 | 4 | AAB76951 | Aab76951 Full leng |
| 249 | 37 | 74.0 | 1238 | 8 | ADSI17761 | Adsi17761 GAL4 + hu | 322 | 35 | 70.0 | 218 | 4 | AAB76953 | Aab76953 Variable |
| 250 | 37 | 74.0 | 1273 | 8 | ADSI17777 | Adsi17777 MS2 pepti | 323 | 35 | 70.0 | 218 | 4 | AAB76958 | Aab76958 Variable |
| 251 | 36 | 72.0 | 9 | 8 | ADT75147 | Adt75147 Murine li | 324 | 35 | 70.0 | 218 | 4 | AAB74211 | Aab74211 E27 anti- |
| 252 | 36 | 72.0 | 110 | 2 | AAR60810 | Aar60810 Light cha | 325 | 35 | 70.0 | 218 | 6 | ABU62797 | Abu62797 E27 anti- |
| 253 | 36 | 72.0 | 111 | 2 | AAR60810 | Aar60810 Light cha | 326 | 35 | 70.0 | 218 | 6 | ABU62797 | Abu62797 E27 anti- |
| 254 | 36 | 72.0 | 112 | 2 | AAW00830 | Aaw00830 Variable | 327 | 35 | 70.0 | 218 | 7 | ADF69597 | Adf69597 Human ant |
| 255 | 36 | 72.0 | 112 | 2 | AAW19016 | Aaw19016 Anti-huma | 328 | 35 | 70.0 | 218 | 7 | ADF29038 | Adf29038 Anti-IgE |
| 256 | 36 | 72.0 | 112 | 6 | ABOI0751 | AbOI0751 Consensus | 329 | 35 | 70.0 | 218 | 8 | ADF71903 | Adf71903 Hu3G8VL-4 |
| 257 | 36 | 72.0 | 112 | 6 | ABR44695 | AbR44695 Murine J5 | 329 | 35 | 70.0 | 218 | 8 | ADF71920 | Adf71920 Hu3G8VL-2 |
| 258 | 36 | 72.0 | 112 | 6 | ADU67961 | AdU67961 Mouse ant | 330 | 35 | 70.0 | 218 | 8 | ADN07034 | Adn07034 Anti-IgE |
| 259 | 36 | 72.0 | 113 | 8 | ADQ09083 | Adq09083 Kabat sub | 331 | 35 | 70.0 | 218 | 8 | ADN07045 | Adn07045 Anti-IgE |
| 260 | 36 | 72.0 | 113 | 8 | ADT75140 | Adt75140 Light cha | 332 | 35 | 70.0 | 218 | 8 | ADN07036 | Adn07036 Anti-IgE |
| 261 | 36 | 72.0 | 113 | 8 | ADT75129 | Adt75129 Light cha | 333 | 35 | 70.0 | 218 | 8 | ADN07038 | Adn07038 Anti-IgE |
| 262 | 36 | 72.0 | 113 | 8 | ADT75141 | Adt75141 Light cha | 334 | 35 | 70.0 | 218 | 8 | ADN07040 | Adn07040 Anti-IgE |
| 263 | 36 | 72.0 | 113 | 8 | ADT75141 | Adt75141 Light cha | 335 | 35 | 70.0 | 218 | 8 | ADN07040 | Adn07040 Anti-IgE |
| 264 | 36 | 72.0 | 120 | 2 | AAR48620 | Aar48620 Sequence | 336 | 35 | 70.0 | 218 | 8 | ADT55439 | Adt55439 Anti IgE |
| 265 | 36 | 72.0 | 238 | 5 | AAE18371 | Aae18371 Human pen | 337 | 35 | 70.0 | 218 | 8 | ADT55438 | Adt55438 Anti IgE |
| 266 | 36 | 72.0 | 238 | 5 | ABG76346 | Abg76346 Mouse DAV | 338 | 35 | 70.0 | 218 | 9 | ADW00660 | Adw00660 Human ant |
| 267 | 36 | 72.0 | 238 | 9 | ABE96755 | Abe96755 DAV-1 ant | 339 | 35 | 70.0 | 218 | 9 | ADW00667 | Adw00667 Human ant |
| 268 | 36 | 72.0 | 435 | 8 | ADN24236 | Adn24236 Bacterial | 340 | 35 | 70.0 | 218 | 9 | ADW00656 | Adw00656 Human ant |
| 269 | 36 | 72.0 | 495 | 3 | AAG29957 | Aag29957 Arabidops | 341 | 35 | 70.0 | 218 | 9 | ADW00662 | Adw00662 Human ant |
| 270 | 36 | 72.0 | 513 | 3 | AAG29956 | Aag29956 Arabidops | 342 | 35 | 70.0 | 218 | 9 | ADW00691 | Adw00691 Human ant |
| 271 | 36 | 72.0 | 517 | 3 | AAG29955 | Aag29955 Arabidops | 343 | 35 | 70.0 | 218 | 9 | ADW00692 | Adw00692 Human ant |
| 272 | 36 | 72.0 | 1693 | 4 | ABBS8927 | Abbs8927 Drosophil | 344 | 35 | 70.0 | 218 | 9 | ADW79895 | Adw79895 Anti-IgE |
| 273 | 35 | 70.0 | 9 | 9 | ADZ99437 | Adz99437 Rat anti- | 345 | 35 | 70.0 | 218 | 9 | ADW79893 | Adw79893 Anti-IgE |
| 274 | 35 | 70.0 | 10 | 8 | ADM78101 | Adm78101 Human SUB | 346 | 35 | 70.0 | 218 | 9 | ADW79897 | Adw79897 Anti-IgE |
| 275 | 35 | 70.0 | 20 | 9 | ADW95719 | Adw95719 Anti-hil- | 347 | 35 | 70.0 | 218 | 9 | ADW79902 | Adw79902 Anti-IgE |
| 276 | 35 | 70.0 | 20 | 9 | ADX15724 | Adx15724 Mouse ant | 348 | 35 | 70.0 | 218 | 9 | ADW79891 | Adw79891 Anti-IgE |
| 277 | 35 | 70.0 | 111 | 2 | AAR33305 | Aar33305 MeE11 lig | 349 | 35 | 70.0 | 218 | 9 | ADZ99438 | Adz99438 Humanized |
| 278 | 35 | 70.0 | 111 | 2 | AAW95650 | Aaw95650 Mus muscu | 350 | 35 | 70.0 | 218 | 9 | AEBS6304 | Aeb56304 Anti-IgE |
| 279 | 35 | 70.0 | 111 | 3 | AAW95651 | Aaw95651 Mus muscu | 351 | 35 | 70.0 | 218 | 9 | AEBS6305 | Aeb56305 Anti-IgE |
| 280 | 35 | 70.0 | 111 | 3 | AAW85193 | Aay85193 Light cha | 352 | 35 | 70.0 | 219 | 8 | ADN07066 | Adn07066 F(ab)-pha |
| 281 | 35 | 70.0 | 111 | 4 | AAW76940 | Aab76940 Variable | 353 | 35 | 70.0 | 219 | 8 | ADW00688 | Adw00688 Expressio |
| 282 | 35 | 70.0 | 111 | 8 | AAW76939 | Aab76939 Variable | 354 | 35 | 70.0 | 241 | 8 | ADQ90719 | Adq90719 Anti-IgE |
| 283 | 35 | 70.0 | 111 | 8 | ADT71919 | Adt71919 Hu3G8VL-4 | 355 | 35 | 70.0 | 241 | 8 | ADQ90717 | Adq90717 Anti-IgE |
| 284 | 35 | 70.0 | 111 | 8 | ADN07026 | Adn07026 Murine an | 356 | 35 | 70.0 | 248 | 2 | AAW95668 | Aaw95668 Mus muscu |
| 285 | 35 | 70.0 | 111 | 8 | ADN07027 | Adn07027 Murine an | 357 | 35 | 70.0 | 248 | 2 | AAW95667 | Aaw95667 Mus muscu |
| 286 | 35 | 70.0 | 111 | 9 | ADW00648 | Adw00648 Murine Ma | 358 | 35 | 70.0 | 248 | 4 | AAW76957 | Aab76957 SFV fragm |
| 287 | 35 | 70.0 | 111 | 9 | ADW00649 | Adw00649 Human F(a | 359 | 35 | 70.0 | 248 | 4 | AAW76956 | Aab76956 SFV fragm |
| 288 | 35 | 70.0 | 112 | 9 | ADW95716 | Adw95716 Mouse ant | 360 | 35 | 70.0 | 248 | 8 | ADN07044 | Adn07044 Anti-IgE |
| 289 | 35 | 70.0 | 112 | 9 | ADX15721 | Adx15721 Mouse ant | 361 | 35 | 70.0 | 248 | 8 | ADN07043 | Adn07043 Anti-IgE |
| 290 | 35 | 70.0 | 114 | 2 | AAW95654 | Aaw95654 Mus muscu | 362 | 35 | 70.0 | 248 | 9 | ADW00666 | Adw00666 Human ant |
| 291 | 35 | 70.0 | 114 | 2 | AAW95655 | Aaw95655 Mus muscu | 363 | 35 | 70.0 | 248 | 9 | ADW00665 | Adw00665 Human ant |
| 292 | 35 | 70.0 | 114 | 2 | AAW95655 | Aaw95655 Mus muscu | 364 | 35 | 70.0 | 248 | 9 | ADW79900 | Adw79900 Anti-IgE |
| 293 | 35 | 70.0 | 114 | 2 | AAW76944 | Aab76944 Variable | 365 | 35 | 70.0 | 248 | 9 | ADW79901 | Adw79901 Anti-IgE |
| 294 | 35 | 70.0 | 114 | 4 | AAW76942 | Aab76942 Variable | 366 | 35 | 70.0 | 282 | 3 | AAG41486 | Aag41486 Arabidops |
| 295 | 35 | 70.0 | 114 | 4 | AAW76943 | Aab76943 Variable | 367 | 35 | 70.0 | 301 | 3 | AAG41485 | Aag41485 Arabidops |
| 296 | 35 | 70.0 | 114 | 8 | AAW7031 | Adw7031 Anti-IgE | 368 | 35 | 70.0 | 301 | 8 | ADN73669 | Adn73669 Thale cre |
| 297 | 35 | 70.0 | 114 | 8 | ADN07029 | Adn07029 Anti-IgE | 369 | 35 | 70.0 | 304 | 4 | AAE02541 | Aae02541 A. thalia |
| 298 | 35 | 70.0 | 114 | 8 | ADN07030 | Adn07030 Anti-IgE | 370 | 35 | 70.0 | 304 | 5 | AAU92994 | Aau92994 Arabidops |
| 299 | 35 | 70.0 | 114 | 8 | ADW00690 | Adw00690 Human ant | 371 | 35 | 70.0 | 304 | 7 | ADD30740 | AdD30740 Plant yie |
| 300 | 35 | 70.0 | 114 | 9 | ADW00653 | Adw00653 Human ant | 372 | 35 | 70.0 | 304 | 7 | ADZ37249 | Adz37249 Plant yie |
| 301 | 35 | 70.0 | 114 | 9 | ADW00651 | Adw00651 Human ant | 373 | 35 | 70.0 | 304 | 8 | AD143793 | Ad143793 Plant tra |
| 302 | 35 | 70.0 | 114 | 9 | ADW00652 | Adw00652 Human ant | 374 | 35 | 70.0 | 304 | 8 | ADO01705 | Ado01705 Thalescres |
| 303 | 35 | 70.0 | 114 | 9 | ADW79888 | Adw79888 Anti-IgE | 375 | 35 | 70.0 | 304 | 9 | AEA27069 | Aea27069 Stress to |
| 304 | 35 | 70.0 | 114 | 9 | ADW79887 | Adw79887 Anti-IgE | 376 | 35 | 70.0 | 318 | 3 | AAG41484 | Aag41484 Arabidops |
| 305 | 35 | 70.0 | 114 | 9 | ADW79886 | Adw79886 Anti-IgE | 377 | 35 | 70.0 | 430 | 8 | ADY08610 | Ady08610 Plant ful |
| 306 | 35 | 70.0 | 117 | 8 | ADW78053 | Adm78053 Human SKB | 378 | 35 | 70.0 | 584 | 2 | AAE88425 | Aae88425 Arabidops |
| 307 | 35 | 70.0 | 121 | 2 | AAW33346 | Aar33346 Sequence | 379 | 35 | 70.0 | 584 | 4 | AEF01922 | Aae01922 Arabidops |
| 308 | 35 | 70.0 | 121 | 2 | AAW48615 | Aar48615 Sequence | 380 | 35 | 70.0 | 584 | 5 | AAU93140 | Aau93140 Arabidops |
| 309 | 35 | 70.0 | 121 | 2 | AAW09274 | Aaw09274 MAB NM-01 | 381 | 35 | 70.0 | 584 | 7 | ADD30785 | AdD30785 Plant yie |
| 310 | 35 | 70.0 | 218 | 2 | AAW95660 | Aaw95660 Mus muscu | 382 | 35 | 70.0 | 584 | 8 | AD144001 | Ad144001 Plant tra |
| 311 | 35 | 70.0 | 218 | 2 | AAW95664 | Aaw95664 Mus muscu | 383 | 35 | 70.0 | 584 | 8 | ADO02219 | Ado02219 Thalescres |
| 312 | 35 | 70.0 | 218 | 2 | AAW95662 | Aaw95662 Mus muscu | 384 | 35 | 70.0 | 703 | 6 | ABE62416 | AbE62416 V AtPase |
| 313 | 35 | 70.0 | 218 | 2 | AAW95669 | Aaw95669 Mus muscu | 385 | 35 | 70.0 | 832 | 6 | ADP86408 | AdP86408 Aspergill |
| 314 | 35 | 70.0 | 218 | 2 | AAW95658 | Aaw95658 Mus muscu | 386 | 35 | 70.0 | 1592 | 6 | ABR53869 | ABr53869 Protein s |
| 315 | 35 | 70.0 | 218 | 2 | AAW50030 | Aay50030 Human E27 | 387 | 35 | 70.0 | 1592 | 7 | ADK64886 | AdK64886 Disease t |
| 316 | 35 | 70.0 | 218 | 3 | AAW85200 | Aay85200 Light cha | 388 | 34 | 68.0 | 9 | 4 | AAW62875 | Anti-SAF- |
| | | | | | | | 389 | 34 | 68.0 | 9 | 9 | AEA45474 | Apolioppr |

| | | | | | | | | |
|-----|----|------|-----|---|-----------|-----------|--------------|-----|
| 390 | 34 | 68.0 | 11 | 6 | ADAS1564 | AdaS1564 | Human | her |
| 391 | 34 | 68.0 | 12 | 6 | ADAS1565 | AdaS1565 | Human | her |
| 392 | 34 | 68.0 | 12 | 6 | ADAS1574 | AdaS1574 | Human | her |
| 393 | 34 | 68.0 | 13 | 6 | ADAS1575 | AdaS1575 | Human | her |
| 394 | 34 | 68.0 | 13 | 6 | ADAS1583 | AdaS1583 | Human | her |
| 395 | 34 | 68.0 | 13 | 6 | ADAS1566 | AdaS1566 | Human | her |
| 396 | 34 | 68.0 | 14 | 6 | ADAS1591 | AdaS1591 | Human | her |
| 397 | 34 | 68.0 | 14 | 6 | ADAS1567 | AdaS1567 | Human | her |
| 398 | 34 | 68.0 | 14 | 6 | ADAS1584 | AdaS1584 | Human | her |
| 399 | 34 | 68.0 | 14 | 6 | ADAS1576 | AdaS1576 | Human | her |
| 400 | 34 | 68.0 | 15 | 6 | ADAS1598 | AdaS1598 | Human | her |
| 401 | 34 | 68.0 | 15 | 6 | ADAS1577 | AdaS1577 | Human | her |
| 402 | 34 | 68.0 | 15 | 6 | ADAS1592 | AdaS1592 | Human | her |
| 403 | 34 | 68.0 | 15 | 6 | ADAS1568 | AdaS1568 | Human | her |
| 404 | 34 | 68.0 | 15 | 6 | ADAS1585 | AdaS1585 | Human | her |
| 405 | 34 | 68.0 | 16 | 6 | ADAS1578 | AdaS1578 | Human | her |
| 406 | 34 | 68.0 | 16 | 6 | ADAS1599 | AdaS1599 | Human | her |
| 407 | 34 | 68.0 | 16 | 6 | ADAS1569 | AdaS1569 | Human | her |
| 408 | 34 | 68.0 | 16 | 6 | ADAS1593 | AdaS1593 | Human | her |
| 409 | 34 | 68.0 | 16 | 6 | ADAS1586 | AdaS1586 | Human | her |
| 410 | 34 | 68.0 | 16 | 6 | ADAS1604 | AdaS1604 | Human | her |
| 411 | 34 | 68.0 | 17 | 6 | ADAS1579 | AdaS1579 | Human | her |
| 412 | 34 | 68.0 | 17 | 6 | ADAS1605 | AdaS1605 | Human | her |
| 413 | 34 | 68.0 | 17 | 6 | ADAS1594 | AdaS1594 | Human | her |
| 414 | 34 | 68.0 | 17 | 6 | ADAS1600 | AdaS1600 | Human | her |
| 415 | 34 | 68.0 | 17 | 6 | ADAS1587 | AdaS1587 | Human | her |
| 416 | 34 | 68.0 | 17 | 6 | ADAS1570 | AdaS1570 | Human | her |
| 417 | 34 | 68.0 | 17 | 6 | ADAS1609 | AdaS1609 | Human | her |
| 418 | 34 | 68.0 | 18 | 6 | ADAS1588 | AdaS1588 | Human | her |
| 419 | 34 | 68.0 | 18 | 6 | ADAS1595 | AdaS1595 | Human | her |
| 420 | 34 | 68.0 | 18 | 6 | ADAS1613 | AdaS1613 | Human | her |
| 421 | 34 | 68.0 | 18 | 6 | ADAS1571 | AdaS1571 | Human | her |
| 422 | 34 | 68.0 | 18 | 6 | ADAS1606 | AdaS1606 | Human | her |
| 423 | 34 | 68.0 | 18 | 6 | ADAS1610 | AdaS1610 | Human | her |
| 424 | 34 | 68.0 | 18 | 6 | ADAS1580 | AdaS1580 | Human | her |
| 425 | 34 | 68.0 | 18 | 6 | ADAS1601 | AdaS1601 | Human | her |
| 426 | 34 | 68.0 | 19 | 6 | ADAS1589 | AdaS1589 | Human | her |
| 427 | 34 | 68.0 | 19 | 6 | ADAS1602 | AdaS1602 | Human | her |
| 428 | 34 | 68.0 | 19 | 6 | ADAS1596 | AdaS1596 | Human | her |
| 429 | 34 | 68.0 | 19 | 6 | ADAS1607 | AdaS1607 | Human | her |
| 430 | 34 | 68.0 | 19 | 6 | ADAS1581 | AdaS1581 | Human | her |
| 431 | 34 | 68.0 | 19 | 6 | ADAS1611 | AdaS1611 | Human | her |
| 432 | 34 | 68.0 | 19 | 6 | ADAS1572 | AdaS1572 | Human | her |
| 433 | 34 | 68.0 | 19 | 6 | ADAS1614 | AdaS1614 | Human | her |
| 434 | 34 | 68.0 | 19 | 6 | ADAS1616 | AdaS1616 | Human | her |
| 435 | 34 | 68.0 | 19 | 8 | ADH373200 | Adh373200 | Epstein B | her |
| 436 | 34 | 68.0 | 20 | 6 | ADAS1608 | AdaS1608 | Human | her |
| 437 | 34 | 68.0 | 20 | 6 | ADAS1582 | AdaS1582 | Human | her |
| 438 | 34 | 68.0 | 20 | 6 | ADAS1603 | AdaS1603 | Human | her |
| 439 | 34 | 68.0 | 20 | 6 | ADAS1618 | AdaS1618 | Human | her |
| 440 | 34 | 68.0 | 20 | 6 | ADAS1590 | AdaS1590 | Human | her |
| 441 | 34 | 68.0 | 20 | 6 | ADAS1615 | AdaS1615 | Human | her |
| 442 | 34 | 68.0 | 20 | 6 | ADAS1597 | AdaS1597 | Human | her |
| 443 | 34 | 68.0 | 20 | 6 | ADAS1617 | AdaS1617 | Human | her |
| 444 | 34 | 68.0 | 20 | 6 | ADAS1612 | AdaS1612 | Human | her |
| 445 | 34 | 68.0 | 20 | 6 | ADAS1573 | AdaS1573 | Human | her |
| 446 | 34 | 68.0 | 20 | 8 | ADH373298 | Adh373298 | Epstein B | her |
| 447 | 34 | 68.0 | 20 | 8 | ADH373299 | Adh373299 | Epstein B | her |
| 448 | 34 | 68.0 | 20 | 8 | ADG223228 | Adg223228 | Cyanophag | her |
| 449 | 34 | 68.0 | 107 | 6 | ABR54902 | Abr54902 | Light cha | her |
| 450 | 34 | 68.0 | 107 | 6 | ABR19278 | Abr19278 | IgG kappa | her |
| 451 | 34 | 68.0 | 112 | 4 | ABO62872 | Abi19278 | Anti-i- SAF- | her |
| 452 | 34 | 68.0 | 156 | 8 | ADO05624 | Ado05624 | Human EXM | her |
| 453 | 34 | 68.0 | 166 | 3 | AAQ42947 | Aaq42947 | Arabidops | her |
| 454 | 34 | 68.0 | 166 | 3 | AAQ17261 | Aaq17261 | Arabidops | her |
| 455 | 34 | 68.0 | 166 | 3 | AAG25223 | Aag25223 | Arabidops | her |
| 456 | 34 | 68.0 | 189 | 3 | AAG25222 | Aag25222 | Arabidops | her |
| 457 | 34 | 68.0 | 208 | 2 | AAR231998 | Aar231998 | EGF/HB-EH | her |
| 458 | 34 | 68.0 | 208 | 2 | AAR80785 | Aar80785 | Human pre | her |
| 459 | 34 | 68.0 | 208 | 2 | AAR80788 | Aar80788 | Rat precu | her |
| 460 | 34 | 68.0 | 208 | 2 | AAR92899 | Aar92899 | Rat HBEGF | her |
| 461 | 34 | 68.0 | 208 | 2 | AAR92897 | Aar92897 | Human HBE | her |
| 462 | 34 | 68.0 | 208 | 3 | AAV58999 | Aav58999 | Human hsp | her |

| | | | | | |
|-----|----|------|------|---|-----------|
| 463 | 34 | 58.0 | 208 | 3 | AA9Y90400 |
| 464 | 34 | 68.0 | 208 | 4 | AA9Y90409 |
| 465 | 34 | 68.0 | 208 | 4 | AA670125 |
| 466 | 34 | 68.0 | 208 | 5 | AAE15908 |
| 467 | 34 | 68.0 | 208 | 5 | AAE25775 |
| 468 | 34 | 68.0 | 208 | 6 | ABP96795 |
| 469 | 34 | 68.0 | 208 | 6 | ABU07422 |
| 470 | 34 | 68.0 | 208 | 6 | ABU09519 |
| 471 | 34 | 68.0 | 208 | 6 | AAO24019 |
| 472 | 34 | 68.0 | 208 | 7 | ADC34571 |
| 473 | 34 | 68.0 | 208 | 7 | ADC34574 |
| 474 | 34 | 68.0 | 208 | 7 | ADE56940 |
| 475 | 34 | 68.0 | 208 | 7 | ADE56944 |
| 476 | 34 | 68.0 | 208 | 7 | ADE56942 |
| 477 | 34 | 68.0 | 208 | 7 | ADE56946 |
| 478 | 34 | 68.0 | 208 | 7 | ADE29191 |
| 479 | 34 | 68.0 | 208 | 7 | ADH91398 |
| 480 | 34 | 68.0 | 208 | 7 | ADH91995 |
| 481 | 34 | 68.0 | 208 | 8 | ADF42794 |
| 482 | 34 | 68.0 | 208 | 8 | ADF42796 |
| 483 | 34 | 68.0 | 208 | 8 | ADF42792 |
| 484 | 34 | 68.0 | 208 | 8 | ADN04000 |
| 485 | 34 | 68.0 | 208 | 8 | ADR51542 |
| 486 | 34 | 68.0 | 208 | 8 | ADS85061 |
| 487 | 34 | 68.0 | 208 | 8 | ADP22946 |
| 488 | 34 | 68.0 | 208 | 8 | ADU17993 |
| 489 | 34 | 68.0 | 208 | 8 | ADU69326 |
| 490 | 34 | 68.0 | 208 | 9 | ADX69331 |
| 491 | 34 | 68.0 | 208 | 9 | ADX69302 |
| 492 | 34 | 68.0 | 208 | 9 | ADZ09757 |
| 493 | 34 | 68.0 | 248 | 2 | ABO23402 |
| 494 | 34 | 68.0 | 251 | 7 | AEO23402 |
| 495 | 34 | 68.0 | 251 | 8 | ADR20790 |
| 496 | 34 | 68.0 | 304 | 7 | ADP58733 |
| 497 | 34 | 68.0 | 312 | 3 | AG428946 |
| 498 | 34 | 68.0 | 312 | 3 | AG17260 |
| 499 | 34 | 68.0 | 320 | 3 | AG17259 |
| 500 | 34 | 68.0 | 320 | 3 | AG42945 |
| 501 | 34 | 68.0 | 320 | 3 | AAE02556 |
| 502 | 34 | 68.0 | 320 | 5 | AAU93119 |
| 503 | 34 | 68.0 | 320 | 6 | ADA5513 |
| 504 | 34 | 68.0 | 320 | 7 | ADD5760 |
| 505 | 34 | 68.0 | 320 | 7 | ADD31021 |
| 506 | 34 | 68.0 | 320 | 8 | AD143801 |
| 507 | 34 | 68.0 | 320 | 8 | AD001731 |
| 508 | 34 | 68.0 | 320 | 9 | AEA27071 |
| 509 | 34 | 68.0 | 324 | 8 | ADY25074 |
| 510 | 34 | 68.0 | 335 | 9 | ADW17421 |
| 511 | 34 | 68.0 | 497 | 8 | ADR09423 |
| 512 | 34 | 68.0 | 665 | 5 | ABJ06974 |
| 513 | 34 | 68.0 | 735 | 6 | ABJ25382 |
| 514 | 34 | 68.0 | 842 | 6 | ABJ25982 |
| 515 | 34 | 68.0 | 1543 | 4 | ABB69373 |
| 516 | 33 | 66.0 | 9 | 2 | AA24716 |
| 517 | 33 | 66.0 | 9 | 5 | AAE28902 |
| 518 | 33 | 66.0 | 9 | 5 | AAE28855 |
| 519 | 33 | 66.0 | 9 | 6 | ABJ26795 |
| 520 | 33 | 66.0 | 9 | 6 | ABJ26748 |
| 521 | 33 | 66.0 | 9 | 7 | ADD24464 |
| 522 | 33 | 66.0 | 9 | 7 | ADD24399 |
| 523 | 33 | 66.0 | 9 | 7 | ADD80841 |
| 524 | 33 | 66.0 | 9 | 7 | ADD80776 |
| 525 | 33 | 66.0 | 9 | 8 | ADK18317 |
| 526 | 33 | 66.0 | 9 | 8 | ADK18252 |
| 527 | 33 | 66.0 | 9 | 9 | ADV14589 |
| 528 | 33 | 66.0 | 9 | 9 | ADX58329 |
| 529 | 33 | 66.0 | 10 | 6 | AEA45388 |
| 530 | 33 | 66.0 | 10 | 6 | ADA51553 |
| 531 | 33 | 66.0 | 11 | 6 | ADA51554 |
| 532 | 33 | 66.0 | 12 | 6 | ADA51555 |
| 533 | 33 | 66.0 | 13 | 6 | ADA51556 |
| 534 | 33 | 66.0 | 14 | 6 | ADA51557 |
| 535 | 33 | 66.0 | 15 | 6 | ADA51558 |

| | |
|-----------|--------------|
| Aay90406 | Human HBEGF |
| Aay90409 | Rat HBEGF |
| Aab70125 | Human HB-EGF |
| Aae15908 | Human dip |
| Aae25775 | Human hep |
| Aap96795 | Human COP |
| Abu07422 | Protein d |
| Abu09519 | Human hep |
| Aac24019 | Human hep |
| Aac34571 | Human hep |
| Aac34574 | Rat hepar |
| Ade56940 | Rat Prote |
| Ade56944 | Rat Prote |
| Ade56942 | Human Pro |
| Ade56946 | Human Pro |
| Ade29191 | Human hep |
| Adh91398 | Rat hepar |
| Adh91995 | Human hep |
| Adf42794 | Mouse EGF |
| Adf42796 | Rat EGF-1 |
| Adf42792 | Human EGF |
| Adn04000 | Antipsori |
| Adr51542 | Human lip |
| Adh85061 | Mouse ato |
| Adp22946 | PRO polypr |
| Adul17993 | Human can |
| Adx69326 | Human hep |
| Adx69331 | Human hep |
| Adx69302 | Human hep |
| Adz09757 | Human bre |
| Asa01829 | scFY(1.1A |
| Abc23402 | Amino aci |
| Adr20790 | Human sec |
| Adf58733 | Human pol |
| Ag942946 | Arabidops |
| Agsl17260 | Arabidops |
| Agsl17259 | Arabidops |
| Asg42945 | Arabidops |
| Aae02556 | A. thalia |
| Aau93119 | Arabidops |
| Ada15513 | A. thalia |
| Add55760 | Thalecres |
| Add31021 | Plant yie |
| Adi43801 | Plant tra |
| Ado01731 | Thalecres |
| Aea27071 | Stress to |
| Ady25074 | Plant ful |
| Adw17421 | Eucalyptu |
| Adr09423 | Human pro |
| Abb06974 | Human EGF |
| Abj25382 | Aspergill |
| Abj25982 | Aspergill |
| Abb69373 | Drosophil |
| Aar24716 | Sequence |
| Aae28902 | Human KDR |
| Aae28855 | Human KDR |
| Abj26795 | VEGF bind |
| Add24464 | Human lig |
| Add24399 | Human K l |
| Add80841 | Human vari |
| Add80776 | Human vari |
| Adk18317 | KDR bindi |
| Adk18252 | KDR bindi |
| Adv14589 | CDR3 pept |
| Adv58329 | Amino aci |
| Aea45388 | Apolipop |
| Ada51553 | Human her |
| Ada51554 | Human her |
| Ada51555 | Human her |
| Ada51556 | Human her |
| Ada51557 | Human her |
| Ada51558 | Human her |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|-----------|---------------------|-----|----|------|-----|---|----------|---------------------|
| 536 | 33 | 66.0 | 16 | 6 | ADA51559 | Ada51559 Human her | 609 | 33 | 66.0 | 273 | 9 | ADY22017 | Ady22017 Single ch |
| 537 | 33 | 66.0 | 17 | 6 | ADA51560 | Ada51560 Human her | 610 | 33 | 66.0 | 273 | 9 | ADY22021 | Ady22021 Antibody |
| 538 | 33 | 66.0 | 18 | 6 | ADA51561 | Ada51561 Human her | 611 | 33 | 66.0 | 281 | 2 | AAW82314 | Aaw82314 Human ScF |
| 539 | 33 | 66.0 | 19 | 6 | ADA51562 | Ada51562 Human her | 612 | 33 | 66.0 | 288 | 2 | AAW82317 | Aaw82317 Mouse bis |
| 540 | 33 | 66.0 | 20 | 6 | ADA51563 | Ada51563 Human her | 613 | 33 | 66.0 | 288 | 2 | AAW82316 | Aaw82316 Mouse OKT |
| 541 | 33 | 66.0 | 58 | 5 | ABP06444 | Abp06444 Human ORF | 614 | 33 | 66.0 | 304 | 3 | AAG14463 | Aagi14463 Arabidops |
| 542 | 33 | 66.0 | 67 | 4 | ABP064287 | Abp064287 Propionib | 615 | 33 | 66.0 | 316 | 8 | AAW82316 | Aaw82316 Mouse OKT |
| 543 | 33 | 66.0 | 67 | 4 | ABM60806 | Abm60806 Propionib | 616 | 33 | 66.0 | 375 | 8 | AAG14463 | Aagi14463 Arabidops |
| 544 | 33 | 66.0 | 69 | 8 | ADT40940 | Adt40940 hSARS vir | 617 | 33 | 66.0 | 375 | 8 | AAG14462 | Aagi14462 Arabidops |
| 545 | 33 | 66.0 | 69 | 8 | ADT40940 | Adt40940 hSARS vir | 618 | 33 | 66.0 | 375 | 8 | ADN72867 | Adn72867 Thale cre |
| 546 | 33 | 66.0 | 69 | 8 | ADT38470 | Adt38470 hSARS vir | 619 | 33 | 66.0 | 379 | 8 | ADP46580 | Adp46580 Human col |
| 547 | 33 | 66.0 | 97 | 6 | ABO04877 | Ab004877 Human col | 620 | 33 | 66.0 | 379 | 8 | ADP46579 | Adp46579 Human col |
| 548 | 33 | 66.0 | 97 | 8 | ADX80230 | Adx80230 Plant ful | 621 | 33 | 66.0 | 382 | 8 | ADP46579 | Adp46579 Human col |
| 549 | 33 | 66.0 | 98 | 8 | ADU86529 | Adu86529 Immunoglo | 622 | 33 | 66.0 | 393 | 7 | ADO80277 | Ado80277 Mycobacte |
| 550 | 33 | 66.0 | 101 | 8 | ADI33189 | Adi33189 Human rbe | 623 | 33 | 66.0 | 393 | 8 | ADP30742 | Adp30742 Plant yie |
| 551 | 33 | 66.0 | 101 | 9 | ABE31471 | Ab31471 Human rbe | 624 | 33 | 66.0 | 404 | 5 | ADI43799 | Adi43799 Plant tra |
| 552 | 33 | 66.0 | 107 | 2 | AAR24723 | Aar24723 Sequence | 625 | 33 | 66.0 | 411 | 7 | ABE54664 | Ab54664 Rat Prote |
| 553 | 33 | 66.0 | 107 | 5 | AAR28880 | Aar28880 Human KDR | 626 | 33 | 66.0 | 411 | 7 | ADP90602 | Adp90602 Mouse BHL |
| 554 | 33 | 66.0 | 107 | 5 | AAR28874 | Aar28874 Human KDR | 627 | 33 | 66.0 | 411 | 8 | ADP74022 | Adp74022 Murine DE |
| 555 | 33 | 66.0 | 107 | 6 | ABJ26767 | Abj26767 VEGF bind | 628 | 33 | 66.0 | 411 | 9 | ADW42890 | Adw42890 Mouse Str |
| 556 | 33 | 66.0 | 107 | 6 | ABJ26773 | Abj26773 VEGF bind | 629 | 33 | 66.0 | 411 | 9 | ADW42892 | Adw42892 Rat Stral |
| 557 | 33 | 66.0 | 107 | 7 | ADD24426 | Add24426 Human lig | 630 | 33 | 66.0 | 411 | 9 | ADW42892 | Adw42892 Rat Stral |
| 558 | 33 | 66.0 | 107 | 7 | ADD24438 | Add24438 Human lig | 631 | 33 | 66.0 | 411 | 9 | ADW42898 | Adw42898 Mouse Str |
| 559 | 33 | 66.0 | 107 | 7 | ADD80803 | Add80803 Human clo | 632 | 33 | 66.0 | 412 | 2 | AAW08140 | Aaw08140 Human cyt |
| 560 | 33 | 66.0 | 107 | 7 | ADD80815 | Add80815 Human KDR | 633 | 33 | 66.0 | 412 | 2 | AAW99060 | Aaw99060 Human bas |
| 561 | 33 | 66.0 | 107 | 8 | ADK18291 | Adk18291 KDR bindi | 634 | 33 | 66.0 | 412 | 3 | AAW99060 | Aaw99060 Human CR8 |
| 562 | 33 | 66.0 | 107 | 8 | ADK18279 | Adk18279 KDR bindi | 635 | 33 | 66.0 | 412 | 3 | AAW99060 | Aaw99060 Human CR8 |
| 563 | 33 | 66.0 | 107 | 8 | ADT56982 | Adt56982 Plant pol | 636 | 33 | 66.0 | 412 | 5 | ABP50758 | Abp50758 Human she |
| 564 | 33 | 66.0 | 109 | 4 | AAW89629 | Aaw89629 Human imm | 637 | 33 | 66.0 | 412 | 5 | ABP50758 | Abp50758 Human she |
| 565 | 33 | 66.0 | 109 | 6 | ABR54392 | Ab54392 Kappa lig | 638 | 33 | 66.0 | 412 | 7 | ADP54666 | Adp54666 Human Pro |
| 566 | 33 | 66.0 | 109 | 9 | ABE19422 | Ab19422 IgB kappa | 639 | 33 | 66.0 | 412 | 7 | ADP54666 | Adp54666 Human Pro |
| 567 | 33 | 66.0 | 111 | 9 | ADV14593 | Adv14593 VL(CD19) | 640 | 33 | 66.0 | 412 | 8 | ADN03704 | Adn03704 Antipeori |
| 568 | 33 | 66.0 | 111 | 9 | ADV14593 | Adv14593 VL(CD19) | 641 | 33 | 66.0 | 412 | 8 | ADN03704 | Adn03704 Antipeori |
| 569 | 33 | 66.0 | 111 | 9 | ADV14593 | Adv14593 VL(CD19) | 642 | 33 | 66.0 | 412 | 8 | ADN03704 | Adn03704 Antipeori |
| 570 | 33 | 66.0 | 112 | 9 | ADV58342 | Adv58342 Variable | 643 | 33 | 66.0 | 412 | 8 | ADP54189 | Adp54189 Human PRO |
| 571 | 33 | 66.0 | 112 | 9 | ADV58346 | Adv58346 Variable | 644 | 33 | 66.0 | 412 | 8 | ADP54189 | Adp54189 Human PRO |
| 572 | 33 | 66.0 | 123 | 2 | AAR24720 | Aar24720 Chimeric | 645 | 33 | 66.0 | 412 | 8 | ADP54189 | Adp54189 Human PRO |
| 573 | 33 | 66.0 | 129 | 7 | ABO66781 | Ab066781 Human ang | 646 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 574 | 33 | 66.0 | 143 | 7 | ABO66781 | Ab066781 Klebsiell | 647 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 575 | 33 | 66.0 | 145 | 4 | ADM19749 | Adm19749 Protein e | 648 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 576 | 33 | 66.0 | 147 | 9 | ADY22013 | Ady22013 Antibody | 649 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 577 | 33 | 66.0 | 152 | 4 | AAW17626 | Aaw17626 Peptide # | 650 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 578 | 33 | 66.0 | 152 | 4 | ABB36645 | Abb36645 Peptide # | 651 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 579 | 33 | 66.0 | 152 | 4 | AAW30142 | Aaw30142 Peptide # | 652 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 580 | 33 | 66.0 | 152 | 4 | ABB31432 | Abb31432 Peptide # | 653 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 581 | 33 | 66.0 | 152 | 4 | ABB31432 | Abb31432 Peptide # | 654 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 582 | 33 | 66.0 | 152 | 4 | ABW21981 | Abw21981 Protein # | 655 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 583 | 33 | 66.0 | 152 | 4 | AAW69803 | Aaw69803 Human bon | 656 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 584 | 33 | 66.0 | 152 | 4 | AAW57409 | Aaw57409 Human bra | 657 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 585 | 33 | 66.0 | 152 | 4 | ABG51495 | Abg51495 Human liv | 658 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 586 | 33 | 66.0 | 152 | 4 | AAW05284 | Aaw05284 Peptide # | 659 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 587 | 33 | 66.0 | 153 | 8 | ABG39430 | Abg39430 Human pep | 660 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 588 | 33 | 66.0 | 168 | 8 | ADY06237 | Ady06237 Plant ful | 661 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 589 | 33 | 66.0 | 172 | 3 | AAW41200 | Aaw41200 Human pro | 662 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 590 | 33 | 66.0 | 208 | 2 | AAR12300 | Aar12300 ORF-2 of | 663 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 591 | 33 | 66.0 | 219 | 2 | AAR33312 | Aar33312 Humanised | 664 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 592 | 33 | 66.0 | 229 | 8 | ADX95689 | Adx95689 Plant ful | 665 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 593 | 33 | 66.0 | 230 | 8 | ADX65787 | Adx65787 Plant ful | 666 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 594 | 33 | 66.0 | 232 | 3 | AAG14464 | Aagi14464 Arabidops | 667 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 595 | 33 | 66.0 | 234 | 4 | AAW47073 | Aaw47073 Mouse ant | 668 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 596 | 33 | 66.0 | 240 | 4 | AAW45993 | Aaw45993 Human MUC | 669 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 597 | 33 | 66.0 | 242 | 7 | ABO80726 | Ab080726 Pseudomon | 670 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 598 | 33 | 66.0 | 246 | 2 | AAW09434 | Aaw09434 Anti-CD19 | 671 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 599 | 33 | 66.0 | 247 | 2 | AAW09443 | Aaw09443 Modified | 672 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 600 | 33 | 66.0 | 250 | 9 | ADV14571 | Adv14571 VH(CD19) | 673 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 601 | 33 | 66.0 | 250 | 9 | ADV14575 | Adv14575 VL(CD19) | 674 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 602 | 33 | 66.0 | 264 | 7 | ADB29202 | Adb29202 Multivale | 675 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 603 | 33 | 66.0 | 271 | 5 | ABE66384 | Ab666384 Drosophil | 676 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 604 | 33 | 66.0 | 271 | 5 | ABG31022 | Abg31022 Mouse sin | 677 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 605 | 33 | 66.0 | 271 | 7 | ADP25451 | Adp25451 Binding d | 678 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 606 | 33 | 66.0 | 271 | 7 | ADM42726 | Adm42726 Synthetic | 679 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 607 | 33 | 66.0 | 271 | 9 | ABE95394 | Ab95394 Mouse HD3 | 680 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |
| 608 | 33 | 66.0 | 271 | 9 | ABE94428 | Ab94428 Mouse ant | 681 | 33 | 66.0 | 412 | 9 | ADW42888 | Adw42888 Human ins |

| | | | | | | | | | | | | | |
|-----|----|------|------|---|-----------|-----------|-----|----|------|------|----------|-----------|-----------|
| 682 | 33 | 66.0 | 498 | 9 | ADZ83729 | CD3 speci | 755 | 33 | 66.0 | 1027 | 7 | ADJ69803 | Human hea |
| 683 | 33 | 66.0 | 498 | 9 | ADZ83773 | CD3 speci | 756 | 33 | 66.0 | 1028 | 4 | ABG11837 | Novel hum |
| 684 | 33 | 66.0 | 498 | 9 | ADZ83785 | CD3 speci | 757 | 33 | 66.0 | 1028 | 7 | ADG10602 | Human STA |
| 685 | 33 | 66.0 | 498 | 9 | ADZ83560 | Vector pE | 758 | 33 | 66.0 | 1029 | 4 | AAAM39216 | Human pol |
| 686 | 33 | 66.0 | 498 | 9 | ADZ83576 | Vector pE | 759 | 33 | 66.0 | 1029 | 7 | ADZ83576 | Human pol |
| 687 | 33 | 66.0 | 498 | 9 | ADZ83582 | Non-deimm | 760 | 33 | 66.0 | 1062 | 4 | AAAM41002 | Human pol |
| 688 | 33 | 66.0 | 498 | 9 | ADZ83767 | CD3 speci | 761 | 33 | 66.0 | 1062 | 4 | AAAM41003 | Human pol |
| 689 | 33 | 66.0 | 498 | 9 | ADZ83779 | CD3 speci | 762 | 33 | 66.0 | 1145 | 4 | ABB62435 | Drosophil |
| 690 | 33 | 66.0 | 498 | 9 | ADZ83737 | CD3 speci | 763 | 33 | 66.0 | 1149 | 8 | ADQ97214 | Mouse can |
| 691 | 33 | 66.0 | 498 | 9 | ADZ83745 | CD3 speci | 764 | 33 | 66.0 | 1326 | 4 | ABB67237 | Drosophil |
| 692 | 33 | 66.0 | 499 | 9 | ADZ83715 | CD3 speci | 765 | 33 | 66.0 | 1326 | 4 | ABB70051 | Drosophil |
| 693 | 33 | 66.0 | 499 | 9 | ADZ83723 | CD3 speci | 766 | 33 | 66.0 | 1326 | 4 | ABB67238 | Drosophil |
| 694 | 33 | 66.0 | 499 | 9 | ADZ83743 | CD3 speci | 767 | 33 | 66.0 | 1707 | 6 | ABJ25898 | Aspergill |
| 695 | 33 | 66.0 | 499 | 9 | ADZ83763 | CD3 speci | 768 | 33 | 66.0 | 1750 | 6 | ABJ26498 | Aspergill |
| 696 | 33 | 66.0 | 499 | 9 | ADZ83787 | CD3 speci | 769 | 33 | 66.0 | 1849 | 4 | ABB61023 | Drosophil |
| 697 | 33 | 66.0 | 499 | 9 | ADZ83707 | CD3 speci | 770 | 33 | 66.0 | 1960 | 7 | ABM85362 | Mouse pro |
| 698 | 33 | 66.0 | 499 | 9 | ADZ83769 | CD3 speci | 771 | 33 | 66.0 | 9913 | 9 | ABE00351 | SARS coro |
| 699 | 33 | 66.0 | 499 | 9 | ADZ83747 | CD3 speci | 772 | 33 | 66.0 | 9914 | 8 | ADT40602 | hsARS vir |
| 700 | 33 | 66.0 | 499 | 9 | ADZ83765 | CD3 speci | 773 | 33 | 66.0 | 9914 | 8 | ADT38132 | hsARS vir |
| 701 | 33 | 66.0 | 499 | 9 | ADZ83731 | CD3 speci | 774 | 32 | 64.0 | 9 | ADT75016 | Murine li | |
| 702 | 33 | 66.0 | 499 | 9 | ADZ83771 | CD3 speci | 775 | 32 | 64.0 | 10 | ADT75151 | Murine li | |
| 703 | 33 | 66.0 | 499 | 9 | ADZ83739 | CD3 speci | 776 | 32 | 64.0 | 14 | ADD23793 | Breast ca | |
| 704 | 33 | 66.0 | 499 | 9 | ADZ83753 | CD3 speci | 777 | 32 | 64.0 | 24 | ADV13631 | Human pho | |
| 705 | 33 | 66.0 | 499 | 9 | ADZ83759 | CD3 speci | 778 | 32 | 64.0 | 24 | ADV13630 | Human pho | |
| 706 | 33 | 66.0 | 499 | 9 | ADZ83775 | CD3 speci | 779 | 32 | 64.0 | 40 | ABJ25315 | SAC isola | |
| 707 | 33 | 66.0 | 499 | 9 | ADZ83783 | CD3 speci | 780 | 32 | 64.0 | 90 | AAU40560 | Propionib | |
| 708 | 33 | 66.0 | 499 | 9 | ADZ83757 | CD3 speci | 781 | 32 | 64.0 | 90 | ABM37079 | Propionib | |
| 709 | 33 | 66.0 | 499 | 9 | ADZ83711 | CD3 speci | 782 | 32 | 64.0 | 107 | 5 | ABG67137 | Human Igg |
| 710 | 33 | 66.0 | 499 | 9 | ADZ83727 | CD3 speci | 783 | 32 | 64.0 | 108 | 6 | ADA55537 | Human pro |
| 711 | 33 | 66.0 | 499 | 9 | ADZ83719 | CD3 speci | 784 | 32 | 64.0 | 108 | 8 | ADT74998 | Light cha |
| 712 | 33 | 66.0 | 499 | 9 | ADZ83777 | CD3 speci | 785 | 32 | 64.0 | 108 | 8 | ADT75001 | Light cha |
| 713 | 33 | 66.0 | 499 | 9 | ADZ83735 | CD3 speci | 786 | 32 | 64.0 | 112 | 8 | ADT75138 | Light cha |
| 714 | 33 | 66.0 | 499 | 9 | ADZ83751 | CD3 speci | 787 | 32 | 64.0 | 112 | 8 | ADT75139 | Light cha |
| 715 | 33 | 66.0 | 499 | 9 | ADZ83781 | CD3 speci | 788 | 32 | 64.0 | 146 | 4 | AAO69606 | Human pol |
| 716 | 33 | 66.0 | 502 | 9 | ADV14530 | Bispecifi | 789 | 32 | 64.0 | 148 | 2 | AAW86239 | Poxvirus |
| 717 | 33 | 66.0 | 503 | 9 | ADV21509 | Mature fo | 790 | 32 | 64.0 | 148 | 2 | AAW86207 | Poxvirus |
| 718 | 33 | 66.0 | 503 | 9 | ADV21499 | Mature fo | 791 | 32 | 64.0 | 148 | 4 | AAU08442 | Polypepti |
| 719 | 33 | 66.0 | 503 | 9 | ADV14538 | Bispecifi | 792 | 32 | 64.0 | 148 | 8 | ADR31438 | Orf virus |
| 720 | 33 | 66.0 | 503 | 9 | ADV14532 | Bispecifi | 793 | 32 | 64.0 | 154 | 5 | ABB06752 | Chimeric |
| 721 | 33 | 66.0 | 503 | 9 | ADV14540 | Bispecifi | 794 | 32 | 64.0 | 157 | 5 | ABB06754 | Chimeric |
| 722 | 33 | 66.0 | 503 | 9 | AEA52452 | Human CD3 | 795 | 32 | 64.0 | 165 | 3 | AAAG41494 | Arabidops |
| 723 | 33 | 66.0 | 503 | 9 | AEA52450 | Human CD3 | 796 | 32 | 64.0 | 188 | 2 | AAV33436 | Parapox v |
| 724 | 33 | 66.0 | 504 | 9 | ADV14534 | Bispecifi | 797 | 32 | 64.0 | 204 | 4 | AAU53997 | Propionib |
| 725 | 33 | 66.0 | 504 | 9 | ADV14556 | Bispecifi | 798 | 32 | 64.0 | 204 | 6 | ABM50516 | Propionib |
| 726 | 33 | 66.0 | 504 | 9 | ADV14536 | Bispecifi | 799 | 32 | 64.0 | 218 | 6 | ABP96773 | TSH recep |
| 727 | 33 | 66.0 | 504 | 9 | AEA52451 | Human CD3 | 800 | 32 | 64.0 | 218 | 6 | ABP96774 | TSH recep |
| 728 | 33 | 66.0 | 504 | 9 | AEA52447 | Human CD3 | 801 | 32 | 64.0 | 234 | 6 | ADB12387 | Allioicoc |
| 729 | 33 | 66.0 | 504 | 9 | AEA52449 | Human CD3 | 802 | 32 | 64.0 | 235 | 6 | ADB12385 | Allioicoc |
| 730 | 33 | 66.0 | 505 | 9 | ADV14528 | Bispecifi | 803 | 32 | 64.0 | 246 | 5 | ABP46064 | Human Bly |
| 731 | 33 | 66.0 | 505 | 9 | ADY22027 | Antibody | 804 | 32 | 64.0 | 246 | 7 | ADG96891 | Single ch |
| 732 | 33 | 66.0 | 505 | 9 | ADY22025 | Antibody | 805 | 32 | 64.0 | 250 | 7 | ADP05508 | Bacterial |
| 733 | 33 | 66.0 | 505 | 9 | AEA52448 | Human CD3 | 806 | 32 | 64.0 | 255 | 7 | ADH85872 | Enterococ |
| 734 | 33 | 66.0 | 506 | 9 | ADV21505 | Mature fo | 807 | 32 | 64.0 | 265 | 8 | ADT91211 | Single ch |
| 735 | 33 | 66.0 | 506 | 9 | ADV21515 | Mature fo | 808 | 32 | 64.0 | 294 | 4 | AAU17278 | Novel sig |
| 736 | 33 | 66.0 | 521 | 9 | ADY22023 | Antibody | 809 | 32 | 64.0 | 294 | 4 | AAU50900 | Human rep |
| 737 | 33 | 66.0 | 531 | 3 | AAV43749 | Amino aci | 810 | 32 | 64.0 | 294 | 4 | ABR95795 | Human tes |
| 738 | 33 | 66.0 | 539 | 3 | AAV50823 | Fv-antibo | 811 | 32 | 64.0 | 294 | 4 | AAU87245 | Novel cen |
| 739 | 33 | 66.0 | 546 | 3 | AAAM39046 | Human pol | 812 | 32 | 64.0 | 294 | 7 | ADB93986 | Human nov |
| 740 | 33 | 66.0 | 554 | 3 | AAV50822 | Fv-antibo | 813 | 32 | 64.0 | 294 | 8 | ADI54560 | Novel hum |
| 741 | 33 | 66.0 | 558 | 4 | AAAM38969 | Human pol | 814 | 32 | 64.0 | 305 | 3 | AAAG41493 | Arabidops |
| 742 | 33 | 66.0 | 562 | 6 | ABR57059 | Plasmid p | 815 | 32 | 64.0 | 310 | 8 | ADT72328 | Plant ful |
| 743 | 33 | 66.0 | 562 | 6 | ABR57058 | Plasmid p | 816 | 32 | 64.0 | 310 | 8 | ADY25077 | Plant ful |
| 744 | 33 | 66.0 | 562 | 7 | ADC37657 | Human ang | 817 | 32 | 64.0 | 337 | 8 | ADK66558 | Plant ful |
| 745 | 33 | 66.0 | 600 | 4 | ABR68916 | Drosophil | 818 | 32 | 64.0 | 341 | 2 | AAV48224 | Human pro |
| 746 | 33 | 66.0 | 683 | 7 | ADM07079 | Aspergill | 819 | 32 | 64.0 | 341 | 8 | ADY11873 | Plant ful |
| 747 | 33 | 66.0 | 735 | 7 | ADM07030 | Human AML | 820 | 32 | 64.0 | 348 | 4 | AAAG90571 | C glutami |
| 748 | 33 | 66.0 | 801 | 7 | ADC38518 | Human AML | 821 | 32 | 64.0 | 351 | 4 | AAU50778 | Propionib |
| 749 | 33 | 66.0 | 869 | 7 | ADC37654 | Human ang | 822 | 32 | 64.0 | 351 | 6 | ABM47297 | Propionib |
| 750 | 33 | 66.0 | 882 | 7 | ABR56262 | Mouse Jun | 823 | 32 | 64.0 | 359 | 5 | ABG81218 | Mycobacte |
| 751 | 33 | 66.0 | 912 | 6 | ABM69149 | Photorhab | 824 | 32 | 64.0 | 359 | 5 | ABG91564 | Purine/py |
| 752 | 33 | 66.0 | 952 | 4 | ABG20628 | Novel hum | 825 | 32 | 64.0 | 362 | 4 | AAH79379 | Corynebac |
| 753 | 33 | 66.0 | 970 | 4 | AAAM39217 | Human pol | 826 | 32 | 64.0 | 396 | 5 | ABR93348 | Herbicida |
| 754 | 33 | 66.0 | 1027 | 6 | ABO53090 | Human put | 827 | 32 | 64.0 | 430 | 2 | AAW85600 | Hexosamin |

| | | | | | | | | | | | | | |
|-----|----|------|------|---|-----------|---------------------|-----|------|------|------|-----------|-----------|--------------------|
| 828 | 32 | 64.0 | 513 | 3 | AAB19771 | Aab19771 Human den | 901 | 32 | 64.0 | 1972 | 8 | ADO30967 | Ado30967 Human Po |
| 829 | 32 | 64.0 | 513 | 8 | ADC27001 | Adc27001 Bacterial | 902 | 32 | 64.0 | 1972 | 8 | ABM81612 | Abm81612 Tumour-as |
| 830 | 32 | 64.0 | 521 | 7 | ADC30992 | Adc30992 Human nov | 903 | 32 | 64.0 | 2000 | 9 | ADY15314 | Pro polyp |
| 831 | 32 | 64.0 | 569 | 9 | ADC71284 | Adc71284 Human col | 904 | 32 | 64.0 | 2035 | 2 | AAR57141 | Host cell |
| 832 | 32 | 64.0 | 581 | 9 | ABM90728 | Abm90728 M. xanthu | 905 | 32 | 64.0 | 2618 | 4 | ABG02135 | Novel hum |
| 833 | 32 | 64.0 | 583 | 7 | ADG48259 | Adg48259 Human ret | 906 | 32 | 64.0 | 2622 | 4 | ABG06418 | Novel hum |
| 834 | 32 | 64.0 | 583 | 8 | ABM83865 | Abm83865 Human dia | 907 | 32 | 64.0 | 3117 | 9 | ADY17046 | Cyclin-de |
| 835 | 32 | 64.0 | 583 | 8 | ADP56334 | Adp56334 Human PRO | 908 | 32 | 64.0 | 3117 | 9 | ADY17046 | PRO polyp |
| 836 | 32 | 64.0 | 591 | 8 | ADY05244 | Ady05244 Plant ful | 909 | 32 | 64.0 | 5533 | 4 | ABB65772 | Drosophil |
| 837 | 32 | 64.0 | 593 | 4 | ABB64794 | Abb64794 Drosophil | 910 | 32 | 64.0 | 5560 | 4 | ABB71160 | Drosophil |
| 838 | 32 | 64.0 | 600 | 6 | ADA55145 | Ada55145 Human pro | 911 | 32 | 64.0 | 5560 | 8 | ADO01004 | Fruit fly |
| 839 | 32 | 64.0 | 603 | 8 | ADI26809 | Adi26809 Saccharom | 912 | 31.5 | 63.0 | 726 | 7 | ADF07557 | Bacterial |
| 840 | 32 | 64.0 | 604 | 8 | ADRO9402 | Adr09402 Human pro | 913 | 31 | 62.0 | 9 | ADA51541 | Human her | |
| 841 | 32 | 64.0 | 623 | 8 | ADRO5166 | Adr05166 Human mal | 914 | 31 | 62.0 | 9 | ADJ94573 | Humanised | |
| 842 | 32 | 64.0 | 623 | 8 | ADRO30326 | Adr030326 Bacterial | 915 | 31 | 62.0 | 9 | ADR86642 | Epstein-B | |
| 843 | 32 | 64.0 | 624 | 4 | AAE11770 | Aae11770 Human kin | 916 | 31 | 62.0 | 10 | ADA51542 | Human her | |
| 844 | 32 | 64.0 | 647 | 7 | ADG48260 | Adg48260 Human ret | 917 | 31 | 62.0 | 10 | ADV13375 | Human pho | |
| 845 | 32 | 64.0 | 648 | 7 | ADG48256 | Adg48256 Human ret | 918 | 31 | 62.0 | 11 | ADA51543 | Human her | |
| 846 | 32 | 64.0 | 648 | 7 | ADG48258 | Adg48258 Human ret | 919 | 31 | 62.0 | 12 | AAU87883 | PDZ domai | |
| 847 | 32 | 64.0 | 655 | 5 | ABBS7126 | Abbs7126 Mouse isc | 920 | 31 | 62.0 | 12 | ADA51544 | Human her | |
| 848 | 32 | 64.0 | 656 | 2 | AAR444555 | Aar44555 Human EWS | 921 | 31 | 62.0 | 13 | ADA51545 | Human her | |
| 849 | 32 | 64.0 | 656 | 2 | AAW33813 | Aaw33813 Human EWS | 922 | 31 | 62.0 | 14 | ADA51546 | Human her | |
| 850 | 32 | 64.0 | 656 | 8 | ADS16278 | Ads16278 Human Ewi | 923 | 31 | 62.0 | 15 | AA898285 | Anti-A33 | |
| 851 | 32 | 64.0 | 656 | 8 | ABM82330 | Abm82330 Tumour-as | 924 | 31 | 62.0 | 15 | AB97665 | A33 antig | |
| 852 | 32 | 64.0 | 665 | 4 | ABG06460 | Abg06460 Novel hum | 925 | 31 | 62.0 | 15 | ADA51547 | Human her | |
| 853 | 32 | 64.0 | 706 | 4 | AB928866 | Aab92866 Human pro | 926 | 31 | 62.0 | 15 | ADJ38581 | HSV-4 lat | |
| 854 | 32 | 64.0 | 707 | 7 | ADMO4556 | Admo4556 Human pro | 927 | 31 | 62.0 | 15 | ADJ38581 | HSV-4 lat | |
| 855 | 32 | 64.0 | 732 | 4 | ABBG1396 | Abbg1396 Drosophil | 928 | 31 | 62.0 | 15 | ADJ38585 | HSV-4 lat | |
| 856 | 32 | 64.0 | 771 | 8 | ADJ76360 | Adj76360 Marker ge | 929 | 31 | 62.0 | 15 | ADJ38583 | HSV-4 lat | |
| 857 | 32 | 64.0 | 772 | 2 | AAR51478 | Aar51478 Human TLE | 930 | 31 | 62.0 | 16 | ADA51548 | Human her | |
| 858 | 32 | 64.0 | 772 | 2 | AAR51111 | Aar51111 Human TLE | 931 | 31 | 62.0 | 17 | ADA51549 | Human her | |
| 859 | 32 | 64.0 | 772 | 8 | ADNO4243 | Adno4243 Antipsori | 932 | 31 | 62.0 | 18 | ADA51550 | Human her | |
| 860 | 32 | 64.0 | 774 | 2 | AAV37454 | Aay37454 Protein i | 933 | 31 | 62.0 | 19 | ADA51551 | Human her | |
| 861 | 32 | 64.0 | 830 | 8 | ADHO9947 | Adho9947 Human hos | 934 | 31 | 62.0 | 20 | ADA51552 | Human her | |
| 862 | 32 | 64.0 | 831 | 5 | ABBO8457 | Abbo8457 Human tum | 935 | 31 | 62.0 | 55 | ADY22572 | Plant ful | |
| 863 | 32 | 64.0 | 831 | 8 | ADHO9948 | Adho9948 Human hos | 936 | 31 | 62.0 | 57 | AAU46539 | Propionib | |
| 864 | 32 | 64.0 | 831 | 8 | ADHO9952 | Adho9952 Human hos | 937 | 31 | 62.0 | 57 | ABM43058 | Propionib | |
| 865 | 32 | 64.0 | 831 | 8 | ADHO9953 | Adho9953 Human hos | 938 | 31 | 62.0 | 62 | ABU67234 | G-protein | |
| 866 | 32 | 64.0 | 831 | 8 | ADI28837 | Adi28837 Human mod | 939 | 31 | 62.0 | 62 | ABP54015 | Human gas | |
| 867 | 32 | 64.0 | 836 | 8 | ADS23382 | Ads23382 Bacterial | 940 | 31 | 62.0 | 62 | ADO28755 | Camelpox | |
| 868 | 32 | 64.0 | 849 | 3 | ABA41861 | Aab41861 Human ORF | 941 | 31 | 62.0 | 62 | ADO05259 | Gastrin r | |
| 869 | 32 | 64.0 | 873 | 4 | AAE02339 | Aae02339 Drosophil | 942 | 31 | 62.0 | 62 | ADX44574 | Class B G | |
| 870 | 32 | 64.0 | 935 | 4 | ABG10172 | Abg10172 Novel hum | 943 | 31 | 62.0 | 62 | ADY83810 | Gastrin r | |
| 871 | 32 | 64.0 | 941 | 3 | AAV94737 | Aay94737 Protein k | 944 | 31 | 62.0 | 62 | AEA13780 | Human gas | |
| 872 | 32 | 64.0 | 942 | 4 | AAW56699 | Aaw56699 Modified | 945 | 31 | 62.0 | 92 | AAU83176 | Novel sec | |
| 873 | 32 | 64.0 | 942 | 4 | ABG10600 | Abg10600 Novel hum | 946 | 31 | 62.0 | 96 | ABP08604 | Human ORF | |
| 874 | 32 | 64.0 | 942 | 7 | ADP56061 | Adp56061 Human PRO | 947 | 31 | 62.0 | 103 | AAI42650 | Brassica | |
| 875 | 32 | 64.0 | 942 | 7 | ADP38413 | Adp38413 Human pro | 948 | 31 | 62.0 | 103 | AAI01787 | A dehisce | |
| 876 | 32 | 64.0 | 942 | 8 | ADF42748 | Adf42748 Human PRK | 949 | 31 | 62.0 | 103 | ADP19560 | Chick Bfk | |
| 877 | 32 | 64.0 | 942 | 8 | ABM82055 | Abm82055 Tumour-as | 950 | 31 | 62.0 | 105 | AAO10288 | Human pol | |
| 878 | 32 | 64.0 | 942 | 8 | ADN60265 | Adn60265 Human pro | 951 | 31 | 62.0 | 105 | ABO59689 | Human gen | |
| 879 | 32 | 64.0 | 942 | 8 | ADT98140 | Adt98140 Human pro | 952 | 31 | 62.0 | 109 | AA898232 | Rabbit an | |
| 880 | 32 | 64.0 | 1053 | 6 | ABR64181 | Abr64181 Angiogene | 953 | 31 | 62.0 | 109 | AA875151 | Rabbit an | |
| 881 | 32 | 64.0 | 1053 | 8 | ADT66568 | Adt66568 Human Lut | 954 | 31 | 62.0 | 113 | AAI26494 | Human ECL | |
| 882 | 32 | 64.0 | 1068 | 4 | ABB69366 | Abb69366 Drosophil | 955 | 31 | 62.0 | 114 | AAAM86768 | Human imm | |
| 883 | 32 | 64.0 | 1076 | 7 | ADC31075 | Adc31075 Human nov | 956 | 31 | 62.0 | 117 | AAAG15989 | Arabidops | |
| 884 | 32 | 64.0 | 1087 | 6 | ABG74689 | Abg74689 Human CGD | 957 | 31 | 62.0 | 127 | ADA36806 | Acinetoba | |
| 885 | 32 | 64.0 | 1172 | 4 | ABB66466 | Abb66466 Drosophil | 958 | 31 | 62.0 | 131 | AA847138 | CDIFF-19 | |
| 886 | 32 | 64.0 | 1259 | 4 | ABBS8695 | Abbs8695 Drosophil | 959 | 31 | 62.0 | 132 | ADQ66820 | Novel hum | |
| 887 | 32 | 64.0 | 1307 | 5 | ABBS91506 | Abbs91506 Herbicida | 960 | 31 | 62.0 | 137 | AAW47282 | Papilloma | |
| 888 | 32 | 64.0 | 1398 | 5 | ABG97491 | Abg97491 Human NOV | 961 | 31 | 62.0 | 137 | ADX78725 | Plant ful | |
| 889 | 32 | 64.0 | 1400 | 2 | AAW13826 | Aaw13826 Yeast tra | 962 | 31 | 62.0 | 154 | ADP31328 | Human dia | |
| 890 | 32 | 64.0 | 1420 | 2 | AAW13826 | Aaw13826 Yeast tra | 963 | 31 | 62.0 | 155 | ADR66944 | Human pro | |
| 891 | 32 | 64.0 | 1420 | 6 | ABBS3557 | Abbs3557 Protein s | 964 | 31 | 62.0 | 155 | ADR66046 | Human pro | |
| 892 | 32 | 64.0 | 1420 | 7 | ADK64386 | Adk64386 Disease t | 965 | 31 | 62.0 | 156 | ABBS9172 | Drosophil | |
| 893 | 32 | 64.0 | 1445 | 6 | ABR41365 | Abr41365 Human DIT | 966 | 31 | 62.0 | 169 | ADN24293 | Bacterial | |
| 894 | 32 | 64.0 | 1453 | 8 | ADT16257 | Adt16257 Human nuc | 967 | 31 | 62.0 | 169 | ADN24294 | Bacterial | |
| 895 | 32 | 64.0 | 1514 | 4 | ABBT0827 | Abbt0827 Drosophil | 968 | 31 | 62.0 | 170 | ABG04973 | Novel hum | |
| 896 | 32 | 64.0 | 1556 | 8 | ADN19143 | Adn19143 Bacterial | 969 | 31 | 62.0 | 186 | ADZ85034 | PHOS prot | |
| 897 | 32 | 64.0 | 1655 | 7 | ADK62116 | Adk62116 Disease t | 970 | 31 | 62.0 | 196 | AA851816 | Gene 37 h | |
| 898 | 32 | 64.0 | 1938 | 6 | ABR64260 | Abr64260 Angiogene | 971 | 31 | 62.0 | 196 | AA851817 | Human sec | |
| 899 | 32 | 64.0 | 1938 | 9 | ADX07060 | Adx07060 Cyclin-de | 972 | 31 | 62.0 | 202 | ADR66945 | Human pro | |
| 900 | 32 | 64.0 | 1972 | 5 | AAG78488 | Aag78488 Human p53 | 973 | 31 | 62.0 | 202 | ADR66047 | Human pro | |

974 31 62.0 204 9 ADZ85059 Partial F
 975 31 62.0 205 8 ADR66725 Human pro
 976 31 62.0 205 8 ADR66383 Human pro
 977 31 62.0 214 4 ABG04974 Novel hum
 978 31 62.0 218 3 ABG15988 Arabidops
 979 31 62.0 218 4 AAU30048 Novel hum
 980 31 62.0 218 6 ABP96770 TSH recep
 981 31 62.0 218 6 ABP96769 TSH recep
 982 31 62.0 219 4 AAG74850 Human col
 983 31 62.0 223 4 AAU62649 Propionib
 984 31 62.0 223 4 ABG03803 Novel hum
 985 31 62.0 223 6 ABM59168 Propionib
 986 31 62.0 225 8 ABO59377 Human gen
 987 31 62.0 229 7 ABM88389 Rice abio
 988 31 62.0 232 4 AAM39787 Human pol
 989 31 62.0 234 7 ABM88766 Rice abio
 990 31 62.0 243 8 ADI58084 Reg IV-sp
 991 31 62.0 248 5 ABP45093 Human Bly
 992 31 62.0 248 7 ADG95920 Single ch
 993 31 62.0 258 4 AAM39788 Human pol
 994 31 62.0 258 8 ABM82415 Tumour-as
 995 31 62.0 259 8 ABO58603 Human gen
 996 31 62.0 279 4 AAM41573 Human pol
 997 31 62.0 279 4 AAM41574 Human pol
 998 31 62.0 286 8 ABO58900 Human gen
 999 31 62.0 289 9 ADW17490 Eucalyptu
 1000 31 62.0 292 8 ADX73314 Plant ful

ALIGNMENTS

RESULT 1
 AAR70197
 ID AAR70197 standard; protein; 9 AA.
 XX
 AC AAR70197;

DT 25-MAR-2003 (revised)
 DT 20-SEP-1995 (first entry)

XX MAB 3B9 light chain CDR.

XX Chimeric antibody; humanized antibody; antibody engineering;
 KW monoclonal antibody; MAB; interleukin-4; IL-4; allergy; CDR;
 KW complementarity determining region.

XX Mus sp.

XX WO9507301-A1.

XX 16-MAR-1995.

XX 07-SEP-1994; 94WO-US010308.

XX 07-SEP-1993; 93US-00117366.

XX 14-OCT-1993; 93US-00136783.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Holmes S, Gross MS, Sylvester DR;

XX WPI; 1995-123387/16.

XX Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from
 PT high affinity mAbs - useful in treatment of IL-4-mediated and IgE-
 PT mediated allergic conditions.

XX Disclosure; Page 56; 97pp; English.

XX Spleen cells from mice immunized with human IL-4 were used to prepare
 CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only clone

CC 3B9 was positive. cDNA clones of the 3B9 light and heavy chains were
 CC cloned into pGEM7f+ and transformed into E. coli DH5-alpha. A light chain
 CC cDNA clone was sequenced (AAQ83490) that encoded the protein given in
 CC AAR70189. 3 CDRs (AAR70195-97) were identified. (Updated on 25-MAR-2003
 XX to correct PN field.)

SQ Sequence 9 AA;

Query Match 100.0%; Score 50; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNEDEPPT 9

DB 1 QQSNEDEPPT 9

RESULT 2

AAZ23774
 ID AAZ23774 standard; peptide; 9 AA.

XX AAZ23774;

XX 13-SEP-1999 (first entry)

DE CDR of the light chain variable region of antibody 3B9.

XX Light chain variable region; interleukin-4; IL-4; antibody 3B9;
 KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
 KW Immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy;
 KW complementarity determining region.

XX Mus sp.

XX US928904-A.

XX 27-JUL-1999.

XX 07-JUN-1995; 95US-00483632.

XX 07-SEP-1993; 93US-00117366.

XX 14-OCT-1993; 93US-00136783.

XX 07-SEP-1994; 94WO-US010308.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Holmes SD, Sylvester DR, Gross MS;

XX WPI; 1999-429500/36.

XX N-PSDB; AAX85891.

XX New DNA molecules encoding recombinant antibodies useful for treating IL4
 PT -mediated conditions.

XX Example 3; Col 45; 50pp; English.

XX The present sequence represents a complementarity determining region
 CC (CDR) of the light chain variable region of murine interleukin-4 (IL-4)
 CC antibody 3B9. The specification describes chimeric and humanised IL-4
 CC monoclonal antibodies. The antibodies of the invention are used in
 CC therapeutic and pharmaceutical compositions for treating IL-4 mediated
 CC and immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis,
 CC conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock,
 CC rheumatoid arthritis, host-versus-graft disease and renal disease. They
 CC are also useful in the diagnosis of an allergy or condition associated
 CC with excess IL-4 production through the measurement e.g. by ELISA of
 CC circulating endogenous IL-4 levels in humans

XX Sequence 9 AA;

Query Match 100.0%; Score 50; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNEPPT 9
 |||||
 Db 1 QQSNEPPT 9

RESULT 3
 AAY18116
 ID AAY18116 standard; peptide; 9 AA.
 XX
 AC AAY18116;
 XX
 DT 11-AUG-1999 (first entry)
 XX
 DE Light chain CDR for hIL-4 specific antibody.
 XX
 KW Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;
 KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
 KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
 KW autoimmune disease; graft versus host disease;
 KW complementarity determining region; CDR.
 XX
 OS Synthetic.
 XX
 PN US5914110-A.
 XX
 PD 22-JUN-1999.
 XX
 PF 07-JUN-1995; 95US-00483636.
 XX
 PR 07-SEP-1993; 93US-00117366.
 PR 14-OCT-1993; 93US-00136783.
 PR 07-SEP-1994; 94WO-US010308.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 PI Sylvester DR, Holmes SD, Gross MS;
 XX
 DR WPI; 1999-370482/31.
 DR N-PSDB; AAX79515.
 XX
 PT Recombinant IL4 antibodies useful for treatment of allergic rhinitis,
 PT atopic asthma and anaphylactic shock.
 XX
 PS Claim 7; Col 45; 50pp; English.
 CC This sequence represents a light chain complementarity determining region
 CC (CDR) from an antibody of the invention. The antibody is a chimeric or
 CC humanised interleukin-4 (IL4) monoclonal antibody for the treatment of
 CC immunoglobulin E (IgE) mediated diseases. The antibodies are useful for
 CC the treatment of allergic disorders such as allergic rhinitis,
 CC conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.
 CC The antibodies are also useful for regulating B and T cell proliferation
 CC and as such are useful in the treatment of autoimmune diseases and graft
 CC versus host disease
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 50; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNEPPT 9
 |||||
 Db 1 QQSNEPPT 9

RESULT 4
 ABUS6909

ID ABUS6909 standard; protein; 52 AA.
 XX AC
 XX ABUS6909;
 XX
 DT 04-APR-2003 (first entry)
 XX
 DE BoNT/A Hc binding antibody scTv VL region from 1B6 #2.
 XX
 KW Botulinum neurotoxin type A; BoNT/A; mouse; light chain variable region;
 KW scFv; antibody; botulism; antibacterial; single chain antibody; VL;
 KW immunoglobulin.
 XX
 OS Mus sp.
 XX
 PN US2002155114-A1.
 XX
 PD 24-OCT-2002.
 XX
 PF 31-AUG-1998; 98US-00144886.
 XX
 PR 31-AUG-1998; 98US-00144886.
 XX
 PA (MARK/) MARKS J D.
 PA (AMER/) AMERSDORFER P.
 XX
 PI Marks JD, Amersdorfer P;
 XX
 DR WPI; 2003-182618/18.
 XX
 PT Novel antibody that specifically binds and neutralizes botulinum
 PT neurotoxin type A useful for neutralizing botulinum neurotoxin and
 PT treating botulism.
 XX
 PS Claim 8; Page 23; 31pp; English.
 XX
 CC The invention relates to an isolated antibody that specifically binds to
 CC an epitope specifically bound by an antibody expressed by a clone such as
 CC clone S25, C25, C39, IC6 and clone IF3, where the antibody binds to and
 CC neutralises botulinum neurotoxin type A (BoNT/A). Also included are a
 CC polypeptide comprising BoNT/A neutralising epitope comprising an epitope
 CC which is specifically bound by the antibody, where the polypeptide is not
 CC a full-length botulinum neurotoxin H₃ fragment and making an anti-BoNT/A
 CC antibody that neutralises BoNT/A (by contacting several antibodies with
 CC an epitope specifically bound by an antibody expressed by any of the
 CC novel clones and isolating an antibody that specifically binds to the
 CC epitope). The antibody is useful for neutralising a BoNT/A, by contacting
 CC botulinum neurotoxin type A with the antibody comprising VH CDR (heavy
 CC chain variable region complementarity determining region) and with a
 CC second anti-BoNT/A antibody which comprises a VH CDR, where the second
 CC antibody binds to a different epitope than the first anti-BoNT/A
 CC antibody. The antibody is useful in the treatment of pathologies
 CC associated with botulinum neurotoxin poisoning, for rapid
 CC detection/diagnosis of botulism and in the detection and/or
 CC quantification of BoNT/A in a biological sample obtained from an organism
 CC which is indicative of a Clostridium botulinum infection of the organism.
 CC The present sequence is a light chain variable region (VL) of a single
 CC chain antibody (scFv) of the invention
 XX
 SQ Sequence 52 AA;

Query Match 100.0%; Score 50; DB 6; Length 52;
 Best Local Similarity 100.0%; Pred. No. 0.27;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNEPPT 9
 |||||
 Db 33 QQSNEPPT 41

RESULT 5
 ADR38683
 ID ADR38683 standard; peptide; 107 AA.
 XX

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AC ADR38683;
XX 02-DEC-2004 (first entry)
XX Mouse light chain variable region scFv seqid 85.
XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse;
KW light chain variable region; single chain antibody; scFv.
XX Mus sp.
XX US2004175385-A1.
XX 09-SEP-2004.
XX 01-AUG-2003; 2003US-00632706.
XX 31-AUG-1998; 98US-00144886.
PR 01-AUG-2002; 2002US-0400721P.
XX (REGC ) UNIV CALIFORNIA.
XX Marks JD, Amersdorfer P;
XX WPI; 2004-652009/63.
XX New isolated antibody that neutralizes botulinum neurotoxin type A,
XX useful for diagnosing botulism or for treating pathologies associated
XX with botulinum neurotoxin poisoning.
XX Example 1; SEQ ID NO 85; 110pp; English.
XX The invention describes an isolated antibody (I) that specifically binds
XX to an epitope specifically bound by an antibody expressed by a specific
XX clone where (I) binds to and neutralises botulinum neurotoxin type A
XX (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
XX specifically bound by an antibody expressed by a clone chosen from clone
XX S25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
XX 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum
XX neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
XX comprising BoNT/A neutralising epitope having an epitope that is
XX specifically bound by an antibody expressed by clones as mentioned in (I)
XX ; producing (I); and a composition (III) comprising several anti-
XX botulinum neurotoxin antibodies, where each antibody is specific for a
XX different epitope of a botulinum neurotoxin and the combination of
XX antibodies shows greater toxin neutralisation than the single antibodies
XX in surplus. The following are disclosed: a pharmaceutical composition
XX comprising (I); and a kit comprising (I). (I) is useful for neutralising
XX BoNT/A antibody and for neutralising a botulinum neurotoxin which
XX involves contacting neurotoxin with (I) in surplus, where each of (I) is
XX specific for a different epitope of the botulinum neurotoxin and the
XX combination of antibodies shows greater toxin neutralisation than the
XX single antibodies in surplus. (I) is useful for diagnosing the botulism
XX or for treating pathologies associated with botulinum neurotoxin
XX poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
XX enables rapid detection or diagnosis of botulism. This is the amino acid
XX sequence of a mouse light chain variable fragment anti-botulinum toxin
XX scFv.
XX SQ Sequence 107 AA;
Query Match 100.0%; Score 50; DB 8; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QQSNEPDPT 9
DB 88 QQSNEPDPT 96
RESULT 6
Query Match 100.0%; Score 50; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QQSNEPDPT 9
DB 93 QQSNEPDPT 101
RESULT 7
AAV18123
ID AAV18123 standard; protein; 111 AA.
XX AAV18123;
AC AAV18123;
XX 11-AUG-1999 (first entry)
XX Light chain sequence for humanised 3B9 antibody.
AAV23781
ID AAV23781 standard; protein; 111 AA.
XX AAV23781;
XX 13-SEP-1999 (first entry)
XX Light chain variable region of Ig REI.
XX Light chain variable region; interleukin-4; IL-4; antibody 3B9;
KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
KW Immunoglobulin E-mediated allergic reaction; allergic rhinitis;
KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy;
KW Ig REI.
XX Synthetic.
XX US5928904-A.
XX 27-JUL-1999.
XX 07-JUN-1995; 95US-00483632.
XX 07-SEP-1993; 93US-00117366.
PR 14-OCT-1993; 93US-00136783.
PR 07-SEP-1994; 94WO-US010308.
XX (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX Holmes SD, Sylvester DR, Gross MS;
XX WPI; 1999-429500/36.
XX N-PSDB; AAX85937.
XX New DNA molecules encoding recombinant antibodies useful for treating IL4
XX -mediated conditions.
XX Disclosure; Col 69-70; 50pp; English.
XX The specification describes chimeric and humanised IL-4 monoclonal
XX antibodies. The antibodies of the invention are used in therapeutic and
XX pharmaceutical compositions for treating IL-4 mediated and immunoglobulin
XX E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis,
XX atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid
XX arthritis, host-versus-graft disease and renal disease. They are also
XX useful in the diagnosis of an allergy or condition associated with excess
XX IL-4 production through the measurement e.g. by ELISA of circulating
XX endogenous IL-4 levels in humans. The present sequence represents the
XX light chain variable region of Ig REI, and is used in the course of the
XX invention
XX SQ Sequence 111 AA;
Query Match 100.0%; Score 50; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QQSNEPDPT 9
DB 93 QQSNEPDPT 101
RESULT 7
AAV18123
ID AAV18123 standard; protein; 111 AA.
XX AAV18123;
AC AAV18123;
XX 11-AUG-1999 (first entry)
XX Light chain sequence for humanised 3B9 antibody.

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XX Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;
 KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
 KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
 KW autoimmune disease; graft versus host disease.

XX Synthetic.

PN US5914110-A.

PD 22-JUN-1999.

PF 07-JUN-1995; 95US-00483636.

XX 07-SEP-1993; 93US-00117366.

PR 14-OCT-1993; 93US-00136783.

PR 07-SEP-1994; 94WO-US010308.

XX (SMIK) SMITHKLINE BEECHAM PLC.

PA (SMIK) SMITHKLINE BEECHAM CORP.

XX Sylvester DR, Holmes SD, Gross MS;

XX WPI; 1999-370482/31.

DR N-PSDB; AAX79531.

XX Recombinant IL4 antibodies useful for treatment of allergic rhinitis,
 KW atopic asthma and anaphylactic shock.

XX Example 3; Col 69-70; 50pp; English.

XX This sequence represents the light chain of the humanised 3B9 antibody of
 CC the invention. The antibody is a chimeric or humanised interleukin-4
 CC (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE)
 CC mediated diseases. The antibodies are useful for the treatment of
 CC allergic disorders such as allergic rhinitis, conjunctivitis, atopic
 CC dermatitis, atopic asthma and anaphylactic shock. The antibodies are also
 CC useful for regulating B and T cell proliferation and as such are useful
 CC in the treatment of autoimmune diseases and graft versus host disease

XX Sequence 111 AA;

Query Match 100.0%; Score 50; DB 2; Length 111;

Best Local Similarity 100.0%; Pred. No. 0.57;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNEDPPT 9

DB 93 QOSNEDPPT 101

RESULT 8

ADR15140

ID ADR15140 standard; protein; 111 AA.

XX AC

XX ADR15140;

DT 21-OCT-2004 (first entry)

XX Mouse anti-protein C inhibitor antibody #14.

XX anti-protein C inhibitor antibody; anti-PCI antibody;

KW activated protein C; APC; sepsis; disseminated intravascular coagulation;

KW arterial thrombosis; protein C inhibitor; mouse; murine.

XX Mus musculus.

OS WO2004065418-A1.

XX WPI; 2004-652009/63.

XX 05-AUG-2004.

XX 20-JAN-2004; 2004WO-JP000429.

XX

PR 20-JAN-2003; 2003JP-00011529.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Koga T, Kimura N, Yoshino T, Ono K;

PI WPI; 2004-593430/57.

XX New anti-protein C inhibitor (PCI) antibody, inhibiting PCI with respect

XX to activation protein C (apc) activity, and apc production by

XX thrombin/thrombomodulin composite, useful for treating sepsis, arterial

XX thrombosis.

XX Disclosure; SEQ ID NO 21; 105pp; Japanese.

XX The invention comprises anti-protein C inhibitor (PCI) antibody. The anti

XX -PCI antibody of the invention is useful for treating or preventing a

XX disease which develops and/or progresses due to reduced activated protein

XX C (apc) activity. Such diseases include: sepsis, disseminated

XX intravascular coagulation, and arterial thrombosis. The present amino

XX acid sequence represents a mouse anti-protein C inhibitor antibody.

XX Sequence 111 AA;

Query Match 100.0%; Score 50; DB 8; Length 111;

Best Local Similarity 100.0%; Pred. No. 0.57;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNEDPPT 9

DB 93 QOSNEDPPT 101

RESULT 9

ADR38675

ID ADR38675 standard; peptide; 112 AA.

XX ADR38675;

XX 02-DEC-2004 (first entry)

XX Mouse light chain variable region scFv seqid 77.

XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;

XX BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;

XX toxin neutralisation; botulinum neurotoxin poisoning; mouse;

XX light chain variable region; single chain antibody; scFv.

XX Mus sp.

XX US2004175385-A1.

XX 09-SEP-2004.

XX 01-AUG-2003; 2003US-00632706.

XX 31-AUG-1998; 98US-00144886.

XX 01-AUG-2002; 2002US-0400721P.

XX (REGC) UNIV CALIFORNIA.

XX Marks JD, Amersdorfer P;

XX WPI; 2004-652009/63.

XX New isolated antibody that neutralizes botulinum neurotoxin type A,

XX useful for diagnosing botulism or for treating pathologies associated

XX with botulinum neurotoxin poisoning.

XX Example 1; SEQ ID NO 77; 110pp; English.

XX The invention describes an isolated antibody (I) that specifically binds

XX to an epitope specifically bound by an antibody expressed by a specific

CC clone where (I) binds to and neutralises botulinum neurotoxin type A
 CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC S25, C25, C39, 1C6, 3D12, B4, 1F3, hUC25, Ar1, Ar2, WR1(T), 3-1,
 CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
 CC comprising BoNT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of a mouse light chain variable fragment anti-botulinum toxin
 CC scFv.

XX Sequence 112 AA;

Query Match 100.0%; Score 50; DB 8; Length 112;
 Best Local Similarity 100.0%; Pred. No. 0.58;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQSNEDEPPT 9
 Db 93 QQSNEDEPPT 101
 |||||

RESULT 10
 AAR29008
 ID AAR29008 standard; protein; 131 AA.

XX AAR29008;

DT 25-MAR-2003 (revised)
 DT 30-MAR-1993 (first entry)

DE p64-k4 protein product.

KW Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
 KW heavy chain; variable region; mouse; monoclonal; hybridoma; AUK64-7;
 KW plasmid; p64-k4; p64-h2.

XX Synthetic.

PH Key Location/Qualifiers
 FT Peptide 1..20
 FT /note= "Signal peptide"
 FT Protein 21..131
 FT /note= "Mature peptide"

XX WO9219759-A1.

PD 12-NOV-1992.

XX 24-APR-1992; 92WO-JP000544.

XX 25-APR-1991; 91JP-00095476.

PR 19-FEB-1992; 92JP-00032084.

XX (CHUS) CHUGAI SEIYAKU KK.

PI Tsuchiya M, Sato K, Bendig MM, Jones ST, Saldanha JW;

XX WPI; 1992-398882/48.

DR N-PSDB; AAQ30757.

XX Reconstituted human antibody to human interleukin-6 receptor - has low
 PT antigenicity and contains mouse V-region complementarily determining
 PT regions.

XX Disclosure; Page 124-125; 207pp; Japanese.

XX The sequences given in AAR29008-09 were encoded by plasmids which were
 CC used in example to illustrate the production of a human antibody which
 CC recognises human interleukin-6 receptor (IL-6R). The antibody comprises
 CC light (L) chain and heavy (H) chain variable regions which were derived
 CC from a mouse monoclonal antibody produced from the hybridoma AUK64-7
 CC which contained the plasmids p64-K4 and p64-h2. (Updated on 25-MAR-2003
 CC to correct PN field.)

XX Sequence 131 AA;

Query Match 100.0%; Score 50; DB 2; Length 131;
 Best Local Similarity 100.0%; Pred. No. 0.67;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQSNEDEPPT 9
 Db 113 QQSNEDEPPT 121
 |||||

RESULT 11
 AAR70202
 ID AAR70202 standard; protein; 131 AA.

XX AAR70202;

DT 25-MAR-2003 (revised)
 DT 20-SEP-1995 (first entry)

DE Humanized antibody 3B9 light chain.

XX Humanized antibody; antibody engineering; monoclonal antibody; MAb;
 KW interleukin-4; IL-4; allergy.

XX Homo sapiens.

XX WO9507301-A1.

XX 16-MAR-1995.

PF 07-SEP-1994; 94WO-US010308.

XX 07-SEP-1993; 93US-00117366.

PR 14-OCT-1993; 93US-00136783.

XX (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Holmes S, Gross MS, Sylvester DR;

XX WPI; 1995-123387/16.

DR N-PSDB; AAQ83520.

XX Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from
 PT high affinity mAbs - useful in treatment of IL-4-mediated and IgE-
 PT mediated allergic conditions.

XX Disclosure; Page 71-72; 97pp; English.

XX A humanized antibody light chain variable region and signal sequence is
 CC given in AAR75355. The signal sequence is also provided in AAR70194. The
 CC sequences of the 3 CDRs are identical to mouse anti-human IL-4 MAb 3B9
 CC light chain CDRs (given in AAR70195-97). (Updated on 25-MAR-2003 to
 CC correct PN field.)

XX Sequence 131 AA;

Query Match 100.0%; Score 50; DB 2; Length 131;
 Best Local Similarity 100.0%; Pred. No. 0.67;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNEDPPT 9
 |||||
 Db 112 QOSNEDPPT 120

RESULT 12
 AAW30278
 ID AAW30278 standard; protein; 131 AA.
 XX AC AAW30278;
 XX DT 07-JUL-1998 (first entry)
 XX DE Light chain of MuM4TS.11.
 XX KW MuM4TS.11; antibody; platelet; beta receptor; PDGF-R beta; inhibition;
 XX KW intimal hyperplasia; vasculature; restenosis; angioplasty; light chain.
 XX OS Mus sp.

FT Key Location/Qualifiers
 FT Protein 20..131
 FT Binding-site 43..58 /note= "Mature protein"
 FT Binding-site 73..80 /note= "Complementarity determining region 1"
 FT Binding-site 112..120 /note= "Complementarity determining region 2"
 FT Binding-site 112..120 /note= "Complementarity determining region 3"

XX WO9737029-A1.
 XX PD 09-OCT-1997.
 XX PF 19-MAR-1997; 97WO-US004198.
 XX PR 22-MAR-1996; 96US-00621751.
 XX PA (PROT-) PROTEIN DESIGN LABS INC.
 XX PA (BOEF) BOEHRINGER MANNHEIM GMBH.
 XX PI Chang C, Landolfi NF, Martin U;
 XX WPI; 1997-503114/46.
 XX DR N-PSDB; AAT90985.

XX PT Antibodies to platelet derived growth factor beta receptor - inhibit PDGF
 XX PT BB-induced proliferation of cells expressing the receptor, used
 XX PT particularly for inhibiting intimal hyperplasia.
 XX PS Claim 11; Fig 7B; 87pp; English.

XX This is the amino acid sequence for the light chain of muM4TS.11, a novel
 XX antibody which specifically binds to the platelet derived growth beta
 XX receptor (PDGF-R beta), but not within the fifth extracellular Ig-like
 XX domain, where the antibody inhibits PDGF BB-induced proliferation of a
 XX cell expressing the PDGF beta receptor. The antibody can be used in a
 XX method of inhibiting intimal hyperplasia in the vasculature of a mammal.
 XX The antibodies can be used for the treatment of disorders related to PDGF
 XX activity such as disorders involving proliferation of smooth muscle
 XX cells, and including restenosis following angioplasty

XX SQ Sequence 131 AA;

Query Match 100.0%; Score 50; DB 2; Length 131;
 Best Local Similarity 100.0%; Pred. No. 0.67;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNEDPPT 9
 |||||
 Db 113 QOSNEDPPT 121

RESULT 13
 AAW30274
 ID AAW30274 standard; protein; 131 AA.
 XX AC AAW30274;
 XX DT 07-JUL-1998 (first entry)
 XX DE Light chain of HuM4TS.11.
 XX KW HuM4TS.11; antibody; platelet; beta receptor; PDGF-R beta; inhibition;
 XX KW intimal hyperplasia; vasculature; restenosis; angioplasty; light chain.
 XX OS Homo sapiens.

XX Key Location/Qualifiers
 XX FT Misc-difference 23 /note= "Optionally Val at position 3 of the mature
 XX FT protein"
 XX FT Misc-difference 24 /note= "Optionally Leu at position 4 of the mature
 XX FT protein"
 XX FT Misc-difference 25 /note= "Optionally Ile or Val at position 25 of the
 XX FT mature protein"
 XX FT Binding-site 43..58 /note= "Complementarity determining region 1"
 XX FT Protein 61..393 /note= "Mature protein"
 XX FT Binding-site 73..80 /note= "Complementarity determining region 2"
 XX FT Misc-difference 82 /note= "Optionally Val at position 62 of the mature
 XX FT protein"
 XX FT Binding-site 112..120 /note= "Complementarity determining region 3"

XX WO9737029-A1.
 XX PD 09-OCT-1997.
 XX PF 19-MAR-1997; 97WO-US004198.
 XX PR 22-MAR-1996; 96US-00621751.
 XX PA (PROT-) PROTEIN DESIGN LABS INC.
 XX PA (BOEF) BOEHRINGER MANNHEIM GMBH.
 XX PI Chang C, Landolfi NF, Martin U;
 XX WPI; 1997-503114/46.
 XX DR N-PSDB; AAT90981.

XX Antibodies to platelet derived growth factor beta receptor - inhibit PDGF
 XX BB-induced proliferation of cells expressing the receptor, used
 XX PT particularly for inhibiting intimal hyperplasia.

XX Claim 13; Fig 8B; 87pp; English.

XX This is the amino acid sequence for the light chain of HuM4TS.11, a novel
 XX antibody which specifically binds to the platelet derived growth beta
 XX receptor (PDGF-R beta), but not within the fifth extracellular Ig-like
 XX domain, where the antibody inhibits PDGF BB-induced proliferation of a
 XX cell expressing the PDGF beta receptor. The antibody can be used in a
 XX method of inhibiting intimal hyperplasia in the vasculature of a mammal.
 XX The antibodies can be used for the treatment of disorders related to PDGF
 XX activity such as disorders involving proliferation of smooth muscle
 XX cells, and including restenosis following angioplasty

```

XX SQ Sequence 131 AA;
Query Match 100.0%; Score 50; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOSNEDPPT 9
Db 113 QOSNEDPPT 121

RESULT 14
AA23779
ID AAY23779 standard; protein; 131 AA.
XX AC AAY23779;
DT 13-SEP-1999 (first entry)
XX DE Light chain variable region of humanised murine IL-4 antibody 3B9.
XX KW Light chain variable region; interleukin-4; IL-4; antibody 3B9;
XX KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
XX KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;
XX KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
XX KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.
XX OS Synthetic.
XX OS Mus sp.
XX OS Homo sapiens.
XX FN US528904-A.
XX PD 27-JUL-1999.
XX PF 07-JUN-1995; 95US-00483632.
XX PR 07-SEP-1993; 93US-00117366.
XX PR 14-OCT-1993; 93US-00136783.
XX PR 07-SEP-1994; 94WO-US010308.
XX XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX PI Holmes SD, Sylvester DR, Gross MS;
XX WPI; 1999-429500/36.
XX DR N-PSDB; AAX85924.
XX XX New DNA molecules encoding recombinant antibodies useful for treating IL4
PT -mediated conditions.
XX PS Disclosure; Col 61-62; 50pp; English.
XX CC The present sequence represents the light chain variable region of a
CC humanised murine interleukin-4 (IL-4) antibody 3B9. The specification
CC describes chimeric and humanised IL-4 monoclonal antibodies. The
CC antibodies of the invention are used in therapeutic and pharmaceutical
CC compositions for treating IL-4 mediated and immunoglobulin E-mediated
CC allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic
CC dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host
CC -versus-graft disease and renal disease. They are also useful in the
CC diagnosis of an allergy or condition associated with excess IL-4
CC production through the measurement e.g. by ELISA of circulating
CC endogenous IL-4 levels in humans
XX SQ Sequence 131 AA;
Query Match 100.0%; Score 50; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOSNEDPPT 9
Db 113 QOSNEDPPT 121

RESULT 15
AA18126
ID AAY18126 standard; protein; 131 AA.
XX AC AAY18126;
DT 11-AUG-1999 (first entry)
XX DE Light chain sequence for humanised 3B9 antibody.
XX KW Antibody; interleukin-4; IL4; immunoglobulin E; IGE mediated disease;
XX KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
XX KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
XX KW autoimmune disease; graft versus host disease.
XX OS Synthetic.
XX OS US5914110-A.
XX PD 22-JUN-1999.
XX PF 07-JUN-1995; 95US-00483636.
XX PR 07-SEP-1993; 93US-00117366.
XX PR 14-OCT-1993; 93US-00136783.
XX PR 07-SEP-1994; 94WO-US010308.
XX XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX PI Sylvester DR, Holmes SD, Gross MS;
XX WPI; 1999-370482/31.
XX DR N-PSDB; AAX79543.
XX XX Recombinant IL4 antibodies useful for treatment of allergic rhinitis,
PT atopic asthma and anaphylactic shock.
XX PS Disclosure; Col 59-62; 50pp; English.
XX CC This sequence represents the light chain of the humanised 3B9 antibody of
CC the invention. The antibody is a chimeric or humanised interleukin-4
CC (IL4) monoclonal antibody for the treatment of immunoglobulin E (IGE)
CC mediated diseases. The antibodies are useful for the treatment of
CC allergic disorders such as allergic rhinitis, conjunctivitis, atopic
CC dermatitis, atopic asthma and anaphylactic shock. The antibodies are also
CC useful for regulating B and T cell proliferation and as such are useful
CC in the treatment of autoimmune diseases and graft versus host disease
XX SQ Sequence 131 AA;
Query Match 100.0%; Score 50; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOSNEDPPT 9
Db 112 QOSNEDPPT 120

RESULT 16
AAR70189
ID AAR70189 standard; protein; 132 AA.
XX AC AAR70189;
DT 25-MAR-2003 (revised)
DT 20-SEP-1995 (first entry)

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XX Mouse MAb 3B9 light chain.
 XX Chimeric antibody; humanized antibody; antibody engineering;
 KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy.
 XX Mus sp.
 XX Key Location/Qualifiers
 FT Peptide 1..20
 FT /label= Sig_peptide
 FT Region 44..58
 FT /label= CDR
 FT /note= "complementarity determining region"
 FT Region 74..80
 FT /label= CDR
 FT /note= "complementarity determining region"
 FT Region 113..121
 FT /label= CDR
 FT /note= "complementarity determining region"
 XX WO9507301-A1.
 PN 16-MAR-1995.
 XX 07-SEP-1994; 94WO-US010308.
 XX 07-SEP-1993; 93US-00117366.
 PR 14-OCT-1993; 93US-00136783.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX Holmes S, Gross MS, Sylvester DR;
 XX WPI; 1995-123387/16.
 DR N-PSDB; AAQ83490.
 XX Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from
 PT high affinity mAbs - useful in treatment of IL-4-mediated and IGE-
 PT mediated allergic conditions.
 XX Disclosure; Fig 1; 97pp; English.
 XX Spleen cells from mice immunized with human IL-4 were used to prepare
 CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only clone
 CC 3B9 was positive. cDNA clones of the 3B9 light and heavy chains were
 CC cloned into pGEM7f+ and transformed into E. coli DH5-alpha. The clones
 CC were sequenced (AAQ83490-91), and used for antibody engineering. (Updated
 CC on 25-MAR-2003 to correct PN field.)
 XX Sequence 132 AA;
 SQ
 Query Match 100.0%; Score 50; DB 2; Length 132;
 Best Local Similarity 100.0%; Pred. No. 0.68;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QQSNEPDPT 9
 Db 113 QQSNEPDPT 121
 RESULT 17
 AAY23767
 ID AAY23767 standard; protein; 132 AA.
 XX AC AAY23767;
 XX 13-SEP-1999 (first entry)
 DE Light chain variable region of murine IL-4 antibody 3B9.
 KW Light chain variable region; interleukin-4; IL-4; antibody 3B9;

KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
 KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.
 XX Mus sp.
 XX US928904-A.
 XX 27-JUL-1999.
 XX 07-JUN-1995; 95US-00483632.
 PR 07-SEP-1993; 93US-00117366.
 PR 14-OCT-1993; 93US-00136783.
 PR 07-SEP-1994; 94WO-US010308.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX Holmes SD, Sylvester DR, Gross MS;
 XX WPI; 1999-429500/36.
 DR N-PSDB; AAX85884.
 XX New DNA molecules encoding recombinant antibodies useful for treating IL4
 PT -mediated conditions.
 XX Example 3; Fig 1; 50pp; English.
 PS The present sequence represents the light chain variable region of murine
 CC interleukin-4 (IL-4) antibody 3B9. The sequences are used in the
 CC production chimeric and humanised IL-4 monoclonal antibodies. The
 CC antibodies of the invention are used in therapeutic and pharmaceutical
 CC compositions for treating IL-4 mediated and immunoglobulin E-mediated
 CC allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic
 CC dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host
 CC -versus-graft disease and renal disease. They are also useful in the
 CC diagnosis of an allergy or condition associated with excess IL-4
 CC production through the measurement e.g. by ELISA of circulating
 CC endogenous IL-4 levels in humans
 XX Sequence 132 AA;
 SQ
 Query Match 100.0%; Score 50; DB 2; Length 132;
 Best Local Similarity 100.0%; Pred. No. 0.68;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QQSNEPDPT 9
 Db 113 QQSNEPDPT 121
 RESULT 18
 AAY18120
 ID AAY18120 standard; protein; 132 AA.
 XX AC AAY18120;
 XX 11-AUG-1999 (first entry)
 DE Light chain sequence for murine 3B9 antibody.
 KW Antibody; interleukin-4; IL4; immunoglobulin E; IGE mediated disease;
 KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
 KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
 KW autoimmune disease; graft versus host disease.
 XX Mus sp.
 XX US5914110-A.
 PN 22-JUN-1999.

```

XX 07-JUN-1995; 95US-00483636.
PF 07-SEP-1993; 93US-00117366.
PR 14-OCT-1993; 93US-00136783.
PR 07-SEP-1994; 94WO-US010308.
XX (SMIK ) SMITHKLINE BEECHAM PLC.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX Sylvester DR, Holmes SD, Gross MS;
XX WPI; 1999-370482/31.
DR N-PSDB; AAX79519.
XX Recombinant IL4 antibodies useful for treatment of allergic rhinitis,
PT atopic asthma and anaphylactic shock.
PT Claim 24; Fig 1; 50pp; English.
XX This sequence represents the light chain of the murine 3B9 antibody of
CC the invention. The antibody is a chimeric or humanised interleukin-4
CC (IL4) monoclonal antibody for the treatment of immunoglobulin E (IGE)
CC mediated diseases. The antibodies are useful for the treatment of
CC allergic disorders such as allergic rhinitis, conjunctivitis, atopic
CC dermatitis, atopic asthma and anaphylactic shock. The antibodies are also
CC useful for regulating B and T cell proliferation and as such are useful
CC in the treatment of autoimmune diseases and graft versus host disease
XX
XX SQ Sequence 132 AA;
Query Match 100.0%; Score 50; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QQSNEPDPT 9
DB 113 QQSNEPDPT 121
RESULT 19
ADT75077
ID ADT75077 standard; peptide; 9 AA.
XX
AC ADT75077;
XX
DT 13-JAN-2005 (first entry)
XX
DE Murine light chain CDR3 region IgG1k antibody binds hDC-SIGNR Seq 123.
XX
KW autoimmune disease; antibody; antigen presenting cell; APC;
KW diabetes mellitus; immune tolerance; antidiabetic; immunosuppressive;
KW vaccine; hDC-SIGNR; IgG1k.
XX
OS Mus sp.
XX
PN WO2004091543-A2.
XX
PD 28-OCT-2004.
XX
PF 04-MAR-2004; 2004WO-US006570.
XX
PR 04-MAR-2003; 2003US-0451816P.
PR 15-DEC-2003; 2003US-0529500P.
PR 28-FEB-2004; 2004US-0548385P.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Bowdish KS, Kretz-Rommel A, Dakappagari N;
XX WPI; 2004-758274/74.
XX
PT Treating an autoimmune disease comprises providing an
antibody/autoantigen construct containing an autoantigen linked to an
antibody to a receptor of an antigen presenting cell and administering
the construct to a subject.
Example 10; SEQ ID NO 123; 71pp; English.
XX
CC This invention relates to the novel treatment of an autoimmune disease
CC that utilises an antibody/ autoantigen construct. Specifically, it refers
CC to a peptide autoantigen that is linked to an antibody raised against an
CC antigen presenting cell (APC) receptor. The present invention describes a
CC method for treating diabetes mellitus by inducing an immune tolerance to
CC an autoantigen, which can be chosen from glutamic acid decarboxylase
CC (GAD), insulin or a heat shock protein (HSP), as well as epitopes derived
CC from each thereof or beta cell antigens that are linked to an APC
CC receptor antibody. In particular, the antibody recognises a receptor
CC chosen from DC-SIGNR, MHC, toll receptor or mannose receptor amongst
CC others, which is expressed on the surface of the APC. The antibody/
CC autoantigen construct then works to interfere with the interaction
CC between the APC and immune cells such as autoreactive T cells, and hence
CC inhibits T-cell proliferation. Accordingly, such compositions exhibit
CC antidiabetic and immunosuppressive activities and can be used in the
CC development of vaccines. Note that the single chain antibodies (scFvs)
CC used in this specification contain both variable light and heavy chain
CC regions connected by a linker, their short length makes these antibody
CC fragments particularly suitable for antigen linkage, and the capacity for
CC binding to the receptor is preserved. This peptide sequence is a heavy
CC chain murine anti-human DC-SIGNR (hDC-SIGNR) CDR3 peptide of the
XX invention.
XX SQ Sequence 9 AA;
Query Match 94.0%; Score 47; DB 8; Length 9;
Best Local Similarity 88.9%; Pred. No. 2e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 QQSNEPDPT 9
DB 1 QQNNEDPPT 9
RESULT 20
ADT75056
ID ADT75056 standard; protein; 113 AA.
XX
AC ADT75056;
XX
DT 13-JAN-2005 (first entry)
XX
DE Light chain murine anti-hDC-SIGNR IgG1k antibody protein D10 Seq 102.
XX
KW autoimmune disease; antibody; antigen presenting cell; APC;
KW diabetes mellitus; immune tolerance; antidiabetic; immunosuppressive;
KW vaccine; hDC-SIGNR; IgG1k.
XX
OS Mus sp.
XX
PN WO2004091543-A2.
XX
PD 28-OCT-2004.
XX
PF 04-MAR-2004; 2004WO-US006570.
XX
PR 04-MAR-2003; 2003US-0451816P.
PR 15-DEC-2003; 2003US-0529500P.
PR 28-FEB-2004; 2004US-0548385P.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Bowdish KS, Kretz-Rommel A, Dakappagari N;
XX WPI; 2004-758274/74.
XX
PT Treating an autoimmune disease comprises providing an

```

PT antibody/autoantigen construct containing an autoantigen linked to an
 PT antibody to a receptor of an antigen presenting cell and administering
 the construct to a subject.
 PS Example 10; Fig 11; 71pp; English.
 XX
 CC This invention relates to the novel treatment of an autoimmune disease
 CC that utilises an antibody/ autoantigen construct. Specifically, it refers
 CC to a peptide autoantigen that is linked to an antibody raised against an
 CC antigen presenting cell (APC) receptor. The present invention describes a
 CC method for treating diabetes mellitus by inducing an immune tolerance to
 CC an autoantigen, which can be chosen from glutamic acid decarboxylase
 CC (GAD), insulin or a heat shock protein (HSP), as well as epitopes derived
 CC from each thereof or beta cell antigens that are linked to an APC
 CC receptor antibody. In particular, the antibody recognises a receptor
 CC chosen from DC-SIGNR, MHC, toll receptor or mannose receptor amongst
 CC others, which is expressed on the surface of the APC. The antibody/
 CC autoantigen construct then works to interfere with the interaction
 CC between the APC and immune cells such as autoreactive T cells, and hence
 CC inhibits T-cell proliferation. Accordingly, such compositions exhibit
 CC antidiabetic and immunosuppressive activities and can be used in the
 CC development of vaccines. Note that the single chain antibodies (scFvs)
 CC used in this specification contain both variable light and heavy chain
 CC regions connected by a linker, their short length makes these antibody
 CC fragments particularly suitable for antigen linkage, and the capacity for
 CC binding to the receptor is preserved. This polypeptide sequence is a
 CC light chain murine anti-human DC-SIGNR (HDC-SIGNR) IgG1k antibody protein
 CC of the invention.
 XX
 SQ Sequence 113 AA;

Query Match 94.0%; Score 47; DB 8; Length 113;
 Best Local Similarity 88.9%; Pred. No. 2;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QQSNEDPPT 9
 ||:|||||
 Db 93 QQNNEDPPT 101

RESULT 21
 AAR70201
 ID AAR70201 standard; protein; 9 AA.
 AC AAR70201;
 XX
 XX
 DT 25-MAR-2003 (revised)
 DT 20-SEP-1995 (first entry)
 XX
 DE Humanized antibody 3B9 light chain CDR.
 XX
 KW Humanized antibody; antibody engineering; monoclonal antibody; Mab;
 KW interleukin-4; IL-4; allergy; CDR; complementarity determining region.
 XX
 OS Homo sapiens.
 XX
 XX WO9507301-A1.
 XX
 PD 16-MAR-1995.
 XX
 PF 07-SEP-1994; 94WO-US010308.
 XX
 XX 07-SEP-1993; 93US-00117366.
 PR 14-OCT-1993; 93US-00136783.
 XX
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Holmes S, Gross MS, Sylvester DR;
 XX
 DR WPI; 1995-123387/16.
 XX
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from

PT high affinity mAbs - useful in treatment of IL-4-mediated and Ige-
 PT mediated allergic conditions.
 XX
 PS Disclosure; Page 28; 97pp; English.
 XX
 CC A humanized antibody light chain variable region and signal sequence is
 CC given in AAR70194. The signal sequence is also provided in AAR70194. The
 CC sequences of the first 2 CDRs are identical to mouse anti-human IL-4 Mab.
 CC 3B9 light chain CDRs (given in AAR70195-96), but the third (AAR70201).
 CC differs by a single amino acid from the native mouse CDR (AAR70197).
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 9 AA;
 Query Match 90.0%; Score 45; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QQSNEDPPP 8
 ||:|||||
 Db 1 QQSNEDPPP 8
 RESULT 22
 AAY23778
 ID AAY23778 standard; peptide; 9 AA.
 AC AAY23778;
 XX
 DT 13-SEP-1999 (first entry)
 XX
 DE CDR of the light chain variable region of antibody 3B9.
 KW Light chain variable region: interleukin-4; IL-4; antibody 3B9;
 KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
 KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 XX US5928904-A.
 XX
 PD 27-JUL-1999.
 XX
 PF 07-JUN-1995; 95US-00483632.
 XX
 PR 07-SEP-1993; 93US-00117366.
 PR 14-OCT-1993; 93US-00136783.
 PR 07-SEP-1994; 94WO-US010308.
 XX
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 XX Holmes SD, Sylvester DR, Gross MS;
 XX
 DR WPI; 1999-429500/36.
 DR N-PSDB; AAX85895.
 XX
 PF New DNA molecules encoding recombinant antibodies useful for treating IL4
 PT -mediated conditions.
 XX
 PS Example 3; Col 49; 50pp; English.
 XX
 CC The present sequence represents a complementarity determining region
 CC (CDR) of the light chain variable region of murine interleukin-4 (IL-4)
 CC antibody 3B9. The specification describes chimeric and humanised IL-4
 CC monoclonal antibodies. The antibodies of the invention are used in
 CC therapeutic and pharmaceutical compositions for treating IL-4 mediated
 CC and immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis,
 CC conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock,
 CC rheumatoid arthritis, host-versus-graft disease and renal disease. They

CC are also useful in the diagnosis of an allergy or condition associated
 CC with excess IL-4 production through the measurement e.g. by ELISA of
 CC circulating endogenous IL-4 levels in humans
 XX
 XX SQ Sequence 9 AA;

Query Match 90.0%; Score 45; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNEPPP 8
 |||||

Db 1 QQSNEPPP 8

RESULT 23
 AAY18119
 ID AAY18119 standard; peptide; 9 AA.
 XX
 AC AAY18119;
 XX
 DT 11-AUG-1999 (first entry)
 XX
 DE Light chain CDR for hIL-4 specific antibody.
 XX
 KW Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;
 KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
 KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
 KW autoimmune disease; graft versus host disease;
 KW complementarity determining region; CDR.
 XX
 OS Synthetic.
 XX
 PN US5914110-A.
 XX
 PD 22-JUN-1999.
 XX
 PF 07-JUN-1995; 95US-00483636.
 XX
 PR 07-SEP-1993; 93US-00117366.
 PR 14-OCT-1993; 93US-00136783.
 PR 07-SEP-1994; 94WO-0010308.
 XX
 PA (SMK) SMITHKLINE BEECHAM PLC.
 PA (SMK) SMITHKLINE BEECHAM CORP.
 XX
 PI Sylvester DR, Holmes SD, Gross MS;
 XX
 DR WPI; 1999-370482/31.
 DR N-PSDB; AAX79518.
 XX
 PT Recombinant IL4 antibodies useful for treatment of allergic rhinitis,
 PT atopic asthma and anaphylactic shock.
 XX
 PS Claim 18; Col 47; 50pp; English.
 XX
 CC This sequence represents a light chain complementarity determining region
 CC (CDR) from an antibody of the invention. The antibody is a chimeric or
 CC humanised interleukin-4 (IL4) monoclonal antibody for the treatment of
 CC immunoglobulin E (IGE) mediated diseases. The antibodies are useful for
 CC the treatment of allergic disorders such as allergic rhinitis,
 CC conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.
 CC The antibodies are also useful for regulating B and T cell proliferation
 CC and as such are useful in the treatment of autoimmune diseases and graft
 CC versus host disease
 XX
 XX SQ Sequence 9 AA;

Query Match 90.0%; Score 45; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNEPPP 8
 |||||

Db 1 QQSNEPPP 8

RESULT 24
 AAY51138
 ID AAY51138 standard; protein; 9 AA.
 XX
 AC AAY51138;
 XX
 DT 31-MAR-2000 (first entry)
 XX
 DE Murine CD4/CD34 recognizing antibody light chain CDR-3 region #1.
 XX
 KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
 KW HIV infection; autoimmune disease; complementarity determining region;
 KW CDR-3; light chain; murine.
 XX
 OS Mus sp.
 XX
 PN WO9961629-A1.
 XX
 PD 02-DEC-1999.
 XX
 PF 24-MAY-1999; 99WO-JP002711.
 XX
 PR 25-MAY-1998; 98JP-00159957.
 PR 26-MAY-1998; 98JP-00163023.
 XX
 PA (ASAH) ASAH KASEI KOGYO KK.
 PA (ASAH) ASAH MEDICAL CO LTD.
 XX
 PI Ono M, Soka T, Morimoto I, Miyamura K;
 XX
 DR WPI; 2000-086720/07.
 XX
 PT Devices containing antibodies recognising CD4 or CD34 and their use for
 PT the separation of CD4 or CD34 positive cells.
 XX
 PS Claim 3; Page 77; 111pp; Japanese.
 XX
 CC This invention describes a novel device (I) for separating cluster
 CC differentiation (CD)-positive cells using a recombinant (chimeric or
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful
 CC for the separation of CD4 or CD34 positive cells, which is useful for the
 CC collection of hematopoietic undifferentiated cells, elimination of
 CC lymphocytes from cells to be used in bone marrow transplantation, the
 CC detection of leukemic cells and the production of medicinal compositions
 CC for the treatment of HIV infection and autoimmune diseases. This sequence
 CC represents a murine derived complementarity determining region CDR-3
 CC protein fragment which is used to illustrate the method of the invention
 XX
 XX SQ Sequence 9 AA;

Query Match 90.0%; Score 45; DB 3; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+06;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNEPPP 9
 |||||

Db 1 QQSNEPPP 9

RESULT 25
 AAY59261
 ID AAY59261 standard; peptide; 9 AA.
 XX
 AC AAY59261;
 XX
 DT 17-APR-2000 (first entry)
 XX
 DS Antibody 4H5 L chain variable region CDR3 fragment.

XX CD4 antigen; anti-human; antibody; 4H5; drug; CDR;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX JP11332563-A.
 PN
 XX 07-DEC-1999.
 PD
 XX 26-MAY-1998; 98JP-00163034.
 PF
 XX 26-MAY-1998; 98JP-00163034.
 PR
 XX (ASAH) ASahi KASEI KOGYO KK.
 PA
 XX WPI; 2000-091351/08.
 DR
 XX An antibody and the nucleic acid coding the antibody.
 PT
 XX Claim 2; Page 14; 25pp; Japanese.
 PS
 XX The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. Sequences
 CC AAY59259-61 represent the complementarity determining region (CDR)-1, CDR
 CC -2 and CDR-3 fragments in the L chain variable region of the antibody 4H5
 CC respectively
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 90.0%; Score 45; DB 3; Length 9;
 Best Local Similarity 88.9%; Pred. NO. 2e+06;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QOSNEPPT 9
 DB 1 QOSSEDPPT 9
 ||:|||||
 RESULT 26
 AAU70354
 ID AAU70354 standard; peptide; 10 AA.
 XX
 AC AAU70354;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Mouse Kappa III light chain CDR3.
 XX
 KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
 KW complementarity determining region; framework region; IgB;
 KW transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
 KW IgD; IgE; IgY; IgW; Kappa; lambda; CHBP.
 XX
 OS Mus musculus.
 XX
 PN WO200183806-A1.
 XX
 XX 08-NOV-2001.
 PD
 XX 02-MAY-2001; 2001WO-US014349.
 PF
 XX 02-MAY-2000; 2000US-00563222.
 PR
 XX (EPIC-) EPICYTE PHARM INC.
 PA
 XX Hiatt AC, Hein MB;
 PI
 XX WPI; 2002-055482/07.
 DR
 XX Preparing immunoglobulin binding protein array in plant cells by
 PT transforming the cells with different polynucleotides encoding binding

PT protein polypeptides specific to ligand, selecting plant cells for
 PT preparing array.
 XX
 PS Disclosure; Page 14; 129pp; English.
 XX
 CC The invention relates to transforming a population of cells (e.g. plant
 CC cells), comprising using a library of two different polynucleotides
 CC encoding different immunoglobulin binding protein (IgBP) polypeptides
 CC that specifically bind to a ligand or form one or more disulphide bonds
 CC with polypeptides in transfected cells, to generate an IgBP that binds to
 CC a ligand, and transformed plant cells are selected, and preparing an IgBP
 CC array in plant cells. At least one peptide sequence has at least 75%
 CC sequence identity to a framework region (FR) of a native IgM, IgG, IgA,
 CC IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
 CC useful for preparing an immunoglobulin binding protein array, preferably
 CC heavy chain binding protein (CHBP) array in eukaryotic cells especially
 CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
 CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for
 CC discovery of e.g. screening assays of IgBPs having desired
 CC characteristics. The present sequence is a mammalian immunoglobulin
 CC derived peptide that may be incorporated into an IgBP of the invention
 XX
 XX Sequence 10 AA;
 SQ
 Query Match 90.0%; Score 45; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. NO. 0.42;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QOSNEPPT 8
 DB 1 QOSNEPPT 8
 ||:|||||
 RESULT 27
 AAY51140
 ID AAY51140 standard; protein; 103 AA.
 XX
 AC AAY51140;
 XX
 DT 31-MAR-2000 (first entry)
 XX
 DE Murine derived protein fragment #2.
 XX
 KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
 KW HIV infection; autoimmune disease; murine.
 XX
 OS Mus sp.
 XX
 PN WO9961629-A1.
 XX
 PD 02-DEC-1999.
 XX
 PF 24-MAY-1999; 99WO-JP002711.
 XX
 XX 25-MAY-1998; 98JP-00159957.
 PR
 XX 26-MAY-1998; 98JP-00163023.
 XX
 XX (ASAH) ASahi KASEI KOGYO KK.
 PA
 XX (ASAH) ASahi MEDICAL CO LTD.
 XX
 PI Ono M, Soka T, Morimoto I, Miyamura K;
 XX
 XX WPI; 2000-086720/07.
 DR
 XX N-PSDB; AA244204.
 DR
 XX Devices containing antibodies recognising CD4 or CD34 and their use for
 PT the separation of CD4 or CD34 positive cells.
 XX
 XX Claim 22; Page 79; 111pp; Japanese.
 PS
 XX This invention describes a novel device (I) for separating cluster
 CC differentiation (CD)-positive cells using a recombinant (chimeric or

CC single-chain) antibody recognising CD4 or CD34. The devices are useful
 CC for the separation of CD4 or CD34 positive cells, which is useful for the
 CC collection of hematopoietic undifferentiated cells, elimination of
 CC lymphocytes from cells to be used in bone marrow transplantation, the
 CC detection of leukemic cells and the production of medicinal compositions
 CC for the treatment of HIV infection and autoimmune diseases. This sequence
 CC represents a murine derived protein fragment which is used to illustrate
 CC the method of the invention
 XX
 SQ Sequence 103 AA;

Query Match 90.0%; Score 45; DB 3; Length 103;
 Best Local Similarity 88.9%; Pred. No. 4;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNEPDPT 9
 |||:||||
 Db 85 QQSSEDPPT 93

RESULT 28
 AAY59263
 ID AAY59263 standard; protein; 103 AA.

XX
 AC AAY59263;

XX
 DT 17-APR-2000 (first entry)

XX
 DE Antibody 4H5 L chain variable region.

XX
 KW CD4 antigen; anti-human; antibody; 4H5; drug.

XX
 OS Mus sp.

XX
 PN JP11332563-A.

XX
 PD 07-DEC-1999.

XX
 PF 26-MAY-1998; 98JP-00163034.

XX
 PR 26-MAY-1998; 98JP-00163034.

XX
 PA (ASAH) ASahi KASEI KOGYO KK.

XX
 WIPI; 2000-091351/08.

DR N-PSDB; AAZ58662.

PT An antibody and the nucleic acid coding the antibody.

XX
 PS Claim 5; Page 15-16; 25pp; Japanese.

XX
 CC The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. The present
 CC sequence represents the L chain variable region of the antibody 4H5
 XX

SQ Sequence 103 AA;

Query Match 90.0%; Score 45; DB 3; Length 103;
 Best Local Similarity 88.9%; Pred. No. 4;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNEPDPT 9
 |||:||||
 Db 85 QQSSEDPPT 93

RESULT 29
 AAY51146
 ID AAY51146 standard; protein; 111 AA.

XX
 AC AAY51146;

DT 31-MAR-2000 (first entry)
 XX
 DE Murine derived protein fragment #8.
 XX
 KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
 KW HIV infection; autoimmune disease; murine.
 XX

OS Mus sp.

PN WO9961629-A1.

XX
 PD 02-DEC-1999.

XX
 PF 24-MAY-1999; 99WO-JP002711.

XX
 PR 25-MAY-1998; 98JP-00159957.

XX
 PR 26-MAY-1998; 98JP-00163023.

XX
 PA (ASAH) ASahi KASEI KOGYO KK.

XX
 PA (ASAH) ASahi MEDICAL CO LTD.

PI Ono M, Soka T, Morimoto I, Miyamura K;

XX
 WIPI; 2000-086720/07.

DR N-PSDB; AAZ44232.

XX
 PT Devices containing antibodies recognising CD4 or CD34 and their use for
 the separation of CD4 or CD34 positive cells.

XX
 PS Disclosure; Page 97-98; 111pp; Japanese.

XX
 CC This invention describes a novel device (I) for separating cluster
 CC differentiation (CD)-positive cells using a recombinant (chimeric or
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful
 CC for the separation of CD4 or CD34 positive cells, which is useful for the
 CC collection of hematopoietic undifferentiated cells, elimination of
 CC lymphocytes from cells to be used in bone marrow transplantation, the
 CC detection of leukemic cells and the production of medicinal compositions
 CC for the treatment of HIV infection and autoimmune diseases. This sequence
 CC represents a murine derived protein fragment which is used to illustrate
 CC the method of the invention
 XX

SQ Sequence 111 AA;

Query Match 90.0%; Score 45; DB 3; Length 111;
 Best Local Similarity 88.9%; Pred. No. 4.3;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNEPDPT 9

Db 93 QQSSEDPPT 101

RESULT 30

AAY51144
 ID AAY51144 standard; protein; 111 AA.

XX
 AC AAY51144;

XX
 DT 31-MAR-2000 (first entry)

XX
 DE Murine derived protein fragment #6.

XX
 KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
 KW HIV infection; autoimmune disease; murine.
 XX

OS Mus sp.

PN WO9961629-A1.

XX
 PD 02-DEC-1999.

XX 24-MAY-1999; 99WO-JP002711.
 XX 25-MAY-1998; 98JP-00159957.
 PR 26-MAY-1998; 98JP-00163023.
 XX (ASAH) ASAH KASEI KOGYO KK.
 PA (ASAH) ASAH MEDICAL CO LTD.
 XX Ono M, Soka T, Morimoto I, Miyamura K;
 XX WPI; 2000-086720/07.
 DR Devices containing antibodies recognising CD4 or CD34 and their use for
 PT the separation of CD4 or CD34 positive cells.
 XX
 XX Disclosure; Page 95; 111pp; Japanese.
 XX This invention describes a novel device (I) for separating cluster
 CC differentiation (CD)-positive cells using a recombinant (chimeric or
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful
 CC for the separation of CD4 or CD34 positive cells, which is useful for the
 CC collection of hematopoietic undifferentiated cells, elimination of the
 CC lymphocytes from cells to be used in bone marrow transplantation, the
 CC detection of leukemic cells and the production of medicinal compositions
 CC for the treatment of HIV infection and autoimmune diseases. This sequence
 CC represents a murine derived protein fragment which is used to illustrate
 CC the method of the invention
 XX
 XX Sequence 111 AA;
 SQ
 Query Match 90.0%; Score 45; DB 3; Length 111;
 Best Local Similarity 88.9%; Pred. NO. 4.3;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QOSNEDPPT 9
 DB 93 QOSSEDPPT 101
 RESULT 31
 AAY59267
 ID AAY59267 standard; protein; 111 AA.
 XX
 AC AAY59267;
 XX
 DT 17-APR-2000 (first entry)
 XX
 DE Antibody 4H5 L chain fragment.
 XX
 KW CD4 antigen; anti-human; antibody; 4H5; drug.
 XX
 OS Mus sp.
 XX
 XX JP11332563-A.
 XX
 PD 07-DEC-1999.
 XX
 XX 26-MAY-1998; 98JP-00163034.
 PF
 XX 26-MAY-1998; 98JP-00163034.
 PR
 XX (ASAH) ASAH KASEI KOGYO KK.
 PA
 XX WPI; 2000-091351/08.
 DR
 DR N-PSDB; AA258690.
 XX
 XX An antibody and the nucleic acid coding the antibody.
 PT
 XX Disclosure; Page 22-23; 25pp; Japanese.
 PS
 XX The invention provides an antibody having affinity to CD4 antigen. The
 XX anti-human CD4 antibody 4H5 is used for the detection of antigen and

CC application for drugs. It is highly safe in human dose. The present
 CC sequence represents a L chain fragment of the antibody 4H5
 XX
 SQ Sequence 111 AA;
 Query Match 90.0%; Score 45; DB 3; Length 111;
 Best Local Similarity 88.9%; Pred. NO. 4.3;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QOSNEDPPT 9
 DB 93 QOSSEDPPT 101
 RESULT 32
 ABO10750
 ID ABO10750 standard; protein; 112 AA.
 XX
 AC ABO10750;
 XX
 DT 20-AUG-2003 (first entry)
 XX
 DE Variable region of murine antibody MuVL-3.
 XX
 KW Modified antibody; deimmunised antibody; anti-PSMA antibody;
 KW prostate specific membrane antigen; immunogenic; CDR; murine;
 KW complementarity determining region; J591; J415; J533; E99; mouse;
 KW prostatic disorder; cancerous disorder; genitourinary inflammation;
 KW prostatitis; benign enlargement; prostatic cancer; testicular cancer;
 KW solid tumour; soft tissue tumour; metastatic lesion; pain; analgesic;
 KW antiinflammatory; cytostatic; framework region; variable heavy chain;
 KW variable light chain; VH; VL; variable region.
 XX
 OS Mus musculus.
 XX
 XX WO200298897-A2.
 XX
 PD 12-DEC-2002.
 XX
 XX 30-MAY-2002; 2002WO-US017068.
 PF
 XX 01-JUN-2001; 2001US-0295214P.
 PR
 XX 20-SEP-2001; 2001US-0323585P.
 PR
 XX 08-MAR-2002; 2002US-0362810P.
 XX
 XX (CORR) CORNELL RES FOUND INC.
 XX
 XX Bander N, Carr FJ, Hamilton A;
 XX
 XX WPI; 2003-156839/15.
 XX
 XX New modified anti-prostate specific membrane antigen (PSMA)
 PT immunoglobulins, useful for treating or preventing a prostatic or
 PT cancerous disorder, e.g. genitourinary inflammation, prostatitis, or
 PT prostatic or testicular cancer.
 XX
 XX Disclosure; Fig 10B; 254pp; English.
 XX
 XX The present invention relates to modified (e.g. deimmunised) antibodies
 CC to prostate specific membrane antigen (PSMA). The modified anti-PSMA
 CC antibodies are less immunogenic compared to the unmodified anti-PSMA
 CC antibodies. The modified antibodies comprise complementarity determining
 CC regions (CDRs) from a non-human antibody (e.g. murine antibody J591, J415,
 CC J533 or E99), and framework sequences that are less immunogenic in humans
 CC (e.g. less antigenic than the murine frameworks in which a murine CDR
 CC naturally occurs). The modified antibodies bind with PSMA, preferably
 CC human PSMA, with high affinity and specificity. The anti-PSMA antibodies
 CC are useful for treating or preventing a prostatic or cancerous disorder,
 CC e.g. genitourinary inflammation, prostatitis, benign enlargement,
 CC prostatic cancer or testicular cancer, or solid tumours, soft tissue
 CC tumours or metastatic lesions, and its associated pain. The present
 CC sequence represents a variable region from a murine antibody
 XX

SQ Sequence 112 AA;
Query Match 90.0%; Score 45; DB 6; Length 112;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QQSNEDEPP 8
DB 93 QQSNEDEPP 100
RESULT 33
ABR44694
ID ABR44694 standard; protein; 112 AA.
XX AC
XX ABR44694;
XX 25-JUL-2003 (first entry)
XX Murine MuVU-3 antibody amino acid sequence SEQ ID NO:81.
XX Mouse; murine; antibody; skin disorder; binding agent; PSMA; cytostatic;
KW prostate specific membrane antigen; antipsoriatic; antiarthritic;
KW dermatological; antiinflammatory; antiallergic; vaccine; dermal disorder;
KW epidermal disorder; psoriasis; inflammatory disorder; epidermis; dermis;
KW neoplastic disorder.
XX OS Mus musculus.
XX WO2003024398-A2.
XX PD 27-MAR-2003.
XX PF 30-MAY-2002; 2002WO-US017204.
XX PR 20-SEP-2001; 2001US-0324100P.
XX PR 08-WAR-2002; 2002US-0362612P.
XX XX (CORR) CORNELL RES FOUND INC.
XX Bander N;
XX WPI; 2003-313319/30.
XX DR
XX AB
XX Ablating/killing aberrant prostate specific membrane antigen-expressing
PT cells for treating skin disorders, by contacting the cell with an
PT antibody that binds to the extracellular domain of prostate specific
PT membrane antigen.
XX PS Disclosure; Page 38; 225pp; English.
XX CC The present invention describes a method (M1) for ablating or killing an
CC aberrant prostate specific membrane antigen (PSMA)-expressing cell (e.g.
CC an epidermal and a dermal cell). M1 comprises contacting the cell, or a
CC vascular endothelial cell proximate to the cell, with an antibody (or its
CC antigen-binding fragment), which binds specifically to the extracellular
CC domain of PSMA in an amount sufficient to ablate or kill the cell. The
CC antibodies have antipsoriatic, antiarthritic, dermatological, cytostatic,
CC antiinflammatory and antiallergic activities, and can be used in
CC vaccines. M1 is useful for treating a skin disorder in a subject, by
CC administering to the subject, an amount of an antibody which binds
CC specifically to the extracellular domain of PSMA (the subject is a
CC mammal, preferably human and is having, or at risk of, a skin disorder).
CC The skin disorder is a dermal or an epidermal disorder, and is selected
CC from psoriasis (preferably chronic stationary psoriasis, psoriasis
CC vulgaris, eruptive (glutiate) psoriasis, psoriatic erythroderma,
CC generalised pustular psoriasis (Von Zumbusch), annular pustular,
CC psoriasis, and localised pustular psoriasis), psoriatic arthritis,
CC exfoliative dermatitis, pityriasis rubra pilaris, pityriasis roseacea,
CC parapsoriasis, pityriasis lichenoides, lichen planus, lichen nitidus,
CC ichthyosiform dermatosis, keratoderma, dermatosis, and prokeratosis,
CC preferably psoriasis. M1 is useful for treating a skin disorder such as
CC an inflammatory or neoplastic disorder of the epidermis or dermis,

CC preferably an epidermal precancerous or cancerous lesion. M1 is also
CC useful to treat or prevent disorders involving aberrant activity of PSMA-
CC expressing cell, e.g. kidney, liver or brain cell. ACC69816 to ACC69837
CC and ABR44613 to ABR44733 represent sequences used in the exemplification
CC of the present invention
XX
SQ Sequence 112 AA;
Query Match 90.0%; Score 45; DB 6; Length 112;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QQSNEDEPP 8
DB 93 QQSNEDEPP 100
RESULT 34
ADU67960
ID ADU67960 standard; protein; 112 AA.
XX AC
XX ADU67960;
XX DT 10-FEB-2005 (first entry)
XX DE Mouse Kabat subgroup VKIII light chain variable region.
XX antibody; antibody engineering; antibody therapy; prostate tumor;
KW cytostatic; prostate specific membrane antigen; PSMA;
KW heavy chain variable region; light chain variable region.
XX OS Mus musculus.
XX WO2004098535-A2.
XX PD 18-NOV-2004.
XX PF 03-MAR-2004; 2004WO-US006586.
XX PR 03-MAR-2003; 2003US-00379838.
XX PR 30-MAY-2003; 2003US-00449379.
XX (MILL-) MILLENNIUM PHARM INC.
XX Horvath CV, Webb IJ;
XX WPI; 2004-805058/79.
XX Use of an anti-prostate specific membrane antigen (anti-PSMA) antibody or
PT antigen-binding fragment for treating prostate cancer or monitoring a
PT patient receiving an anti-PSMA antibody to treat prostate cancer.
XX Disclosure; SEQ ID NO 81; 284pp; English.
XX The invention relates to the use of an anti-prostate specific membrane
CC antigen (anti-PSMA) antibody or antigen-binding fragment for treating
CC prostate cancer, monitoring a patient receiving an anti-PSMA antibody to
CC treat prostate cancer, or selecting a patient for treatment with an anti-
CC PSMA antibody. Also included are a method of treating prostate cancer in
CC a subject, a method of monitoring a patient receiving an anti-PSMA
CC antibody to treat prostate cancer and a method of selecting a patient for
CC treatment with an anti-PSMA antibody. Also disclosed are anti-PSMA
CC antibodies. The antibody or antigen-binding fragment is a human antibody
CC (or antigen-binding fragment), a modified antibody (or an antigen-binding
CC fragment). The modified antibody is selected from CDR-grafted fragments,
CC humanized antibody, deimmunized antibody, or antigen binding fragments.
CC The modified antibody or antigen-binding fragment has one or more CDRs
CC (complementarity determining region) from a mouse monoclonal antibody
CC selected from J591, J415, J533, or E99. The anti-PSMA antibody or antigen
CC -binding fragment is useful for treating prostate cancer, monitoring a
CC patient receiving an anti-PSMA antibody to treat prostate cancer, or
CC selecting a patient for treatment with an anti-PSMA antibody. The present
CC sequence is a mouse kabat subgroup consensus sequence for a light or

CC heavy chain variable region used to compare to a sequence from one of the
 CC mouse monoclonal antibodies listed above.

SQ Sequence 112 AA;

Query Match 90.0%; Score 45; DB 8; Length 112;
 Best Local Similarity 100.0%; Pred. No. 4.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNEPPP 8
 |||||
 Db 93 QQSNEPPP 100

RESULT 35
 ADQ90832
 ID ADQ90832 standard; protein; 113 AA.

XX ADQ90832;

XX 07-OCT-2004 (first entry)

XX Kabat subgroup murine VKIII.

XX insulin-related disorder; prostate specific membrane antigen; PSMA;
 KW obesity; hyperglycaemia; hypoglycaemia; hyperinsulinaemia;
 KW insulin-resistance; impaired glucose tolerance; impaired fasting glucose;
 KW Type 1 diabetes mellitus; Type 2 diabetes mellitus; gestational diabetes;
 KW antibody; mouse.

XX Mus musculus.

XX US2004136998-A1.

XX 15-JUL-2004.

XX 17-OCT-2003; 2003US-00688015.

XX 30-OCT-2002; 2002US-0422396P.

XX (BAND/) BANDER N H.

XX Bander NH;

XX WPI; 2004-533338/51.

XX Use of anti-prostate specific membrane antigen antibodies for treating or
 PT preventing insulin-related disorders, e.g. obesity, hyperglycemia,
 PT hypoglycemia, hyperinsulinemia, insulin-resistance, or Type 1 or 2
 PT diabetes mellitus.

PS Disclosure; SEQ ID NO 81; 89pp; English.

XX The invention relates to a method of treating or preventing an insulin-
 CC related disorder in a subject which comprises administering an antibody
 CC or its antigen-binding portion specific for prostate specific membrane
 CC antigen (PSMA). The method is useful for treating an insulin-related
 CC disorder, including obesity, hyperglycaemia, hypoglycaemia,
 CC hyperinsulinaemia, insulin-resistance, impaired glucose tolerance,
 CC impaired fasting glucose, Type 1 diabetes mellitus, Type 2 diabetes
 CC mellitus, and gestational diabetes. The present sequence represents Kabat
 CC subgroup murine VKIII.

SQ Sequence 113 AA;

Query Match 90.0%; Score 45; DB 8; Length 113;
 Best Local Similarity 100.0%; Pred. No. 4.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNEPPP 8
 |||||
 Db 94 QQSNEPPP 101

RESULT 36

AAR32123
 ID AAR32123 standard; protein; 131 AA.

XX AAR32123;

XX 25-MAR-2003 (revised)

DT 10-MAR-2003 (revised)

DT 02-JUN-1993 (first entry)

XX Anti-CD4 antibody MT 3.10 light chain variable region.

XX immunosuppression; tissue transplantation; graft; L chain; V region;
 KW T-helper cell inhibition; transplant rejection; Mab;
 KW interleukin-2 receptor.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..20

FT Region /label= signal

FT Region 21..120

FT Region /label= Variable

FT Region 121..131

PN /label= J1

XX DE4143214-A1.

XX 28-JAN-1993.

XX 30-DEC-1991; 91DE-04143214.

XX 25-JUL-1991; 91DE-04124759.

XX (BOEF) BOEHRINGER MANNHEIM GMBH.

XX Weidle U, Scheuer W, Kaluza B, Riethmuller G;

XX WPI; 1993-037582/05.

XX N-PSDB; AAQ36609.

XX Synergistic antibody compsn. for use as immunosuppressant - comprises
 PT monoclonal anti-CD4 antibodies and monoclonal anti-IL2R alpha- or anti-
 PT IL2R beta antibodies.

XX Claim 5; Page 11; 18pp; German.

XX This sequence is the light chain variable region of a preferred anti-CD4
 CC monoclonal antibody for use in the claimed synergistic composition. Mab
 CC MT 3.10 is deposited as clone 3.101/8B10 (ECACC 90090702). The anti-CD4
 CC antibody is used with at least one anti-IL2R alpha or beta antibody.
 CC Individually the antibodies are strongly inhibiting and when used
 CC together their immunosuppressive properties are improved; they
 CC synergistically inhibit T-helper cell proliferation to effectively
 CC inhibit transplant rejection at low doses without significantly reducing
 CC the general immune response. See also AAQ36608-Q36616. (Updated on 10-MAR
 CC -2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX Sequence 131 AA;

Query Match 90.0%; Score 45; DB 2; Length 131;
 Best Local Similarity 88.9%; Pred. No. 5;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNEPPP 9

DB 113 QQSNEPPP 121

RESULT 37

AAR75355

```

ID  AAR75355 standard; protein; 131 AA.
XX
AC  AAR75355;
XX
DT  25-MAR-2003 (revised)
DE  20-SEP-1995 (first entry)
XX
XX  Humanized antibody 3B9 light chain.
XX
DE  Humanized antibody; antibody engineering; monoclonal antibody; MAb;
KW  interleukin-4; IL-4; allergy.
XX
OS  Homo sapiens.
XX
FH  Key Location/Qualifiers
FT  Peptide 1..20
FT  Region 43..57
FT  /label= Sig_peptide
FT  /label= CDR
FT  /note= "complementarity determining region"
FT  Region 73..79
FT  /label= CDR
FT  /note= "complementarity determining region"
FT  Region 112..120
FT  /label= CDR
FT  /note= "complementarity determining region"
XX
XX  WO9507301-A1.
XX
XX  16-MAR-1995.
XX
XX  07-SEP-1994; 94WO-US010308.
XX
XX  07-SEP-1993; 93US-00117366.
XX  14-OCT-1993; 93US-00136783.
XX
XX  (SMIK ) SMITHKLINE BEECHAM CORP.
XX  (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX  Holmes S, Gross MS, Sylvester DR;
XX
XX  WPI; 1995-123387/16.
XX  N-PSDB; AAQ73986.
XX
XX  Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from
XX  high affinity mAbs - useful in treatment of IL-4-mediated and IgE-
XX  mediated allergic conditions.
XX
XX  Disclosure; Fig 5; 97pp; English.
XX
XX  A humanized antibody light chain variable region and signal sequence is
XX  given in AAR75355. The signal sequence is also provided in AAR70194. The
XX  sequences of the first 2 CDRs are identical to mouse anti-human IL-4 MAb
XX  3B9 light chain CDRs (given in AAR70195-96), but the third (AAR70201)
XX  differs by a single amino acid from the native mouse CDR (AAR70197).
XX  (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ  Sequence 131 AA;

  Query Match          90.0%; Score 45; DB 2; Length 131;
  Best Local Similarity 100.0%; Pred. No. 5;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 QQSNEPPP 8
Db  112 QQSNEPPP 119

RESULT 38
ID  AAY23771
XX  AAY23771 standard; protein; 131 AA.
XX
AC  AAY23771;

```

```

XX  13-SEP-1999 (first entry)
XX
XX  Light chain variable region of humanised murine IL-4 antibody 3B9.
XX
XX  Light chain variable region; interleukin-4; IL-4; antibody 3B9;
XX  chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
XX  immunoglobulin E-mediated allergic reaction; allergic rhinitis;
XX  conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
XX  rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.
XX
OS  Synthetic.
OS  Mus sp.
OS  Homo sapiens.
XX
XX  US5928904-A.
XX
XX  27-JUL-1999.
XX
XX  07-JUN-1995; 95US-00483632.
XX
XX  07-SEP-1993; 93US-00117366.
XX  14-OCT-1993; 93US-00136783.
XX  07-SEP-1994; 94WO-US010308.
XX
XX  (SMIK ) SMITHKLINE BEECHAM CORP.
XX  (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX  Holmes SD, Sylvester DR, Gross MS;
XX
XX  WPI; 1999-429500/36.
XX  N-PSDB; AAX85888.
XX
XX  New DNA molecules encoding recombinant antibodies useful for treating IL4
XX  -mediated conditions.
XX
XX  Example 3; Fig 5; 50pp; English.
XX
XX  The present sequence represents the light chain variable region of a
XX  humanised murine interleukin-4 (IL-4) antibody 3B9. The specification
XX  describes chimeric and humanised IL-4 monoclonal antibodies. The
XX  antibodies of the invention are used in therapeutic and pharmaceutical
XX  compositions for treating IL-4 mediated and immunoglobulin E-mediated
XX  allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic
XX  dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host
XX  -versus-graft disease and renal disease. They are also useful in the
XX  diagnosis of an allergy or condition associated with excess IL-4
XX  production through the measurement e.g. by ELISA of circulating
XX  endogenous IL-4 levels in humans
XX
SQ  Sequence 131 AA;

  Query Match          90.0%; Score 45; DB 2; Length 131;
  Best Local Similarity 100.0%; Pred. No. 5;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 QQSNEPPP 8
Db  112 QQSNEPPP 119

RESULT 39
ID  AAY18118
XX  AAY18118 standard; protein; 131 AA.
XX
XX  AAY18118;
XX
XX  11-AUG-1999 (first entry)
XX
XX  Light chain sequence for humanised 3B9 antibody.
XX
XX  Antibody; interleukin-4; IL4; immunoglobulin E; IGE mediated disease;
XX  allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
XX

```

KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
 KW autoimmune disease; graft versus host disease.

XX Synthetic.

XX US5914110-A.

XX 22-JUN-1999.

XX 07-JUN-1995; 95US-00483636.

XX 07-SEP-1993; 93US-00117366.

XX 14-OCT-1993; 93US-00136783.

XX 07-SEP-1994; 94WO-US010308.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Sylvester DR, Holmes SD, Grosse MS;

XX WPI; 1999-370482/31.

XX N-PSDB; AAX79517.

XX Recombinant IL4 antibodies useful for treatment of allergic rhinitis,

XX atopic asthma and anaphylactic shock.

XX Claim 16; Fig 5; 50pp; English.

XX This sequence represents the light chain of the humanised 3B9 antibody of

XX the invention. The antibody is a chimeric or humanised interleukin-4

XX (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE)

XX mediated diseases. The antibodies are useful for the treatment of

XX allergic disorders such as allergic rhinitis, conjunctivitis, atopic

XX dermatitis, atopic asthma and anaphylactic shock. The antibodies are also

XX useful for regulating B and T cell proliferation and as such are useful

XX in the treatment of autoimmune diseases and graft versus host disease

XX Sequence 131 AA;

XX Query Match 90.0%; Score 45; DB 2; Length 131;

XX Best Local Similarity 100.0%; Pred. No. 5;

XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 QQSNEPDP 8

XX Db 112 QQSNEPDP 119

XX RESULT 40

XX AAY51142

XX ID AAY51142 standard; protein; 305 AA.

XX AC AAY51142;

XX 31-MAR-2000 (first entry)

XX Murine derived protein fragment #4.

XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;

XX hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;

XX HIV infection; autoimmune disease; murine.

XX Mus sp.

XX WO9961629-A1.

XX 02-DEC-1999.

XX 24-MAY-1999; 99WO-JP002711.

XX 25-MAY-1998; 98JP-00159957.

XX 26-MAY-1998; 98JP-00163023.

XX

PA (ASAH) ASAH KASEI KOGYO KK.

XX (ASAH) ASAH MEDICAL CO LTD.

XX Ono M, Soka T, Morimoto I, Miyamura K;

XX WPI; 2000-086720/07.

XX N-PSDB; AA244206.

XX Devices containing antibodies recognising CD4 or CD34 and their use for

XX the separation of CD4 or CD34 positive cells.

XX Claim 22; Page 82-84; 11pp; Japanese.

XX This invention describes a novel device (I) for separating cluster

XX differentiation (CD)-positive cells using a recombinant (chimeric or

XX single-chain) antibody recognising CD4 or CD34. The devices are useful

XX for the separation of CD4 or CD34 positive cells, which is useful for the

XX collection of hematopoietic undifferentiated cells, elimination of the

XX lymphocytes from cells to be used in bone marrow transplantation, the

XX detection of leukemic cells and the production of medicinal compositions

XX for the treatment of HIV infection and autoimmune diseases. This sequence

XX represents a murine derived protein fragment which is used to illustrate

XX the method of the invention

XX Sequence 305 AA;

XX Query Match 90.0%; Score 45; DB 3; Length 305;

XX Best Local Similarity 88.9%; Pred. No. 11;

XX Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 QQSNEPDP 9

XX Db 248 QQSNEPDP 256

XX RESULT 41

XX AAY51141

XX ID AAY51141 standard; protein; 305 AA.

XX AC AAY51141;

XX 31-MAR-2000 (first entry)

XX Murine derived protein fragment #3.

XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;

XX hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;

XX HIV infection; autoimmune disease; murine.

XX Mus sp.

XX WO9961629-A1.

XX 02-DEC-1999.

XX 24-MAY-1999; 99WO-JP002711.

XX 25-MAY-1998; 98JP-00159957.

XX 26-MAY-1998; 98JP-00163023.

XX (ASAH) ASAH KASEI KOGYO KK.

XX (ASAH) ASAH MEDICAL CO LTD.

XX Ono M, Soka T, Morimoto I, Miyamura K;

XX WPI; 2000-086720/07.

XX N-PSDB; AA244205.

XX Devices containing antibodies recognising CD4 or CD34 and their use for

XX the separation of CD4 or CD34 positive cells.

XX Claim 22; Page 80-82; 11pp; Japanese.

XX

CC This invention describes a novel device (I) for separating cluster
 CC differentiation (CD)-positive cells using a recombinant (chimeric or
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful
 CC for the separation of CD4 or CD34 positive cells, which is useful for the
 CC collection of hematopoietic undifferentiated cells, elimination of
 CC lymphocytes from cells to be used in bone marrow transplantation, the
 CC detection of leukemic cells and the production of medicinal compositions
 CC for the treatment of HIV infection and autoimmune diseases. This sequence
 CC represents a murine derived protein fragment which is used to illustrate
 CC the method of the invention
 XX
 XX SQ Sequence 305 AA;

Query Match 90.0%; Score 45; DB 3; Length 305;
 Best Local Similarity 88.9%; Pred. No. 11;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QQSNEDEPPT 9
 |||:||||
 Db 115 QQSSEDPPT 123

RESULT 42
 AAY59264
 ID AAY59264 standard; protein; 305 AA.

XX AC AAY59264;

XX DT 17-APR-2000 (first entry)

XX DE Antibody 4H5 H chain sequence.

XX KW CD4 antigen; anti-human; antibody; 4H5; drug.

XX OS Mus sp.

XX FN JP11332563-A.

XX PD 07-DEC-1999.

XX PF 26-MAY-1998; 98JP-00163034.

XX PR 26-MAY-1998; 98JP-00163034.

XX PA (ASAH) ASAH KASEI KOGYO KK.

XX DR WPI; 2000-091351/08.

XX DR N-PSDB; AAZ58663.

XX PT An antibody and the nucleic acid coding the antibody.

XX PS Disclosure; Page 16-17; 25pp; Japanese.

XX CC The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. The present
 CC sequence represents the H chain sequence of the antibody 4H5

XX SQ Sequence 305 AA;

Query Match 90.0%; Score 45; DB 3; Length 305;
 Best Local Similarity 88.9%; Pred. No. 11;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNEDEPPT 9

|||:||||
 Db 115 QQSSEDPPT 123

RESULT 43
 AAY59265
 ID AAY59265 standard; protein; 305 AA.

XX

AC AAY59265;
 XX 17-APR-2000 (first entry)
 DT Antibody 4H5 L chain sequence.
 DE
 XX CD4 antigen; anti-human; antibody; 4H5; drug.
 XX Mus sp.
 OS
 XX JP11332563-A.
 PN
 XX 07-DEC-1999.
 PD
 XX 26-MAY-1998; 98JP-00163034.
 PF
 XX 26-MAY-1998; 98JP-00163034.
 PR
 XX (ASAH) ASAH KASEI KOGYO KK.
 PA
 XX WPI; 2000-091351/08.
 DR
 XX N-PSDB; AAZ58664.
 DR
 XX An antibody and the nucleic acid coding the antibody.
 PT
 XX Disclosure; Page 17-18; 25pp; Japanese.
 PS
 XX The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. The present
 CC sequence represents the L chain sequence of the antibody 4H5

XX SQ Sequence 305 AA;

Query Match 90.0%; Score 45; DB 3; Length 305;
 Best Local Similarity 88.9%; Pred. No. 11;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNEDEPPT 9

|||:||||
 Db 248 QQSSEDPPT 256

RESULT 44

AAR66145

ID AAR66145 standard; peptide; 17 AA.

XX AC AAR66145;

XX DT 12-JUL-1995 (first entry)

XX DE CD-4 antibody variable region complementary peptide.

XX KW CD-4 antibody variable region; complementary peptide;
 KW extra-corporeal blood circulation; cell filter material.

XX OS Synthetic.

XX PN JP06269663-A.

XX PD 27-SEP-1994.

XX PF 17-MAR-1993; 93JP-00057206.

XX PR 17-MAR-1993; 93JP-00057206.

XX PA (TOYM) TOYOBO KK.

XX DR WPI; 1994-346316/43.

XX PT Material for collecting cells positive for CD-4 antibody - comprises
 PT nonwoven fabric having keto-alkyl halide functional gp.


```

PS Example 3; Page 8; 9pp; Japanese.
XX
CC AAR66140-R66146 are peptides complementary to the variable region of the
CC CD-4 antibody, these peptides are fixed onto a claimed nonwoven fabric
CC (average fibre dia. of 1-30 microns) coated with keto-alkyl halide
CC functional groups. This material can be used as a filter for CD-4
CC positive cells in a medical treatment involving the extra-corporeal
CC circulation of blood
XX
SQ Sequence 17 AA;
    Query Match      84.0%; Score 42; DB 2; Length 17;
    Best Local Similarity 88.9%; Pred. No. 2.3;
    Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSNEDEPPT 9
Db 9 QQSNEDEPPT 17

RESULT 45
AAR04134
ID AAR04134 standard; protein; 115 AA.
XX
AC AAR04134;
XX
DT 25-MAR-2003 (revised)
DT 06-SEP-1990 (first entry)
XX
DE Anti-Leu 3a light chain variable region gene product, KOL/206 V1.
XX
KW HIV; AIDS; anti-Leu3A; vaccine; ds.
XX
OS Mus musculus.
XX
PN EP365209-A.
XX
PD 25-APR-1990.
XX
PF 11-OCT-1989; 89EP-00310415.
XX
PR 17-OCT-1988; 88US-00260558.
XX
PA (BECT ) BECTON DICKINSON CO.
XX
PI Hinton R, Oi VT;
XX
DR WPI; 1990-126329/17.
XX
N-PSDB; AAQ04039.
XX
PT New chimeric variants of murine antibody anti-leucine - contg. human
XX antibody regions, and DNA encoding sequences.
XX
PS Claim 1; Fig 2; 12pp; English.
XX
CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be used
CC to form chimeric mouse-variable, human-constant region Abs suggested as
CC being useful as a vaccine to HIV. (Updated on 25-MAR-2003 to correct PF
CC field.)
XX
SQ Sequence 131 AA;
    Query Match      84.0%; Score 42; DB 2; Length 131;
    Best Local Similarity 88.9%; Pred. No. 17;
    Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSNEDEPPT 9
Db 113 QQSNEDEPPT 121

RESULT 47
AAR64202
ID AAR64202 standard; protein; 215 AA.
XX
AC AAR64202;
XX
DT 25-MAR-2003 (revised)
DT 08-JUL-1995 (first entry)
XX
DE Monoclonal antibody 28C5 light chain.
XX
KW CD14 receptor; monoclonal antibody; 28C5; hybridoma; antiseptic;
KW therapeutic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 3..20 /note= "FR.1"
FT Region 21..35 /note= "CDR1"
FT Region 36..50 /note= "FR.2"
FT Region 51..57

Query Match      84.0%; Score 42; DB 2; Length 115;
Best Local Similarity 88.9%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSNEDEPPT 9
Db 96 QQSNEDEPPT 104

RESULT 46
AAR04132

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FT Region /note= "CDR2"
FT 58. .89
FT Region /note= "FR.3"
FT 90. .98
FT Region /note= "CDR3"
FT 99. .108
FT Region /note= "FR.4"
FT 109. .215
FT Region /note= "CH-1"
FT
XX
PN W09428025-A1.
XX
XX
XX 08-DEC-1994.
XX
XX 27-MAY-1994; 94WO-US005898.
XX
XX 28-MAY-1993; 93US-00070160.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Leturoq DJ, Moriarty AM, Ulevitch RJ, Tobias PS, Mathison JC;
XX
XX WPI; 1995-022719/03.
XX
XX P-PSDB; AAQ80292.
XX
XX Hybridoma cell lines produce MAb which inhibit CD14-mediated cell
XX activation - for detecting CD14 in a sample and to inhibit the binding of
XX LPS to CD14.
XX
XX Disclosure; Fig 3; 91pp; English.
XX
XX Anti-human soluble CD14 receptor MAB 28C5 may be used to detect CD14 in
XX cell samples, to inhibit binding of LPS to CD14 or a LPS/CD14 complex to
XX a cell, to inhibit CD14-mediated activation of a cell expressing CD14
XX receptor, and for sepsis therapy. (Updated on 25-MAR-2003 to correct PN
XX field.)
XX
XX Sequence 215 AA;
XX
XX Query Match 84.0%; Score 42; DB 2; Length 215;
XX Best Local Similarity 88.9%; Pred. No. 27;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 QQSNEDEPPT 9
XX |||||
XX 90 QQSNEDEPPT 98
XX
XX RESULT 48
XX AAW83029
XX ID AAW83029 standard; peptide; 9 AA.
XX
XX AC AAW83029;
XX
XX 25-MAR-2003 (revised)
XX 15-MAR-1999 (first entry)
XX
XX DE Anti-Fas MAB HFE7A light chain CDR-L3.
XX
XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis;
XX autoimmune disease; Hashimoto's disease; Sjogren syndrome; pernicious anaemia;
XX graft versus host disease; Goodpasture syndrome; Crohn's disease;
XX Addison's disease; scleroderma; autoimmune haemolytic anaemia;
XX sterility; rheumatoid arthritis; autoimmune haemolytic anaemia;
XX myasthenia gravis; multiple sclerosis; Basedow's disease;
XX thrombopenia purpura; insulin-dependent diabetes; allergy; atopy;
XX arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis;
XX hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy;
XX complementarity determining region; CDR.
XX
XX Mus musculus.
XX
XX AU9859701-A.

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XX 08-OCT-1998.
XX
XX 30-MAR-1998; 98AU-00059701.
XX
XX 01-APR-1997; 97JP-00082953.
XX 25-JUN-1997; 97JP-00169088.
XX 08-OCT-1997; 97JP-00276064.
XX
XX (SANY ) SANKYO CO LTD.
XX
XX Nobufusa S, Kimihisa I, Jun O, Masahiko O, Hideyuki H, Tohru T;
XX Hiroko Y, Akio S, Shin Y;
XX
XX WPI; 1998-543440/01.
XX
XX New antibodies and proteins bind conserved epitope of Fas antigen - used
XX to evaluate drugs in animal models and to treat Fas-associated diseases
XX e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis,
XX hepatitis and AIDS.
XX
XX Claim 9; Page 185; 292pp; English.
XX
XX This is the amino acid of complementarity determining region 3 (CDR-L3)
XX of the light chain (see AAW83042) of murine anti-human Fas monoclonal
XX antibody HFE7A. The invention relates to antibodies, especially humanised
XX antibodies (see AAW83031-37), recognising the Fas antigen. Such
XX antibodies preferably comprise a heavy chain and a light chain including
XX CDRs (see AAW83024-29) from the heavy and light chains of HFE7A.
XX Humanised antibodies are produced by CDR grafting. The antibodies are
XX capable of inducing apoptosis in abnormal cells expressing Fas, and of
XX inhibiting Fas-induced apoptosis in normal cells. They are used to
XX evaluate, in animal models, treatments of diseases that involve Fas/Fas
XX ligand interactions, and also to treat such diseases, including
XX autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's
XX disease, graft versus host disease, Sjogren syndrome, pernicious anaemia,
XX Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease,
XX rheumatoid arthritis, autoimmune haemolytic anaemia, sterility,
XX myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia
XX purpura and insulin-dependent diabetes), allergies, atopy,
XX arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis,
XX hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all
XX claimed). (Updated on 25-MAR-2003 to correct DR field.)
XX
XX Sequence 9 AA;
XX
XX Query Match 82.0%; Score 41; DB 2; Length 9;
XX Best Local Similarity 88.9%; Pred. No. 2e+06;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 QQSNEDEPPT 9
XX |||||
XX 1 QQSNEDEPPT 9
XX
XX RESULT 49
XX AAB14746
XX ID AAB14746 standard; peptide; 9 AA.
XX
XX AC AAB14746;
XX
XX 24-NOV-2000 (first entry)
XX
XX DE Mouse anti-Fas antibody HFE7A light chain CDR3.
XX
XX Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine;
XX complementarity determining region; CDR; human Fas; Fas ligand;
XX apoptosis modulator; programmed cell death; autoimmune disease; allergy;
XX atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis;
XX aplastic anaemia; pancytopenia; hepatitis; AIDS; graft rejection;
XX light chain.
XX
XX Mus musculus.
XX
XX AU9859701-A.

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XX JP2000169393-A.
 XX 20-JUN-2000.
 XX
 XX 30-SEP-1999; 99JP-00278301.
 XX 30-SEP-1998; 98JP-00276883.
 XX (SANY) SANKYO CO LTD.
 XX WPI; 2000-485645/43.
 XX Preventive or treating agent for the diseases caused by an abnormality in
 PT the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas
 PT antibody.
 XX
 PS Claim 10; Page 65; 139pp; Japanese.
 XX
 CC The invention relates to compositions for the prevention or treatment or
 CC diseases caused by an abnormality in the Fas/Fas ligand system containing
 CC an anti-Fas antibody as the active component. The anti-Fas antibody is
 CC either the murine anti-human Fas monoclonal antibody HFE7A, or a
 CC humanised version of HFE7A containing identical CDRs (complementarity
 CC determining regions) to antibody HFE7A. Via its interaction with Fas, the
 CC antibody of the invention acts as a modulator of apoptosis. The
 CC compositions of the invention may therefore be used in the treatment or
 CC prevention of conditions such as autoimmune diseases, allergy, atopy,
 CC arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis,
 CC aplastic anaemia (pamylorophthisis), hepatitis, AIDS and organ graft
 CC rejection. Sequences AAB14744-B14746 represent CDRs 1-3 of the light
 CC chain of the murine anti-human Fas monoclonal antibody HFE7A, which is
 CC produced by hybridoma HFE7A (FERM-BP-5828)
 XX
 SQ Sequence 9 AA;
 Query Match 82.0%; Score 41; DB 3; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QOSNEDPPT 9
 DB 1 QOSNEDPPT 9
 RESULT 50
 AAW90896
 ID AAW90896 standard; peptide; 9 AA.
 XX
 AC AAW90896;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Murine anti-Fas antibody peptide fragment #6.
 XX
 KW Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX
 OS Mus musculus.
 XX
 XX EP990663-A2.
 XX
 XX 05-APR-2000.
 XX

PF 29-SEP-1999; 99EP-00307711.
 XX
 PR 30-SEP-1998; 98JP-00276881.
 PR 30-SEP-1998; 98JP-00276882.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX WPI; 2000-258930/23.
 DR
 XX
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems.
 XX
 PS Disclosure; Page 98; 263pp; English.
 XX
 CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antiartherosclerotic, cardiac and hepatotropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (II) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a murine anti-Fas antibody peptide fragment described in the method of
 CC the invention
 XX
 SQ Sequence 9 AA;

Query Match 82.0%; Score 41; DB 3; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QOSNEDPPT 9
 DB 1 QOSNEDPPT 9

Search completed: February 23, 2006, 09:40:10
 Job time : 94.5385 secs

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OM protein - protein search, using sw model

Run on: February 23, 2006, 09:41:24 ; Search time 12.7385 Seconds
(without alignments)
67.979 Million cell updates/sec

Title: US-10-723-872-20
Perfect score: 50
Sequence: 1 QOSNEDPPT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 45 | 90.0 | 112 | 2 | S19971 |
| 2 | 45 | 90.0 | 131 | 2 | PH1226 |
| 3 | 41 | 82.0 | 65 | 2 | C38601 |
| 4 | 40 | 80.0 | 96 | 2 | B49442 |
| 5 | 40 | 80.0 | 107 | 2 | S26344 |
| 6 | 40 | 80.0 | 111 | 1 | KVMS37 |
| 7 | 40 | 80.0 | 111 | 1 | KVMS83 |
| 8 | 40 | 80.0 | 111 | 1 | KVMSCL |
| 9 | 40 | 80.0 | 111 | 2 | S09966 |
| 10 | 40 | 80.0 | 111 | 2 | A33936 |
| 11 | 39 | 78.0 | 107 | 2 | S26343 |
| 12 | 39 | 78.0 | 111 | 1 | KVMS08 |
| 13 | 39 | 78.0 | 111 | 1 | KVMS43 |
| 14 | 39 | 78.0 | 111 | 1 | KVMS69 |
| 15 | 38 | 76.0 | 81 | 2 | S42193 |
| 16 | 38 | 76.0 | 111 | 2 | D45722 |
| 17 | 37 | 74.0 | 692 | 1 | S59833 |
| 18 | 36 | 72.0 | 131 | 1 | KVMSM6 |
| 19 | 36 | 72.0 | 435 | 2 | T19840 |
| 20 | 36 | 72.0 | 508 | 2 | F84921 |
| 21 | 36 | 72.0 | 1123 | 2 | A44766 |
| 22 | 36 | 72.0 | 1589 | 2 | C44766 |
| 23 | 35 | 70.0 | 65 | 2 | B38601 |
| 24 | 35 | 70.0 | 93 | 2 | A38601 |
| 25 | 35 | 70.0 | 102 | 2 | PH1079 |
| 26 | 35 | 70.0 | 112 | 2 | S19972 |
| 27 | 35 | 70.0 | 301 | 2 | T45859 |
| 28 | 35 | 70.0 | 304 | 1 | S71285 |
| 29 | 35 | 70.0 | 584 | 2 | B84668 |

| | | | | | |
|-----|------|------|---|--------|--------------------|
| 30 | 70.0 | 586 | 2 | T20353 | hypothetical prote |
| 31 | 70.0 | 597 | 2 | T23961 | hypothetical prote |
| 32 | 70.0 | 1592 | 2 | S63208 | hypothetical prote |
| 33 | 68.0 | 208 | 1 | A38432 | heparin-binding EG |
| 34 | 68.0 | 208 | 1 | JCL409 | heparin-binding EG |
| 35 | 68.0 | 208 | 1 | JCL410 | heparin-binding EG |
| 36 | 68.0 | 268 | 2 | T51678 | myb-related trans |
| 37 | 68.0 | 320 | 2 | C85440 | myb-related protei |
| 38 | 68.0 | 497 | 1 | WMBELM | membrane protein L |
| 39 | 68.0 | 776 | 2 | E30591 | lipoprotein (impor |
| 40 | 68.0 | 3026 | 2 | T28431 | variant surface pr |
| 41 | 66.0 | 66 | 2 | T02595 | hypothetical prote |
| 42 | 66.0 | 169 | 2 | F87713 | conserved hypothet |
| 43 | 66.0 | 209 | 2 | JQ2347 | hypothetical 23.6K |
| 44 | 66.0 | 375 | 2 | T51854 | RING-H2 finger pro |
| 45 | 66.0 | 382 | 2 | T45301 | homoserine o-acety |
| 46 | 66.0 | 393 | 1 | S22520 | myb-related protei |
| 47 | 66.0 | 412 | 2 | JC5547 | basic helix-loop-h |
| 48 | 66.0 | 496 | 2 | AC1306 | carboxy-terminal p |
| 49 | 66.0 | 496 | 2 | AC1678 | carboxy-terminal p |
| 50 | 66.0 | 705 | 2 | D88536 | acidic protein - C |
| 51 | 66.0 | 705 | 2 | S27786 | acidic protein - C |
| 52 | 66.0 | 925 | 2 | JC2033 | G protein-coupled |
| 53 | 64.0 | 107 | 2 | S36262 | Ig lambda chain v |
| 54 | 64.0 | 142 | 2 | AF0592 | tolR protein (impo |
| 55 | 64.0 | 148 | 2 | D49530 | 16K vascular endot |
| 56 | 64.0 | 179 | 2 | JH0499 | glutamine/glutamic |
| 57 | 64.0 | 301 | 2 | A98214 | hypothetical prote |
| 58 | 64.0 | 327 | 2 | F75061 | signal peptidase r |
| 59 | 64.0 | 359 | 2 | A70978 | probable rmlA2 pro |
| 60 | 64.0 | 386 | 2 | T05781 | hypothetical prote |
| 61 | 64.0 | 387 | 2 | D84885 | hypothetical prote |
| 62 | 64.0 | 420 | 2 | T36532 | probable membrane |
| 63 | 64.0 | 479 | 2 | S48705 | serine/threonine p |
| 64 | 64.0 | 603 | 1 | ORBY8W | probable protein k |
| 65 | 64.0 | 655 | 1 | A55726 | RNA-binding protei |
| 66 | 64.0 | 656 | 1 | A49358 | RNA-binding protei |
| 67 | 64.0 | 661 | 2 | T15073 | hypothetical prote |
| 68 | 64.0 | 666 | 1 | S73445 | MG032 homolog B01 |
| 69 | 64.0 | 771 | 2 | S35681 | ESG protein - mous |
| 70 | 64.0 | 772 | 2 | D56695 | transducin-like en |
| 71 | 64.0 | 838 | 2 | A54163 | vacuolar ATPase (E |
| 72 | 64.0 | 838 | 2 | B38656 | vacuolar proton pu |
| 73 | 64.0 | 885 | 2 | JC4732 | beta-N-acetylhexos |
| 74 | 64.0 | 942 | 2 | JC2129 | protein kinase PKN |
| 75 | 64.0 | 943 | 2 | S28400 | gag-like protein - |
| 76 | 64.0 | 950 | 2 | S27473 | URB1 protein - am |
| 77 | 64.0 | 1163 | 2 | E71481 | probable swf/snf h |
| 78 | 64.0 | 1261 | 2 | T13165 | mutator 2 - fruit |
| 79 | 64.0 | 1307 | 2 | G96711 | unknown protein, 9 |
| 80 | 64.0 | 1420 | 2 | B57062 | SRB9 protein - yea |
| 81 | 64.0 | 1450 | 2 | T30273 | hypothetical prote |
| 82 | 64.0 | 1556 | 2 | S59393 | probable membrane |
| 83 | 64.0 | 1584 | 1 | JN0114 | kinesin-related pr |
| 84 | 64.0 | 1584 | 2 | T15822 | kinesin-like prote |
| 85 | 64.0 | 1655 | 2 | S47446 | nucleoporin Np188 |
| 86 | 64.0 | 1671 | 2 | S71628 | sensory transduci |
| 87 | 64.0 | 1905 | 2 | T18267 | multidrug resistan |
| 88 | 64.0 | 2035 | 2 | A40718 | host cell factor C |
| 89 | 63.0 | 135 | 2 | D82539 | hypothetical prote |
| 90 | 62.0 | 90 | 2 | T27091 | hypothetical prote |
| 91 | 62.0 | 104 | 2 | T29540 | hypothetical prote |
| 92 | 62.0 | 115 | 2 | S63596 | Ig kappa chain v r |
| 93 | 62.0 | 127 | 2 | B84172 | hypothetical prote |
| 94 | 62.0 | 169 | 2 | T21034 | hypothetical prote |
| 95 | 62.0 | 181 | 2 | T21035 | hypothetical prote |
| 96 | 62.0 | 199 | 1 | W2BE46 | gene 46 protein - |
| 97 | 62.0 | 260 | 2 | S42806 | gag-like polyprote |
| 98 | 62.0 | 277 | 1 | Q0BEC2 | HKPFX protein - hu |
| 99 | 62.0 | 286 | 2 | S32480 | hypothetical prote |
| 100 | 62.0 | 297 | 2 | S55085 | hypothetical prote |
| 101 | 62.0 | 303 | 2 | A40807 | membrane glycoprot |
| 102 | 62.0 | 355 | 2 | AE0034 | probable type III |

| | | | | | | | | | | | | | |
|-----|------|------|------|---|--------|--------------------|-----|----|------|------|---|--------|---------------------|
| 103 | 31 | 62.0 | 381 | 2 | S48049 | cholecystokinin B | 176 | 30 | 60.0 | 481 | 2 | F86208 | protein F22G5.30 [|
| 104 | 31 | 62.0 | 381 | 2 | S26812 | transcription fact | 177 | 30 | 60.0 | 488 | 2 | JC7969 | metalloprotease 1 |
| 105 | 31 | 62.0 | 427 | 2 | A84826 | hypothetical prote | 178 | 30 | 60.0 | 490 | 2 | E71486 | probable s/t prote |
| 106 | 31 | 62.0 | 447 | 2 | A47430 | gastrin/cholecysto | 179 | 30 | 60.0 | 491 | 2 | JE0276 | voltage-gated pota |
| 107 | 31 | 62.0 | 450 | 2 | JQ1614 | gastrin receptor - | 180 | 30 | 60.0 | 494 | 1 | WJFFBC | homeotic protein b |
| 108 | 31 | 62.0 | 452 | 2 | JC2459 | gastrin/cholecysto | 181 | 30 | 60.0 | 525 | 2 | AB3539 | bacterial peptide |
| 109 | 31 | 62.0 | 452 | 2 | A46195 | cholecystokinin B | 182 | 30 | 60.0 | 528 | 2 | T02863 | probable membrane |
| 110 | 31 | 62.0 | 453 | 2 | S28177 | gastrin receptor - | 183 | 30 | 60.0 | 536 | 2 | S28501 | hypothetical prote |
| 111 | 31 | 62.0 | 483 | 2 | A84698 | probable RNA-bindi | 184 | 30 | 60.0 | 548 | 2 | T16082 | hypothetical prote |
| 112 | 31 | 62.0 | 492 | 2 | T26502 | hypothetical prote | 185 | 30 | 60.0 | 549 | 2 | C87719 | protein R119.6 (im |
| 113 | 31 | 62.0 | 496 | 2 | T09931 | probable phosphodi | 186 | 30 | 60.0 | 577 | 2 | AE0936 | probable membrane |
| 114 | 31 | 62.0 | 544 | 2 | S46447 | f42h10.1 protein - | 187 | 30 | 60.0 | 596 | 2 | AE1515 | internalin like pr |
| 115 | 31 | 62.0 | 509 | 2 | S45413 | probable membrane | 188 | 30 | 60.0 | 601 | 2 | T11677 | probable transcrip |
| 116 | 31 | 62.0 | 514 | 2 | T26501 | hypothetical prote | 189 | 30 | 60.0 | 603 | 2 | JC7900 | beta-N-acetylgluco |
| 117 | 31 | 62.0 | 539 | 2 | T18116 | hypothetical prote | 190 | 30 | 60.0 | 622 | 1 | ACCH4N | nicotinic acetylch |
| 118 | 31 | 62.0 | 608 | 2 | T19935 | hypothetical prote | 191 | 30 | 60.0 | 639 | 2 | T46577 | arylsulfatase (EC |
| 119 | 31 | 62.0 | 620 | 2 | T16166 | hypothetical prote | 192 | 30 | 60.0 | 660 | 2 | I51684 | epithelial sodium |
| 120 | 31 | 62.0 | 623 | 2 | S68963 | phosphoprotein pho | 193 | 30 | 60.0 | 683 | 2 | H85074 | probable athila tr |
| 121 | 31 | 62.0 | 643 | 2 | S55610 | polyprotein - equi | 194 | 30 | 60.0 | 688 | 2 | H96681 | protein F1E22.10 [|
| 122 | 31 | 62.0 | 661 | 2 | T16597 | hypothetical prote | 195 | 30 | 60.0 | 715 | 2 | T12534 | hypothetical prote |
| 123 | 31 | 62.0 | 678 | 2 | A18441 | Mg chelatase chain | 196 | 30 | 60.0 | 731 | 2 | S46813 | lanosterol synthas |
| 124 | 31 | 62.0 | 689 | 4 | S30392 | hypothetical RTVL- | 197 | 30 | 60.0 | 740 | 1 | T02567 | probable ATP-bindi |
| 125 | 31 | 62.0 | 726 | 2 | T48023 | ATP-dependent RNA | 198 | 30 | 60.0 | 786 | 2 | A55501 | cyclin F - human |
| 126 | 31 | 62.0 | 728 | 2 | S48569 | hypothetical prote | 199 | 30 | 60.0 | 803 | 2 | JC7862 | eukaryotic initiat |
| 127 | 31 | 62.0 | 729 | 2 | H84912 | probable pre-mRNA | 200 | 30 | 60.0 | 833 | 2 | T49782 | related to alkalini |
| 128 | 31 | 62.0 | 794 | 2 | T27870 | hypothetical prote | 201 | 30 | 60.0 | 834 | 1 | WMVXPJ | RNA replicase 2 (E |
| 129 | 31 | 62.0 | 914 | 2 | S46593 | finger protein AZF | 202 | 30 | 60.0 | 856 | 2 | G96814 | hypothetical prote |
| 130 | 31 | 62.0 | 935 | 2 | S15795 | vacuolar proton pu | 203 | 30 | 60.0 | 895 | 2 | T45738 | hypothetical prote |
| 131 | 31 | 62.0 | 966 | 2 | H97717 | hypothetical prote | 204 | 30 | 60.0 | 900 | 2 | T33482 | hypothetical prote |
| 132 | 31 | 62.0 | 1006 | 2 | T00050 | hypothetical prote | 205 | 30 | 60.0 | 917 | 2 | T21870 | hypothetical prote |
| 133 | 31 | 62.0 | 1008 | 2 | T32986 | hypothetical prote | 206 | 30 | 60.0 | 921 | 2 | D86293 | FH2.22 protein - |
| 134 | 31 | 62.0 | 1027 | 2 | I38604 | p53-binding protei | 207 | 30 | 60.0 | 946 | 1 | A29550 | methyltetrahydr |
| 135 | 31 | 62.0 | 1170 | 2 | T31971 | hypothetical prote | 208 | 30 | 60.0 | 1054 | 2 | JC7294 | alpha integrin - |
| 136 | 31 | 62.0 | 1246 | 2 | S60954 | probable membrane | 209 | 30 | 60.0 | 1094 | 2 | S49313 | protein kinase - s |
| 137 | 31 | 62.0 | 1449 | 2 | B84426 | hypothetical prote | 210 | 30 | 60.0 | 1187 | 1 | JC4155 | protein-tyrosine-p |
| 138 | 31 | 62.0 | 1568 | 2 | T08616 | aggregation factor | 211 | 30 | 60.0 | 1189 | 1 | JC2366 | protein-tyrosine-p |
| 139 | 31 | 62.0 | 1784 | 2 | S86921 | polyketide synthas | 212 | 30 | 60.0 | 1214 | 2 | JC2069 | zinc-finger protei |
| 140 | 31 | 62.0 | 2197 | 2 | B71600 | variant-specific s | 213 | 30 | 60.0 | 1245 | 2 | S51255 | probable membrane |
| 141 | 31 | 62.0 | 3005 | 2 | S33642 | homeotic protein z | 214 | 30 | 60.0 | 1257 | 2 | T01020 | hypothetical prote |
| 142 | 31 | 62.0 | 3149 | 1 | Q0BE8 | BPLF1 protein - hu | 215 | 30 | 60.0 | 1272 | 2 | T30248 | fragile X mental r |
| 143 | 31 | 62.0 | 3712 | 1 | YGCEVC | alpha-aminoadipyl- | 216 | 30 | 60.0 | 1284 | 2 | T50993 | hypothetical prote |
| 144 | 30.5 | 61.0 | 467 | 2 | A98989 | heat shock protein | 217 | 30 | 60.0 | 1340 | 2 | D96521 | protein F21D18.16 |
| 145 | 30 | 60.0 | 62 | 1 | N1N7JM | short neurotoxin 1 | 218 | 30 | 60.0 | 1392 | 2 | A43336 | microtubule-vesicl |
| 146 | 30 | 60.0 | 72 | 2 | B82590 | hypothetical prote | 219 | 30 | 60.0 | 1427 | 2 | S22695 | restin - human |
| 147 | 30 | 60.0 | 87 | 2 | C97796 | hypothetical prote | 220 | 30 | 60.0 | 1448 | 2 | T08526 | DNA primase trac2 |
| 148 | 30 | 60.0 | 108 | 1 | W4WLC1 | E4 protein - pygmy | 221 | 30 | 60.0 | 1448 | 2 | S37669 | tracC-2 protein - E |
| 149 | 30 | 60.0 | 128 | 2 | H84457 | probable retroelem | 222 | 30 | 60.0 | 1736 | 2 | T00391 | hypothetical prote |
| 150 | 30 | 60.0 | 133 | 1 | GFPGE | glycophorin - pig | 223 | 30 | 60.0 | 1888 | 2 | T39009 | hypothetical prote |
| 151 | 30 | 60.0 | 151 | 2 | A39392 | RAD6 DNA-repair ho | 224 | 30 | 60.0 | 2216 | 2 | S78398 | hypothetical prote |
| 152 | 30 | 60.0 | 155 | 2 | T00844 | hypothetical prote | 225 | 29 | 58.0 | 107 | 2 | PD0011 | Ig kappa chain V r |
| 153 | 30 | 60.0 | 164 | 1 | TVBE11 | transforming prote | 226 | 29 | 58.0 | 107 | 2 | FC4405 | Ig kappa chain V r |
| 154 | 30 | 60.0 | 167 | 2 | D55224 | hypothetical prote | 227 | 29 | 58.0 | 107 | 2 | C96970 | probable transcrip |
| 155 | 30 | 60.0 | 192 | 2 | T35200 | hypothetical prote | 228 | 29 | 58.0 | 107 | 2 | T22709 | hypothetical prote |
| 156 | 30 | 60.0 | 207 | 2 | D87267 | hypothetical prote | 229 | 29 | 58.0 | 107 | 2 | T27502 | hypothetical prote |
| 157 | 30 | 60.0 | 230 | 2 | H86233 | hypothetical prote | 230 | 29 | 58.0 | 108 | 1 | K1HULY | Ig kappa chain V-I |
| 158 | 30 | 60.0 | 262 | 2 | T22148 | hypothetical prote | 231 | 29 | 58.0 | 109 | 1 | K3HUPM | Ig kappa chain V-I |
| 159 | 30 | 60.0 | 279 | 1 | RGECR1 | regulatory protein | 232 | 29 | 58.0 | 111 | 1 | KVMS40 | Ig kappa chain V r |
| 160 | 30 | 60.0 | 295 | 2 | T22039 | hypothetical prote | 233 | 29 | 58.0 | 111 | 2 | S09965 | Ig kappa chain V-J |
| 161 | 30 | 60.0 | 296 | 2 | B96507 | hypothetical prote | 234 | 29 | 58.0 | 122 | 2 | S40314 | Ig kappa chain - h |
| 162 | 30 | 60.0 | 298 | 2 | T21610 | hypothetical prote | 235 | 29 | 58.0 | 124 | 2 | S17598 | Ig lambda chain - |
| 163 | 30 | 60.0 | 302 | 2 | A96841 | hypothetical prote | 236 | 29 | 58.0 | 132 | 1 | KVMS32 | Ig kappa chain pre |
| 164 | 30 | 60.0 | 313 | 2 | H87731 | protein W10C9.1 [i | 237 | 29 | 58.0 | 134 | 2 | S44430 | synuclein - human |
| 165 | 30 | 60.0 | 325 | 2 | A75415 | homoserine dehydro | 238 | 29 | 58.0 | 134 | 2 | A72730 | hypothetical prote |
| 166 | 30 | 60.0 | 334 | 2 | T11633 | hypothetical prote | 239 | 29 | 58.0 | 140 | 2 | T49027 | hypothetical prote |
| 167 | 30 | 60.0 | 337 | 2 | D84671 | hypothetical prote | 240 | 29 | 58.0 | 144 | 2 | S35331 | apidaecin 22 precu |
| 168 | 30 | 60.0 | 346 | 2 | T07005 | L-lactate dehydrog | 241 | 29 | 58.0 | 145 | 2 | H75310 | hypothetical prote |
| 169 | 30 | 60.0 | 362 | 2 | P84695 | probable protein p | 242 | 29 | 58.0 | 168 | 2 | S35330 | apidaecin 14 precu |
| 170 | 30 | 60.0 | 376 | 2 | A96643 | hypothetical prote | 243 | 29 | 58.0 | 176 | 2 | T47743 | hypothetical prote |
| 171 | 30 | 60.0 | 395 | 2 | T19144 | hypothetical prote | 244 | 29 | 58.0 | 210 | 2 | D85098 | hypothetical prote |
| 172 | 30 | 60.0 | 427 | 2 | S38032 | hypothetical prote | 245 | 29 | 58.0 | 225 | 2 | T13109 | gene 23 protein - |
| 173 | 30 | 60.0 | 451 | 2 | S37933 | aspartate transami | 246 | 29 | 58.0 | 237 | 2 | A84720 | hypothetical prote |
| 174 | 30 | 60.0 | 466 | 2 | A82540 | two-component sens | 247 | 29 | 58.0 | 246 | 1 | S56439 | ammonium transport |
| 175 | 30 | 60.0 | 479 | 2 | D81423 | probable iron-sulf | 248 | 29 | 58.0 | 246 | 2 | AF1054 | cysQ protein (impo |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|--------|---------------------|-----|----|------|------|---|--------|---------------------|
| 249 | 29 | 58.0 | 246 | 2 | H86118 | ammonium transport | 322 | 29 | 58.0 | 681 | 2 | JX0338 | rabphilin-3A - mou |
| 250 | 29 | 58.0 | 246 | 2 | H91277 | ammonium transport | 323 | 29 | 58.0 | 684 | 2 | I58166 | rabphilin-3A - rat |
| 251 | 29 | 58.0 | 247 | 2 | AB0429 | inositol monophosp | 324 | 29 | 58.0 | 699 | 2 | A96529 | hypothetical prote |
| 252 | 29 | 58.0 | 275 | 2 | T32626 | hypothetical prote | 325 | 29 | 58.0 | 715 | 2 | S54628 | hypothetical prote |
| 253 | 29 | 58.0 | 278 | 2 | D83474 | hypothetical prote | 326 | 29 | 58.0 | 724 | 2 | A48569 | antigen Em100 - Ei |
| 254 | 29 | 58.0 | 281 | 2 | AH3629 | taurine transport | 327 | 29 | 58.0 | 731 | 2 | T18632 | hypothetical prote |
| 255 | 29 | 58.0 | 283 | 2 | S35332 | apidaecin 73 precu | 328 | 29 | 58.0 | 734 | 2 | G86171 | hypothetical prote |
| 256 | 29 | 58.0 | 285 | 2 | AB0782 | probable esterase | 329 | 29 | 58.0 | 781 | 2 | S37032 | gene L15 protein - |
| 257 | 29 | 58.0 | 316 | 1 | S15799 | protein-tyrosine-p | 330 | 29 | 58.0 | 788 | 2 | AE3153 | NADP-dependent ald |
| 258 | 29 | 58.0 | 317 | 1 | AB0450 | trehalose operon r | 331 | 29 | 58.0 | 796 | 2 | T20393 | hypothetical prote |
| 259 | 29 | 58.0 | 319 | 1 | LURT5 | annexin V - rat | 332 | 29 | 58.0 | 796 | 2 | UC7355 | peroxisome prolife |
| 260 | 29 | 58.0 | 319 | 2 | PC1137 | DNA primase - Buch | 333 | 29 | 58.0 | 798 | 2 | F98134 | hypothetical prote |
| 261 | 29 | 58.0 | 333 | 2 | D70792 | hypothetical prote | 334 | 29 | 58.0 | 798 | 2 | T34248 | hypothetical prote |
| 262 | 29 | 58.0 | 345 | 2 | T43182 | tetrahydrofolylpol | 335 | 29 | 58.0 | 815 | 1 | T05754 | S-receptor kinase |
| 263 | 29 | 58.0 | 351 | 2 | A45377 | transcription fact | 336 | 29 | 58.0 | 825 | 1 | GLHQ | beta-glucosidase (|
| 264 | 29 | 58.0 | 357 | 2 | S45772 | homoserine kinase | 337 | 29 | 58.0 | 841 | 2 | B82755 | beta-hexosaminidas |
| 265 | 29 | 58.0 | 358 | 2 | AC0740 | probable integrase | 338 | 29 | 58.0 | 858 | 2 | AS7513 | heat shock protein |
| 266 | 29 | 58.0 | 358 | 2 | B87003 | hypothetical prote | 339 | 29 | 58.0 | 859 | 2 | S66666 | heat shock protein |
| 267 | 29 | 58.0 | 364 | 2 | T01184 | hypothetical prote | 340 | 29 | 58.0 | 863 | 2 | S06017 | neuraxin - rat |
| 268 | 29 | 58.0 | 369 | 2 | S77199 | hypothetical prote | 341 | 29 | 58.0 | 863 | 2 | T27958 | hypothetical prote |
| 269 | 29 | 58.0 | 370 | 2 | T49246 | transcription init | 342 | 29 | 58.0 | 880 | 2 | F83386 | hypothetical prote |
| 270 | 29 | 58.0 | 379 | 2 | D70846 | hypothetical prote | 343 | 29 | 58.0 | 883 | 2 | T37208 | hypothetical prote |
| 271 | 29 | 58.0 | 380 | 2 | H95362 | probable metaA prot | 344 | 29 | 58.0 | 913 | 2 | A86237 | protein F14N23.15 |
| 272 | 29 | 58.0 | 386 | 2 | T49335 | hypothetical prote | 345 | 29 | 58.0 | 953 | 2 | B70681 | probable rne prote |
| 273 | 29 | 58.0 | 392 | 2 | T04150 | hypothetical prote | 346 | 29 | 58.0 | 953 | 2 | T08961 | hypothetical prote |
| 274 | 29 | 58.0 | 403 | 2 | T02513 | RAD23 protein homo | 347 | 29 | 58.0 | 961 | 2 | H86181 | hypothetical prote |
| 275 | 29 | 58.0 | 403 | 2 | H64861 | hypothetical prote | 348 | 29 | 58.0 | 1013 | 2 | G87236 | conserved integral |
| 276 | 29 | 58.0 | 415 | 2 | H86204 | probable phosphoes | 349 | 29 | 58.0 | 1014 | 2 | T31109 | myosin III - Atlan |
| 277 | 29 | 58.0 | 417 | 2 | C82840 | conserved hypothet | 350 | 29 | 58.0 | 1021 | 2 | T23252 | hypothetical prote |
| 278 | 29 | 58.0 | 422 | 2 | T05592 | tyrosine transamin | 351 | 29 | 58.0 | 1046 | 2 | T34566 | hypothetical prote |
| 279 | 29 | 58.0 | 427 | 1 | T49031 | acid phosphatase (| 352 | 29 | 58.0 | 1088 | 2 | B34106 | protein kinase (EC |
| 280 | 29 | 58.0 | 428 | 2 | S48174 | variable surface g | 353 | 29 | 58.0 | 1098 | 2 | S36868 | alpha, alpha-trehal |
| 281 | 29 | 58.0 | 430 | 2 | H96580 | hypothetical prote | 354 | 29 | 58.0 | 1148 | 2 | D85360 | hypothetical prote |
| 282 | 29 | 58.0 | 441 | 2 | S37881 | hypothetical prote | 355 | 29 | 58.0 | 1199 | 2 | T15826 | hypothetical prote |
| 283 | 29 | 58.0 | 445 | 2 | I46225 | mucin A, tracheal | 356 | 29 | 58.0 | 1200 | 2 | T48194 | hypothetical prote |
| 284 | 29 | 58.0 | 447 | 2 | AF2295 | hypothetical prote | 357 | 29 | 58.0 | 1209 | 2 | T00373 | hypothetical prote |
| 285 | 29 | 58.0 | 463 | 2 | S10224 | thesaaurin A - Afri | 358 | 29 | 58.0 | 1239 | 2 | T06143 | hypothetical prote |
| 286 | 29 | 58.0 | 468 | 2 | C96818 | hypothetical prote | 359 | 29 | 58.0 | 1274 | 2 | S59405 | probable membrane |
| 287 | 29 | 58.0 | 468 | 2 | T40223 | HMG-box containing | 360 | 29 | 58.0 | 1307 | 2 | T25563 | hypothetical prote |
| 288 | 29 | 58.0 | 468 | 2 | A41518 | transcription fact | 361 | 29 | 58.0 | 1404 | 2 | E36788 | hypothetical prote |
| 289 | 29 | 58.0 | 469 | 2 | T10061 | 3-oxoacyl-lacyl-ca | 362 | 29 | 58.0 | 1430 | 2 | T34516 | hypothetical prote |
| 290 | 29 | 58.0 | 478 | 2 | T09896 | hypothetical prote | 363 | 29 | 58.0 | 1434 | 2 | T30172 | transmembrane prot |
| 291 | 29 | 58.0 | 486 | 2 | S07633 | hematopoietic line | 364 | 29 | 58.0 | 1462 | 1 | A69809 | probable multifunc |
| 292 | 29 | 58.0 | 486 | 2 | I49760 | LckBp1 protein - m | 365 | 29 | 58.0 | 1473 | 2 | T31422 | C-terminal domain |
| 293 | 29 | 58.0 | 488 | 2 | T27532 | hypothetical prote | 366 | 29 | 58.0 | 1570 | 2 | T38792 | probable protein t |
| 294 | 29 | 58.0 | 496 | 2 | JC5261 | salt-tolerant prot | 367 | 29 | 58.0 | 1606 | 2 | T34073 | paranemin - chicke |
| 295 | 29 | 58.0 | 498 | 2 | T34592 | DEAD-box RNA helic | 368 | 29 | 58.0 | 1655 | 2 | T32633 | hypothetical prote |
| 296 | 29 | 58.0 | 505 | 2 | T39645 | folypolyglutamate | 369 | 29 | 58.0 | 1811 | 2 | T39252 | hypothetical prote |
| 297 | 29 | 58.0 | 521 | 2 | S52824 | AEPI protein - yea | 370 | 29 | 58.0 | 1873 | 2 | A30063 | probable protein t |
| 298 | 29 | 58.0 | 521 | 2 | AC1949 | hypothetical prote | 371 | 29 | 58.0 | 2094 | 2 | S33124 | dihydropyridine re |
| 299 | 29 | 58.0 | 532 | 2 | T49467 | related to COp1-in | 372 | 29 | 58.0 | 2145 | 2 | JC4747 | tpx protein - huma |
| 300 | 29 | 58.0 | 540 | 2 | T20563 | probable berberine | 373 | 29 | 58.0 | 2211 | 1 | KFB05 | adenylate cyclase |
| 301 | 29 | 58.0 | 549 | 2 | T23526 | hypothetical prote | 374 | 29 | 58.0 | 2251 | 2 | T24490 | coagulation factor |
| 302 | 29 | 58.0 | 557 | 2 | S6292 | hypothetical prote | 375 | 29 | 58.0 | 2364 | 2 | A56577 | hypothetical prote |
| 303 | 29 | 58.0 | 558 | 2 | S63148 | probable membrane | 376 | 29 | 58.0 | 2464 | 1 | QRMSP1 | microtubule-associ |
| 304 | 29 | 58.0 | 560 | 2 | E64600 | soluble lytic mure | 377 | 29 | 58.0 | 2688 | 2 | I49477 | microtubule-associ |
| 305 | 29 | 58.0 | 573 | 2 | T00320 | hypothetical prote | 378 | 29 | 58.0 | 4660 | 2 | T42737 | alpha-A-crystallin |
| 306 | 29 | 58.0 | 577 | 2 | D91239 | membrane protein (| 379 | 29 | 58.0 | 4725 | 1 | A44357 | gp330 protein prec |
| 307 | 29 | 58.0 | 577 | 2 | A86087 | hypothetical prote | 380 | 29 | 58.0 | 1139 | 2 | S44800 | dynein heavy chain |
| 308 | 29 | 58.0 | 577 | 2 | F65202 | hypothetical prote | 381 | 29 | 58.0 | 20 | 2 | S33001 | FluB9.8 protein - |
| 309 | 29 | 58.0 | 582 | 2 | S08686 | finger protein ZFP | 382 | 29 | 58.0 | 37 | 2 | A10933 | hypothetical prote |
| 310 | 29 | 58.0 | 583 | 2 | H84810 | probable calcium-d | 383 | 29 | 58.0 | 41 | 1 | UOCCIM | hypothetical prote |
| 311 | 29 | 58.0 | 592 | 2 | T16725 | hypothetical prote | 384 | 29 | 58.0 | 94 | 2 | D71284 | hypothetical prote |
| 312 | 29 | 58.0 | 597 | 2 | T25547 | conserved hypothet | 385 | 29 | 58.0 | 97 | 2 | S26341 | Ig light chain v r |
| 313 | 29 | 58.0 | 604 | 2 | G83091 | hypothetical prote | 386 | 29 | 58.0 | 108 | 2 | T05921 | N-carbamyl-L-amino |
| 314 | 29 | 58.0 | 610 | 2 | T32327 | hypothetical prote | 387 | 29 | 58.0 | 108 | 2 | S36283 | Ig lambda chain v |
| 315 | 29 | 58.0 | 634 | 2 | T27959 | hypothetical prote | 388 | 29 | 58.0 | 112 | 2 | S19976 | Ig kappa chain v r |
| 316 | 29 | 58.0 | 638 | 2 | A45287 | gamete lytic enzym | 389 | 29 | 58.0 | 115 | 2 | T26191 | hypothetical prote |
| 317 | 29 | 58.0 | 639 | 2 | E98281 | cobT protein (limp) | 390 | 29 | 58.0 | 131 | 2 | E25733 | T-cell receptor al |
| 318 | 29 | 58.0 | 639 | 2 | AC3002 | cobyrinic acid syn | 391 | 29 | 58.0 | 133 | 2 | S57891 | T cell receptor ps |
| 319 | 29 | 58.0 | 643 | 1 | S24382 | nitrous-oxide redu | 392 | 29 | 58.0 | 134 | 2 | D64744 | exopolysaccharide |
| 320 | 29 | 58.0 | 657 | 2 | S05517 | lamin - chicken | 393 | 29 | 58.0 | 134 | 2 | F85504 | regulator in colan |
| 321 | 29 | 58.0 | 679 | 2 | S48437 | hypothetical prote | 394 | 29 | 58.0 | 134 | 2 | F90653 | regulator in colan |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|--------|--------------------|-----|----|------|-----|---|--------|---------------------|
| 395 | 28 | 56.0 | 136 | 2 | F84041 | hypothetical prote | 468 | 28 | 56.0 | 357 | 2 | S43278 | cell division cont |
| 396 | 28 | 56.0 | 137 | 2 | T47418 | hypothetical prote | 469 | 28 | 56.0 | 357 | 2 | A86434 | protein T17H7.11 [|
| 397 | 28 | 56.0 | 145 | 1 | UOCA1 | urotensin I precur | 470 | 28 | 56.0 | 358 | 2 | T27195 | hypothetical prote |
| 398 | 28 | 56.0 | 146 | 2 | T14667 | hypothetical prote | 471 | 28 | 56.0 | 367 | 2 | G84831 | probable bZIP tran |
| 399 | 28 | 56.0 | 151 | 2 | T14948 | hypothetical prote | 472 | 28 | 56.0 | 367 | 2 | T52624 | b-Zip DNA binding |
| 400 | 28 | 56.0 | 154 | 2 | S55017 | hypothetical prote | 473 | 28 | 56.0 | 368 | 2 | A2840 | ABC transporter, s |
| 401 | 28 | 56.0 | 161 | 2 | S11801 | pullulanase secret | 474 | 28 | 56.0 | 368 | 2 | E97617 | hypothetical prote |
| 402 | 28 | 56.0 | 164 | 2 | D68855 | translation initia | 475 | 28 | 56.0 | 372 | 2 | H89453 | protein F35H12.1 [|
| 403 | 28 | 56.0 | 166 | 1 | RGHJ1B | regenerating islet | 476 | 28 | 56.0 | 375 | 2 | S26059 | probable transform |
| 404 | 28 | 56.0 | 172 | 2 | G83415 | hypothetical prote | 477 | 28 | 56.0 | 380 | 2 | E84238 | quinone oxidoreduc |
| 405 | 28 | 56.0 | 173 | 2 | S70521 | cathelin-related p | 478 | 28 | 56.0 | 383 | 2 | S32975 | gene BCRP2 protein |
| 406 | 28 | 56.0 | 173 | 2 | S38231 | hypothetical prote | 479 | 28 | 56.0 | 387 | 2 | C83398 | hypothetical prote |
| 407 | 28 | 56.0 | 173 | 2 | S41755 | cyclin E type II - | 480 | 28 | 56.0 | 388 | 2 | T29894 | hypothetical prote |
| 408 | 28 | 56.0 | 181 | 2 | AC2053 | hypothetical prote | 481 | 28 | 56.0 | 390 | 2 | T25080 | hypothetical prote |
| 409 | 28 | 56.0 | 188 | 2 | S66001 | conserved hypotet | 482 | 28 | 56.0 | 394 | 2 | E75104 | hypothetical prote |
| 410 | 28 | 56.0 | 190 | 2 | A26630 | nucleoplasmin A - | 483 | 28 | 56.0 | 395 | 2 | A11842 | hypothetical prote |
| 411 | 28 | 56.0 | 195 | 2 | C83854 | hypothetical prote | 484 | 28 | 56.0 | 399 | 1 | C43685 | polymerase-associa |
| 412 | 28 | 56.0 | 200 | 2 | A26169 | nucleoplasmin - Af | 485 | 28 | 56.0 | 401 | 2 | S50533 | hypothetical prote |
| 413 | 28 | 56.0 | 202 | 2 | B82522 | hypothetical prote | 486 | 28 | 56.0 | 401 | 2 | E83955 | flagellar motor sw |
| 414 | 28 | 56.0 | 211 | 2 | AD1053 | conserved hypotet | 487 | 28 | 56.0 | 403 | 2 | T25556 | hypothetical prote |
| 415 | 28 | 56.0 | 214 | 2 | AB2157 | hypothetical prote | 488 | 28 | 56.0 | 404 | 2 | S76573 | transcription init |
| 416 | 28 | 56.0 | 215 | 2 | T16383 | hypothetical prote | 489 | 28 | 56.0 | 411 | 2 | B89024 | protein R02D1.1 [i |
| 417 | 28 | 56.0 | 216 | 2 | T49795 | related to 3-oxoac | 490 | 28 | 56.0 | 413 | 2 | S28172 | ribulose-bisphosph |
| 418 | 28 | 56.0 | 217 | 2 | A70166 | hypothetical prote | 491 | 28 | 56.0 | 416 | 2 | T12511 | hypothetical prote |
| 419 | 28 | 56.0 | 224 | 2 | S56431 | hypothetical prote | 492 | 28 | 56.0 | 428 | 2 | T23363 | hypothetical prote |
| 420 | 28 | 56.0 | 224 | 2 | H91276 | hypothetical prote | 493 | 28 | 56.0 | 439 | 2 | C89890 | hypothetical prote |
| 421 | 28 | 56.0 | 225 | 2 | H86117 | hypothetical prote | 494 | 28 | 56.0 | 445 | 2 | T51018 | hypothetical prote |
| 422 | 28 | 56.0 | 225 | 2 | S73585 | MG068 homolog D02 | 495 | 28 | 56.0 | 446 | 2 | A56733 | hypothetical prote |
| 423 | 28 | 56.0 | 229 | 2 | S64049 | hypothetical prote | 496 | 28 | 56.0 | 449 | 2 | JC5391 | nuclear domain 10 |
| 424 | 28 | 56.0 | 230 | 2 | A29573 | Glx-rich protein - | 497 | 28 | 56.0 | 449 | 2 | A98239 | presenilin-beta - |
| 425 | 28 | 56.0 | 233 | 2 | C75440 | transcription regu | 498 | 28 | 56.0 | 449 | 2 | AC3047 | hypothetical prote |
| 426 | 28 | 56.0 | 240 | 2 | B36724 | hypothetical prote | 499 | 28 | 56.0 | 452 | 2 | A88712 | multicopper oxidas |
| 427 | 28 | 56.0 | 245 | 2 | S66711 | hypothetical prote | 500 | 28 | 56.0 | 472 | 2 | A33312 | protein C17H12.9 [|
| 428 | 28 | 56.0 | 247 | 2 | A38647 | glutamine/glutamat | 501 | 28 | 56.0 | 478 | 2 | C29514 | sarcoplasmic retic |
| 429 | 28 | 56.0 | 247 | 2 | A29545 | submandibular glan | 502 | 28 | 56.0 | 478 | 2 | T34985 | muscarinic acetylch |
| 430 | 28 | 56.0 | 251 | 2 | JC7513 | fibroblast growth | 503 | 28 | 56.0 | 479 | 2 | S33776 | probable sugar tra |
| 431 | 28 | 56.0 | 253 | 2 | B71800 | hypothetical prote | 504 | 28 | 56.0 | 484 | 2 | T07675 | muscarinic acetylch |
| 432 | 28 | 56.0 | 255 | 2 | B38647 | glutamine/glutamat | 505 | 28 | 56.0 | 486 | 2 | G96713 | cyclin a2-type, mi |
| 433 | 28 | 56.0 | 262 | 2 | S18134 | arcelin precursor | 506 | 28 | 56.0 | 492 | 2 | A41907 | probable DNA-bindi |
| 434 | 28 | 56.0 | 265 | 2 | I46986 | albumin - dog (fra | 507 | 28 | 56.0 | 498 | 1 | A56564 | methyl-CpG-binding |
| 435 | 28 | 56.0 | 270 | 2 | H86369 | hypothetical prote | 508 | 28 | 56.0 | 500 | 2 | JC7668 | transcription fact |
| 436 | 28 | 56.0 | 273 | 2 | S28132 | gas vesicle protei | 509 | 28 | 56.0 | 503 | 2 | H70509 | dipeptidyl-peptida |
| 437 | 28 | 56.0 | 275 | 1 | S07442 | interleukin-2 rece | 510 | 28 | 56.0 | 505 | 1 | P1WLRB | hypothetical prote |
| 438 | 28 | 56.0 | 276 | 2 | T21304 | hypothetical prote | 511 | 28 | 56.0 | 505 | 2 | T43488 | Li protein - cotto |
| 439 | 28 | 56.0 | 279 | 2 | AE1873 | phycobilisome rod- | 512 | 28 | 56.0 | 508 | 2 | B81594 | hypothetical prote |
| 440 | 28 | 56.0 | 279 | 2 | J60592 | rod-core linker po | 513 | 28 | 56.0 | 508 | 2 | E86549 | hypothetical prote |
| 441 | 28 | 56.0 | 279 | 2 | S23473 | rod-core linker po | 514 | 28 | 56.0 | 508 | 2 | C72074 | hypothetical prote |
| 442 | 28 | 56.0 | 281 | 2 | T52189 | ethylene responsiv | 515 | 28 | 56.0 | 509 | 1 | D64312 | conserved hypotet |
| 443 | 28 | 56.0 | 285 | 2 | A85079 | probable Athila-li | 516 | 28 | 56.0 | 514 | 1 | VHNZCV | nucleocapsid prote |
| 444 | 28 | 56.0 | 288 | 1 | STW53A | succinate-CoA liga | 517 | 28 | 56.0 | 514 | 1 | E84306 | methylmalonyl-CoA |
| 445 | 28 | 56.0 | 288 | 2 | S57706 | hypothetical prote | 518 | 28 | 56.0 | 516 | 2 | T29834 | hypothetical prote |
| 446 | 28 | 56.0 | 289 | 2 | G86403 | 33.3K hypothetical | 519 | 28 | 56.0 | 518 | 2 | A12426 | hypothetical prote |
| 447 | 28 | 56.0 | 290 | 2 | F89952 | hypothetical prote | 520 | 28 | 56.0 | 519 | 2 | T20158 | hypothetical prote |
| 448 | 28 | 56.0 | 294 | 2 | S13141 | hypothetical prote | 521 | 28 | 56.0 | 520 | 1 | O4BOM | cholesterol monoox |
| 449 | 28 | 56.0 | 296 | 2 | T15550 | hypothetical prote | 522 | 28 | 56.0 | 532 | 2 | A34329 | 60K esterase (EC 3 |
| 450 | 28 | 56.0 | 300 | 2 | F69719 | succinate-CoA liga | 523 | 28 | 56.0 | 537 | 2 | T40507 | probable vacuolar |
| 451 | 28 | 56.0 | 300 | 2 | T20712 | hypothetical prote | 524 | 28 | 56.0 | 542 | 2 | T44094 | site-specific reco |
| 452 | 28 | 56.0 | 302 | 2 | B83958 | succinyl-CoA synth | 525 | 28 | 56.0 | 550 | 2 | A28166 | Kupffer cell recep |
| 453 | 28 | 56.0 | 302 | 2 | AC2018 | hypothetical prote | 526 | 28 | 56.0 | 558 | 2 | T28881 | hypothetical prote |
| 454 | 28 | 56.0 | 305 | 1 | S71284 | myb-related protei | 527 | 28 | 56.0 | 568 | 2 | G02753 | testis specific ba |
| 455 | 28 | 56.0 | 306 | 2 | A71332 | probable integrase | 528 | 28 | 56.0 | 584 | 2 | JQ1229 | cellulase (EC 3.2. |
| 456 | 28 | 56.0 | 315 | 2 | JC5842 | chitinase (EC 3.2. | 529 | 28 | 56.0 | 589 | 2 | T52070 | RNAI protein homol |
| 457 | 28 | 56.0 | 317 | 2 | AF2129 | hypothetical prote | 530 | 28 | 56.0 | 589 | 2 | A36983 | RNAI homolog fugi |
| 458 | 28 | 56.0 | 320 | 2 | A81165 | HPr kinase/phospha | 531 | 28 | 56.0 | 589 | 2 | S60154 | serine/threonine-s |
| 459 | 28 | 56.0 | 321 | 2 | T24410 | hypothetical prote | 532 | 28 | 56.0 | 589 | 2 | S60159 | serine/threonine-s |
| 460 | 28 | 56.0 | 329 | 2 | T23209 | hypothetical prote | 533 | 28 | 56.0 | 598 | 2 | T47254 | serine/threonine k |
| 461 | 28 | 56.0 | 332 | 2 | D84690 | hypothetical prote | 534 | 28 | 56.0 | 601 | 2 | T38736 | hypothetical prote |
| 462 | 28 | 56.0 | 338 | 2 | JC5435 | aspartate-semialde | 535 | 28 | 56.0 | 603 | 2 | E71444 | probable BREFP-4 - |
| 463 | 28 | 56.0 | 338 | 2 | JC5436 | aspartate-semialde | 536 | 28 | 56.0 | 607 | 2 | E84827 | hypothetical prote |
| 464 | 28 | 56.0 | 344 | 2 | T12243 | NADH2 dehydrogenas | 537 | 28 | 56.0 | 610 | 2 | T47725 | hypothetical prote |
| 465 | 28 | 56.0 | 344 | 2 | T12247 | NADH2 dehydrogenas | 538 | 28 | 56.0 | 615 | 2 | JC7576 | transcription fact |
| 466 | 28 | 56.0 | 347 | 2 | I38008 | melanoma antigen M | 539 | 28 | 56.0 | 619 | 1 | S48729 | glucokinase regula |
| 467 | 28 | 56.0 | 348 | 2 | S44628 | f22b7.1 protein - | 540 | 28 | 56.0 | 620 | 2 | S22711 | probable protein k |

| | | | | | | | | | | | | | |
|-----|----|------|------|---|-------------------|----------------------|-----|------|------|------|---|--------|--------------------|
| 541 | 28 | 56.0 | 622 | 2 | T37257 | hypothetical prote | 614 | 28 | 56.0 | 1006 | 2 | S76892 | hypothetical prote |
| 542 | 28 | 56.0 | 627 | 1 | A41745 | glucokinase regula | 615 | 28 | 56.0 | 1009 | 2 | E89792 | hypothetical prote |
| 543 | 28 | 56.0 | 628 | 2 | T29128 | probable ATP/GTP b | 616 | 28 | 56.0 | 1014 | 1 | DEBY | oxoglutarate dehyd |
| 544 | 28 | 56.0 | 633 | 2 | T004179 | hypothetical prote | 617 | 28 | 56.0 | 1015 | 2 | T00726 | probable serine/th |
| 545 | 28 | 56.0 | 635 | 2 | T50661 | receptor-type prot | 618 | 28 | 56.0 | 1038 | 2 | JC6027 | 115K outer membran |
| 546 | 28 | 56.0 | 635 | 2 | S57714 | csbB protein - Clo | 619 | 28 | 56.0 | 1045 | 2 | B30239 | hydroxymethylgluta |
| 547 | 28 | 56.0 | 638 | 2 | T13691 | hypothetical prote | 620 | 28 | 56.0 | 1053 | 1 | QYYC | phosphoenolpyruvat |
| 548 | 28 | 56.0 | 640 | 2 | S64106 | hypothetical prote | 621 | 28 | 56.0 | 1117 | 2 | S63399 | probable membrane |
| 549 | 28 | 56.0 | 646 | 2 | JC5583 | 85K SH3 domain-con | 622 | 28 | 56.0 | 1119 | 2 | T16720 | hypothetical prote |
| 550 | 28 | 56.0 | 652 | 2 | T41162 | hypothetical prote | 623 | 28 | 56.0 | 1123 | 2 | T19713 | hypothetical prote |
| 551 | 28 | 56.0 | 653 | 2 | A46362 | amyloid precursor- | 624 | 28 | 56.0 | 1131 | 2 | D75429 | sensory box sensor |
| 552 | 28 | 56.0 | 655 | 2 | JC7140 | protoxin - Bacillu | 625 | 28 | 56.0 | 1159 | 2 | S62562 | probable nuclear p |
| 553 | 28 | 56.0 | 656 | 2 | T23338 | hypothetical prote | 626 | 28 | 56.0 | 1176 | 2 | A48970 | parasporal crystal |
| 554 | 28 | 56.0 | 659 | 2 | S67175 | probable membrane | 627 | 28 | 56.0 | 1189 | 2 | S00944 | parasporal crystal |
| 555 | 28 | 56.0 | 675 | 2 | T02537 | probable serine/th | 628 | 28 | 56.0 | 1194 | 2 | E96624 | hypothetical prote |
| 556 | 28 | 56.0 | 681 | 2 | T23454 | hypothetical prote | 629 | 28 | 56.0 | 1196 | 2 | S35994 | DNA repair protein |
| 557 | 28 | 56.0 | 682 | 2 | AG2118 | serine/threonine k | 630 | 28 | 56.0 | 1200 | 2 | T17404 | hyalin - sea urchi |
| 558 | 28 | 56.0 | 686 | 2 | S60749 | probable ligand-ga | 631 | 28 | 56.0 | 1205 | 2 | T41987 | hypothetical prote |
| 559 | 28 | 56.0 | 688 | 2 | A47705 | triacylglycerol li | 632 | 28 | 56.0 | 1211 | 2 | T42230 | AF4 protein - mous |
| 560 | 28 | 56.0 | 701 | 2 | D64641 | glycine-tRNA ligas | 633 | 28 | 56.0 | 1221 | 1 | HJNVAV | helicase [EC 3.6.1 |
| 561 | 28 | 56.0 | 701 | 2 | H71874 | glycine-tRNA ligas | 634 | 28 | 56.0 | 1222 | 2 | T41835 | DNA helicase P143 |
| 562 | 28 | 56.0 | 711 | 2 | T48335 | glycine-tRNA ligas | 635 | 28 | 56.0 | 1224 | 2 | T00059 | hypothetical prote |
| 563 | 28 | 56.0 | 721 | 2 | A82941 | receptor like prot | 636 | 28 | 56.0 | 1225 | 2 | A56514 | chromokinesin - ch |
| 564 | 28 | 56.0 | 724 | 2 | A82941 | hypothetical prote | 637 | 28 | 56.0 | 1231 | 2 | AF2220 | hypothetical prote |
| 565 | 28 | 56.0 | 726 | 2 | S22258 | hypothetical prote | 638 | 28 | 56.0 | 1244 | 2 | S73731 | probable lipoprote |
| 566 | 28 | 56.0 | 729 | 2 | T51896 | probable protein k | 639 | 28 | 56.0 | 1253 | 2 | T40302 | hypothetical prote |
| 567 | 28 | 56.0 | 731 | 2 | JC7701 | probable translati | 640 | 28 | 56.0 | 1262 | 2 | T30524 | protein phosphatas |
| 568 | 28 | 56.0 | 732 | 2 | A32626 | ARHGAP9 protein - | 641 | 28 | 56.0 | 1273 | 2 | AP2421 | hypothetical prote |
| 569 | 28 | 56.0 | 738 | 2 | E89552 | Ku antigen 80K cha | 642 | 28 | 56.0 | 1279 | 2 | T13613 | hypothetical prote |
| 570 | 28 | 56.0 | 741 | 2 | B49555 | probable membrane | 643 | 28 | 56.0 | 1297 | 2 | S25714 | son-of-sevenless-2 |
| 571 | 28 | 56.0 | 742 | 2 | T00663 | enhancer of split | 644 | 28 | 56.0 | 1307 | 2 | H84467 | probable retroelem |
| 572 | 28 | 56.0 | 750 | 2 | T10864 | glucosidase I homo | 645 | 28 | 56.0 | 1319 | 2 | T28203 | probable DNA-direc |
| 573 | 28 | 56.0 | 754 | 2 | T06249 | transcription acti | 646 | 28 | 56.0 | 1485 | 2 | S23756 | CFTF protein - Afr |
| 574 | 28 | 56.0 | 769 | 2 | S36657 | protoporphylin IX | 647 | 28 | 56.0 | 1510 | 2 | T33100 | hypothetical prote |
| 575 | 28 | 56.0 | 770 | 2 | B56695 | SWI6 protein - yea | 648 | 28 | 56.0 | 1518 | 2 | T28880 | hypothetical prote |
| 576 | 28 | 56.0 | 775 | 2 | T40647 | transducin-like en | 649 | 28 | 56.0 | 1649 | 2 | T39938 | hypothetical prote |
| 577 | 28 | 56.0 | 778 | 2 | B86218 | ubiquitin carboxyl | 650 | 28 | 56.0 | 1661 | 2 | S64800 | hypothetical prote |
| 578 | 28 | 56.0 | 793 | 1 | S60735 | protein T27G7.20 [| 651 | 28 | 56.0 | 1706 | 2 | I84499 | probable membrane |
| 579 | 28 | 56.0 | 794 | 1 | KXHUF | splicing factor SF | 652 | 28 | 56.0 | 1708 | 2 | A05205 | zinc finger protei |
| 580 | 28 | 56.0 | 797 | 2 | T33098 | fuXin (EC 3.4.21.7 | 653 | 28 | 56.0 | 1735 | 2 | A57607 | hypothetical prote |
| 581 | 28 | 56.0 | 809 | 2 | S64594 | hypothetical prote | 654 | 28 | 56.0 | 1735 | 2 | T23707 | Munc13-1 - rat |
| 582 | 28 | 56.0 | 814 | 2 | T02195 | probable beta-adap | 655 | 28 | 56.0 | 1868 | 2 | T23707 | hypothetical prote |
| 583 | 28 | 56.0 | 818 | 2 | T35872 | hypothetical prote | 656 | 28 | 56.0 | 1879 | 2 | T15962 | hypothetical prote |
| 584 | 28 | 56.0 | 823 | 2 | S04181 | DNA gyrase-like pr | 657 | 28 | 56.0 | 2039 | 2 | T00385 | KIAA0624 protein - |
| 585 | 28 | 56.0 | 823 | 2 | T21943 | parasporal crystal | 658 | 28 | 56.0 | 2039 | 2 | T15347 | ankyrin-related un |
| 586 | 28 | 56.0 | 823 | 2 | T21104 | hypothetical prote | 659 | 28 | 56.0 | 2049 | 2 | T43161 | sodium channel pro |
| 587 | 28 | 56.0 | 825 | 2 | T21944 | hypothetical prote | 660 | 28 | 56.0 | 2140 | 2 | T18543 | probable cell-adhe |
| 588 | 28 | 56.0 | 827 | 2 | A53954 | hypothetical prote | 661 | 28 | 56.0 | 2160 | 2 | T20241 | hypothetical prote |
| 589 | 28 | 56.0 | 832 | 2 | S53396 | Li-cadherin precu | 662 | 28 | 56.0 | 2180 | 2 | A47651 | hypothetical prote |
| 590 | 28 | 56.0 | 832 | 2 | T31878 | Li-cadherin - huma | 663 | 28 | 56.0 | 2368 | 2 | S46005 | ESR1 protein - yea |
| 591 | 28 | 56.0 | 839 | 2 | F64171 | hypothetical prote | 664 | 28 | 56.0 | 2450 | 2 | S71625 | protein-tyrosine-p |
| 592 | 28 | 56.0 | 845 | 2 | T12537 | hypothetical prote | 665 | 28 | 56.0 | 2500 | 2 | G88493 | protein F57B9.2 [i |
| 593 | 28 | 56.0 | 846 | 2 | T13179 | hypothetical prote | 666 | 28 | 56.0 | 2500 | 2 | G71609 | hypothetical prote |
| 594 | 28 | 56.0 | 850 | 2 | B96839 | hypothetical prote | 667 | 28 | 56.0 | 2549 | 2 | A54837 | polyketide synthas |
| 595 | 28 | 56.0 | 851 | 2 | T38648 | hypothetical prote | 668 | 28 | 56.0 | 3125 | 1 | GNVSPP | genome polyprotein |
| 596 | 28 | 56.0 | 852 | 1 | GNLJGA | pol polyprotein - | 669 | 28 | 56.0 | 3140 | 1 | GNVSRA | genome polyprotein |
| 597 | 28 | 56.0 | 852 | 1 | GNLJGB | pol polyprotein - | 670 | 28 | 56.0 | 3140 | 1 | GNVS08 | genome polyprotein |
| 598 | 28 | 56.0 | 852 | 2 | S23358 | pol protein - bovi | 671 | 28 | 56.0 | 3141 | 1 | GNVSPP | genome polyprotein |
| 599 | 28 | 56.0 | 864 | 2 | T02156 | glucosidase homo | 672 | 28 | 56.0 | 3473 | 1 | A46112 | genome polyprotein |
| 600 | 28 | 56.0 | 870 | 2 | C96698 | probable glucosida | 673 | 28 | 56.0 | 3473 | 2 | S27927 | polyprotein - rice |
| 601 | 28 | 56.0 | 880 | 2 | T02245 | hypothetical prote | 674 | 28 | 56.0 | 3839 | 2 | T49799 | related to TOM1 pr |
| 602 | 28 | 56.0 | 880 | 2 | S44833 | F54H12.5 protein - | 675 | 28 | 56.0 | 4351 | 2 | T00252 | MEG1 protein - ra |
| 603 | 28 | 56.0 | 891 | 2 | T21942 | hypothetical prote | 676 | 28 | 56.0 | 4351 | 2 | T41581 | hypothetical coile |
| 604 | 28 | 56.0 | 896 | 2 | F96523 | hypothetical prote | 677 | 28 | 56.0 | 4717 | 2 | T41581 | hypothetical coile |
| 605 | 28 | 56.0 | 908 | 2 | A33280 | sarcoscalmenin precu | 678 | 28 | 56.0 | 5035 | 1 | I46646 | ryanodine receptor |
| 606 | 28 | 56.0 | 926 | 2 | T24923 | hypothetical prote | 679 | 28 | 56.0 | 5170 | 2 | T15348 | hypothetical prote |
| 607 | 28 | 56.0 | 932 | 2 | T33847 | hypothetical prote | 680 | 27.5 | 55.0 | 602 | 2 | S72513 | FOG2 protein - yea |
| 608 | 28 | 56.0 | 935 | 2 | T19011 | hypothetical prote | 681 | 27.5 | 55.0 | 1331 | 2 | T49813 | related to gastric |
| 609 | 28 | 56.0 | 947 | 2 | I49635 | mouse Dhml protein | 682 | 27 | 54.0 | 26 | 2 | S68641 | nicotinic acetylch |
| 610 | 28 | 56.0 | 947 | 2 | T20156 | hypothetical prote | 683 | 27 | 54.0 | 32 | 2 | S55937 | translation initia |
| 611 | 28 | 56.0 | 974 | 2 | T04910 | hypothetical prote | 684 | 27 | 54.0 | 59 | 2 | D41476 | probable antigen 4 |
| 612 | 28 | 56.0 | 976 | 2 | D96714 | hypothetical prote | 685 | 27 | 54.0 | 61 | 1 | N1NJ1B | short neurotoxin 1 |
| 613 | 28 | 56.0 | 1004 | 2 | S51133 | DNA-directed RNA p | 686 | 27 | 54.0 | 61 | 1 | N1NJ1R | short neurotoxin 1 |
| | | | | | transposase Tn452 | | | | | | | | |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|--------|--------------------|-----|----|------|-----|---|--------|--------------------|
| 687 | 27 | 54.0 | 61 | 1 | NINJ1W | short neurotoxin 1 | 760 | 27 | 54.0 | 212 | 1 | W4WLRB | E4 protein - cotto |
| 688 | 27 | 54.0 | 61 | 1 | NINJ2C | short neurotoxin 2 | 761 | 27 | 54.0 | 214 | 2 | S48947 | hypothetical prote |
| 689 | 27 | 54.0 | 61 | 1 | NIRI1 | short neurotoxin 1 | 762 | 27 | 54.0 | 215 | 1 | SDADMS | hexon-associated p |
| 690 | 27 | 54.0 | 61 | 1 | NIRI2 | short neurotoxin 1 | 763 | 27 | 54.0 | 215 | 1 | T19056 | hypothetical prote |
| 691 | 27 | 54.0 | 62 | 2 | S39327 | short neurotoxin 1 | 764 | 27 | 54.0 | 222 | 2 | S22517 | S-allele-associate |
| 692 | 27 | 54.0 | 64 | 2 | S36969 | hypothetical prote | 765 | 27 | 54.0 | 222 | 2 | S51595 | mycinamicin III O- |
| 693 | 27 | 54.0 | 66 | 2 | T06697 | hypothetical prote | 766 | 27 | 54.0 | 226 | 2 | G95278 | hypothetical prote |
| 694 | 27 | 54.0 | 67 | 2 | PHI081 | ig light chain v r | 767 | 27 | 54.0 | 227 | 1 | RHXLIT | thyroliberin precu |
| 695 | 27 | 54.0 | 69 | 2 | PHI080 | ig light chain v r | 768 | 27 | 54.0 | 227 | 2 | AB2008 | hypothetical prote |
| 696 | 27 | 54.0 | 73 | 2 | D64078 | slyX protein homol | 769 | 27 | 54.0 | 234 | 2 | H82730 | ribonuclease HII X |
| 697 | 27 | 54.0 | 82 | 2 | JCS892 | cobrotoxin b - Chi | 770 | 27 | 54.0 | 235 | 2 | S76733 | hypothetical prote |
| 698 | 27 | 54.0 | 83 | 1 | NINJ1F | short neurotoxin 1 | 771 | 27 | 54.0 | 235 | 2 | B42384 | hypothetical prote |
| 699 | 27 | 54.0 | 87 | 2 | E59071 | hypothetical prote | 772 | 27 | 54.0 | 236 | 2 | A99938 | hypothetical lipop |
| 700 | 27 | 54.0 | 91 | 2 | S17638 | ig kappa chain v r | 773 | 27 | 54.0 | 240 | 2 | A46587 | extracellular hemo |
| 701 | 27 | 54.0 | 105 | 2 | PHO087 | ig kappa chain v r | 774 | 27 | 54.0 | 241 | 2 | T37790 | probable 30s ribos |
| 702 | 27 | 54.0 | 106 | 1 | VKLJG3 | trans-regulatory s | 775 | 27 | 54.0 | 243 | 2 | S75330 | hypothetical prote |
| 703 | 27 | 54.0 | 108 | 1 | VKLJ52 | trans-regulatory s | 776 | 27 | 54.0 | 244 | 2 | A22722 | proliferin-related |
| 704 | 27 | 54.0 | 108 | 2 | T34436 | hypothetical prote | 777 | 27 | 54.0 | 244 | 2 | T12458 | hypothetical prote |
| 705 | 27 | 54.0 | 108 | 2 | C97328 | probable transcrip | 778 | 27 | 54.0 | 245 | 2 | T40971 | 20s proteasome com |
| 706 | 27 | 54.0 | 111 | 2 | E53285 | ig kappa chain v a | 779 | 27 | 54.0 | 248 | 2 | S26198 | H+-transporting tw |
| 707 | 27 | 54.0 | 112 | 2 | G02056 | 13kD differentiat | 780 | 27 | 54.0 | 250 | 2 | T05996 | hypothetical prote |
| 708 | 27 | 54.0 | 114 | 2 | D72665 | hypothetical prote | 781 | 27 | 54.0 | 250 | 2 | T29734 | hemolymph 30K prot |
| 709 | 27 | 54.0 | 117 | 2 | H86316 | protein T10022.17 | 782 | 27 | 54.0 | 251 | 2 | S01047 | hypothetical prote |
| 710 | 27 | 54.0 | 118 | 2 | AH2666 | hypothetical prote | 783 | 27 | 54.0 | 251 | 2 | B69142 | hypothetical prote |
| 711 | 27 | 54.0 | 118 | 2 | F37448 | hypothetical prote | 784 | 27 | 54.0 | 252 | 2 | H97287 | rRNA methylase, YA |
| 712 | 27 | 54.0 | 120 | 2 | AH1329 | cell-division prot | 785 | 27 | 54.0 | 253 | 2 | T16918 | hypothetical prote |
| 713 | 27 | 54.0 | 120 | 2 | AH1700 | cell-division prot | 786 | 27 | 54.0 | 254 | 2 | T51562 | hypothetical prote |
| 714 | 27 | 54.0 | 121 | 2 | T17897 | hypothetical prote | 787 | 27 | 54.0 | 259 | 2 | S55936 | translation initia |
| 715 | 27 | 54.0 | 122 | 2 | S60262 | corticotensin - ra | 788 | 27 | 54.0 | 259 | 2 | A83301 | hypothetical prote |
| 716 | 27 | 54.0 | 122 | 2 | T32932 | hypothetical prote | 789 | 27 | 54.0 | 260 | 2 | T37277 | chloride channel p |
| 717 | 27 | 54.0 | 125 | 2 | S40315 | ig kappa chain - h | 790 | 27 | 54.0 | 263 | 2 | AB0812 | probable oxidoredu |
| 718 | 27 | 54.0 | 128 | 2 | S77068 | ycf35 protein - sy | 791 | 27 | 54.0 | 265 | 2 | T52313 | photosystem II pro |
| 719 | 27 | 54.0 | 128 | 2 | T32947 | hypothetical prote | 792 | 27 | 54.0 | 265 | 2 | C83685 | hypothetical prote |
| 720 | 27 | 54.0 | 129 | 2 | S40317 | ig kappa chain - h | 793 | 27 | 54.0 | 267 | 2 | T52381 | zinc finger protei |
| 721 | 27 | 54.0 | 130 | 2 | E87020 | conserved hypotbet | 794 | 27 | 54.0 | 267 | 2 | E85786 | hypothetical prote |
| 722 | 27 | 54.0 | 131 | 2 | S14390 | tap2 protein - gar | 795 | 27 | 54.0 | 267 | 2 | T23516 | hypothetical prote |
| 723 | 27 | 54.0 | 139 | 2 | B69953 | hypothetical prote | 796 | 27 | 54.0 | 267 | 2 | A97762 | hypothetical prote |
| 724 | 27 | 54.0 | 142 | 1 | BVECTR | tolR protein - Esc | 797 | 27 | 54.0 | 270 | 2 | AF2159 | hypothetical prote |
| 725 | 27 | 54.0 | 142 | 2 | E85576 | probable inner mem | 798 | 27 | 54.0 | 270 | 2 | F86177 | hypothetical prote |
| 726 | 27 | 54.0 | 142 | 2 | E90725 | probable inner mem | 799 | 27 | 54.0 | 273 | 2 | AD1855 | ATP-binding protei |
| 727 | 27 | 54.0 | 152 | 2 | S29752 | ubiquitin-activati | 800 | 27 | 54.0 | 273 | 2 | AB2049 | hypothetical prote |
| 728 | 27 | 54.0 | 153 | 2 | C36813 | nodulation protein | 801 | 27 | 54.0 | 274 | 2 | JC8063 | heart-restricted 1 |
| 729 | 27 | 54.0 | 156 | 2 | F88175 | protein T24H7.3 [i | 802 | 27 | 54.0 | 275 | 2 | S75994 | hypothetical prote |
| 730 | 27 | 54.0 | 156 | 2 | C84596 | hypothetical prote | 803 | 27 | 54.0 | 277 | 1 | S68421 | endopeptidase Clp |
| 731 | 27 | 54.0 | 157 | 2 | S28012 | outB protein - Brw | 804 | 27 | 54.0 | 277 | 2 | T60122 | rsu-1 homolog - hu |
| 732 | 27 | 54.0 | 158 | 2 | T33920 | hypothetical prote | 805 | 27 | 54.0 | 277 | 2 | S25770 | RSP-1 protein - mo |
| 733 | 27 | 54.0 | 160 | 2 | T47185 | hypothetical prote | 806 | 27 | 54.0 | 280 | 2 | T19363 | hypothetical prote |
| 734 | 27 | 54.0 | 160 | 2 | AG3311 | monamine oxidase | 807 | 27 | 54.0 | 283 | 2 | AE2081 | hypothetical prote |
| 735 | 27 | 54.0 | 161 | 2 | D86418 | unknown protein, 6 | 808 | 27 | 54.0 | 285 | 2 | E75507 | anti-sigma factor |
| 736 | 27 | 54.0 | 161 | 2 | A97671 | hypothetical prote | 809 | 27 | 54.0 | 285 | 2 | D69975 | F15K9.19 protein - |
| 737 | 27 | 54.0 | 166 | 2 | E90434 | conserved hypotbet | 810 | 27 | 54.0 | 286 | 2 | D86163 | hypothetical prote |
| 738 | 27 | 54.0 | 167 | 2 | C97542 | hypothetical prote | 811 | 27 | 54.0 | 289 | 2 | AE2006 | probable major int |
| 739 | 27 | 54.0 | 168 | 2 | H85071 | hypothetical prote | 812 | 27 | 54.0 | 289 | 2 | A12179 | hypothetical prote |
| 740 | 27 | 54.0 | 169 | 1 | KTHOB | choriogonadotropin | 813 | 27 | 54.0 | 301 | 2 | AC1989 | hypothetical prote |
| 741 | 27 | 54.0 | 171 | 2 | T51674 | myb-related transc | 814 | 27 | 54.0 | 301 | 2 | T51435 | hypothetical prote |
| 742 | 27 | 54.0 | 172 | 2 | ACL820 | photosystem I chai | 815 | 27 | 54.0 | 302 | 2 | E97323 | probable epimerase |
| 743 | 27 | 54.0 | 173 | 1 | CYL2AA | alpha-crystallin c | 816 | 27 | 54.0 | 303 | 2 | A86443 | hypothetical prote |
| 744 | 27 | 54.0 | 178 | 2 | D72064 | conserved hypotbet | 817 | 27 | 54.0 | 303 | 2 | H70716 | hypothetical prote |
| 745 | 27 | 54.0 | 178 | 2 | E86560 | CHUPS euo protein | 818 | 27 | 54.0 | 305 | 2 | T19926 | hypothetical prote |
| 746 | 27 | 54.0 | 181 | 2 | A70639 | hypothetical prote | 819 | 27 | 54.0 | 307 | 1 | GSFF3 | salivary glue prot |
| 747 | 27 | 54.0 | 181 | 2 | S77219 | hypothetical prote | 820 | 27 | 54.0 | 310 | 2 | T47695 | hypothetical prote |
| 748 | 27 | 54.0 | 185 | 2 | AD1183 | hypothetical prote | 821 | 27 | 54.0 | 311 | 2 | T40886 | hypothetical prote |
| 749 | 27 | 54.0 | 186 | 2 | AE1540 | hypothetical prote | 822 | 27 | 54.0 | 311 | 2 | E96714 | probable DNA-bind |
| 750 | 27 | 54.0 | 195 | 2 | S76319 | hypothetical prote | 823 | 27 | 54.0 | 312 | 2 | H89872 | hypothetical prote |
| 751 | 27 | 54.0 | 198 | 2 | F71229 | hypothetical prote | 824 | 27 | 54.0 | 312 | 2 | E70376 | exopolysphatase |
| 752 | 27 | 54.0 | 200 | 2 | S55609 | hypothetical prote | 825 | 27 | 54.0 | 315 | 2 | T46993 | hypothetical prote |
| 753 | 27 | 54.0 | 202 | 2 | G82751 | hypothetical prote | 826 | 27 | 54.0 | 316 | 2 | T00769 | hypothetical prote |
| 754 | 27 | 54.0 | 203 | 2 | D84221 | hypothetical prote | 827 | 27 | 54.0 | 319 | 2 | B83370 | conserved hypotbet |
| 755 | 27 | 54.0 | 204 | 2 | DB1793 | hypothetical prote | 828 | 27 | 54.0 | 324 | 2 | S60118 | RING finger protei |
| 756 | 27 | 54.0 | 204 | 2 | E81216 | conserved hypotbet | 829 | 27 | 54.0 | 324 | 2 | F84913 | probable FCA-relat |
| 757 | 27 | 54.0 | 208 | 2 | B70208 | conserved hypotbet | 830 | 27 | 54.0 | 325 | 2 | D97375 | adenosine deaminas |
| 758 | 27 | 54.0 | 208 | 2 | T36390 | hypothetical prote | 831 | 27 | 54.0 | 325 | 2 | AB2593 | adenosine deaminas |
| 759 | 27 | 54.0 | 211 | 2 | G01654 | spp-24 precursor - | 832 | 27 | 54.0 | 327 | 2 | A81839 | probable periplasm |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|--------|--------------------|-----|----|------|-----|---|--------|--------------------|
| 833 | 27 | 54.0 | 327 | 2 | D81103 | hypothetical prote | 906 | 27 | 54.0 | 446 | 2 | F71069 | hypothetical prote |
| 834 | 27 | 54.0 | 327 | 2 | AH2608 | transcription regu | 907 | 27 | 54.0 | 446 | 2 | I59354 | orphan nuclear rec |
| 835 | 27 | 54.0 | 327 | 2 | G97390 | araC family trans | 908 | 27 | 54.0 | 448 | 2 | D81740 | conserved hypothet |
| 836 | 27 | 54.0 | 328 | 2 | E88866 | protein P52G2.1a [| 909 | 27 | 54.0 | 448 | 2 | T44869 | probable membrane |
| 837 | 27 | 54.0 | 331 | 2 | C87385 | conserved hypothet | 910 | 27 | 54.0 | 450 | 2 | I48756 | gene Sbx protein - |
| 838 | 27 | 54.0 | 334 | 2 | S44299 | hypothetical prote | 911 | 27 | 54.0 | 454 | 2 | S17450 | probable ligand-bi |
| 839 | 27 | 54.0 | 337 | 2 | S31131 | hypothetical prote | 912 | 27 | 54.0 | 456 | 2 | C86624 | hypothetical prote |
| 840 | 27 | 54.0 | 340 | 2 | F88545 | protein F59B2.11 [| 913 | 27 | 54.0 | 456 | 2 | H72000 | hypothetical prote |
| 841 | 27 | 54.0 | 341 | 2 | A95939 | probable spermidin | 914 | 27 | 54.0 | 457 | 2 | A36329 | hypothetical prote |
| 842 | 27 | 54.0 | 340 | 1 | LUPY1 | annexin I type 1 - | 915 | 27 | 54.0 | 458 | 2 | H87624 | peptidase M23/M37 |
| 843 | 27 | 54.0 | 344 | 2 | C84015 | transcription regu | 916 | 27 | 54.0 | 461 | 2 | C84539 | hypothetical prote |
| 844 | 27 | 54.0 | 344 | 2 | T22515 | hypothetical prote | 917 | 27 | 54.0 | 462 | 1 | A39356 | gene 61 protein - |
| 845 | 27 | 54.0 | 345 | 2 | T37685 | probable vanadate | 918 | 27 | 54.0 | 467 | 1 | WZBE61 | 3-oxoacyl-lacyl-ca |
| 846 | 27 | 54.0 | 346 | 2 | T32273 | hypothetical prote | 919 | 27 | 54.0 | 468 | 2 | T32586 | hypothetical prote |
| 847 | 27 | 54.0 | 348 | 2 | C96511 | probable heat choc | 920 | 27 | 54.0 | 471 | 2 | A31103 | membrane glycoprot |
| 848 | 27 | 54.0 | 348 | 2 | D72274 | hypothetical prote | 921 | 27 | 54.0 | 471 | 2 | D95940 | probable urate oxi |
| 849 | 27 | 54.0 | 353 | 2 | F37831 | phenol 2-monooxyge | 922 | 27 | 54.0 | 475 | 2 | A30672 | hypothetical prote |
| 850 | 27 | 54.0 | 353 | 2 | F75581 | hypothetical prote | 923 | 27 | 54.0 | 475 | 2 | E85522 | hypothetical prote |
| 851 | 27 | 54.0 | 354 | 2 | G86251 | protein F25C20.6 [| 924 | 27 | 54.0 | 475 | 2 | C64757 | probable iron-sulf |
| 852 | 27 | 54.0 | 354 | 2 | T48321 | hypothetical prote | 925 | 27 | 54.0 | 475 | 2 | S54511 | hypothetical prote |
| 853 | 27 | 54.0 | 355 | 2 | E83741 | hypothetical prote | 926 | 27 | 54.0 | 475 | 2 | A71110 | hypothetical prote |
| 854 | 27 | 54.0 | 355 | 2 | T29251 | hypothetical prote | 927 | 27 | 54.0 | 480 | 2 | D75050 | hypothetical prote |
| 855 | 27 | 54.0 | 357 | 2 | A98147 | hypothetical prote | 928 | 27 | 54.0 | 480 | 2 | JC7812 | BC16 homologous zi |
| 856 | 27 | 54.0 | 361 | 2 | S63642 | hypothetical COI i | 929 | 27 | 54.0 | 481 | 2 | T27975 | hypothetical prote |
| 857 | 27 | 54.0 | 364 | 2 | T45253 | probable antiporte | 930 | 27 | 54.0 | 482 | 2 | JC5092 | E-selectin - pig |
| 858 | 27 | 54.0 | 369 | 2 | T04917 | hypothetical prote | 931 | 27 | 54.0 | 483 | 2 | T19720 | hypothetical prote |
| 859 | 27 | 54.0 | 371 | 2 | E86578 | flagellar motor sw | 932 | 27 | 54.0 | 490 | 2 | T21365 | hypothetical prote |
| 860 | 27 | 54.0 | 371 | 2 | H72045 | flagellar motor sw | 933 | 27 | 54.0 | 491 | 2 | S51435 | hypothetical prote |
| 861 | 27 | 54.0 | 374 | 2 | T22356 | hypothetical prote | 934 | 27 | 54.0 | 495 | 1 | S31223 | transcription fact |
| 862 | 27 | 54.0 | 379 | 2 | S31719 | proline-rich prote | 935 | 27 | 54.0 | 500 | 2 | B43577 | perfringolysin O p |
| 863 | 27 | 54.0 | 382 | 1 | RGFFAS | GTP-binding regula | 936 | 27 | 54.0 | 501 | 2 | A37858 | alveolysin - Bacil |
| 864 | 27 | 54.0 | 382 | 1 | S22652 | transcription fact | 937 | 27 | 54.0 | 501 | 2 | S34825 | uvr2 protein - Neu |
| 865 | 27 | 54.0 | 384 | 2 | H90496 | iron-sulfur protei | 938 | 27 | 54.0 | 503 | 2 | S36549 | L1 protein - human |
| 866 | 27 | 54.0 | 385 | 1 | RGPFAL | GTP-binding regula | 939 | 27 | 54.0 | 504 | 2 | S52048 | deoxyribodipyrimid |
| 867 | 27 | 54.0 | 388 | 1 | SYEC5B | succinate-CoA liga | 940 | 27 | 54.0 | 506 | 2 | F96772 | probable exonuclea |
| 868 | 27 | 54.0 | 388 | 2 | AF0591 | succinyl-CoA synth | 941 | 27 | 54.0 | 508 | 2 | S36508 | L1 protein - human |
| 869 | 27 | 54.0 | 388 | 2 | A90723 | succinyl-CoA synth | 942 | 27 | 54.0 | 508 | 2 | G84133 | Rieske [2Fe-2S] ir |
| 870 | 27 | 54.0 | 388 | 2 | H85573 | succinyl-CoA synth | 943 | 27 | 54.0 | 508 | 2 | AG2206 | serine/threonine k |
| 871 | 27 | 54.0 | 388 | 2 | T06035 | hypothetical prote | 944 | 27 | 54.0 | 509 | 2 | C70624 | probable two compo |
| 872 | 27 | 54.0 | 389 | 2 | G84245 | NADH dehydrogenase | 945 | 27 | 54.0 | 512 | 2 | A05196 | hypothetical prote |
| 873 | 27 | 54.0 | 392 | 2 | T24666 | hypothetical prote | 946 | 27 | 54.0 | 518 | 2 | T29589 | hypothetical prote |
| 874 | 27 | 54.0 | 393 | 2 | AG1110 | aminotransferase h | 947 | 27 | 54.0 | 519 | 2 | T02600 | hypothetical prote |
| 875 | 27 | 54.0 | 393 | 2 | AC1472 | aminotransferase h | 948 | 27 | 54.0 | 520 | 1 | S57337 | trichodiene oxygen |
| 876 | 27 | 54.0 | 394 | 2 | A71083 | hypothetical prote | 949 | 27 | 54.0 | 524 | 2 | F84511 | hypothetical prote |
| 877 | 27 | 54.0 | 396 | 2 | T11981 | hypothetical prote | 950 | 27 | 54.0 | 527 | 2 | E69351 | phosphoglycerate d |
| 878 | 27 | 54.0 | 397 | 2 | B70763 | probable membrane | 951 | 27 | 54.0 | 529 | 2 | G84295 | hypothetical prote |
| 879 | 27 | 54.0 | 398 | 2 | F69863 | probable transamin | 952 | 27 | 54.0 | 531 | 2 | S09859 | hypothetical prote |
| 880 | 27 | 54.0 | 402 | 1 | BOHUS | sex steroid-bindin | 953 | 27 | 54.0 | 534 | 2 | S77239 | ABC-type transport |
| 881 | 27 | 54.0 | 406 | 2 | A56637 | calreticulin homol | 954 | 27 | 54.0 | 536 | 1 | F0MVME | gag polyprotein - |
| 882 | 27 | 54.0 | 407 | 2 | AG2150 | serine proteinase | 955 | 27 | 54.0 | 539 | 1 | A47610 | cell fusion glycop |
| 883 | 27 | 54.0 | 408 | 2 | T13387 | hypothetical prote | 956 | 27 | 54.0 | 539 | 1 | VGNZH3 | zona pellucida gly |
| 884 | 27 | 54.0 | 410 | 2 | G90362 | hypothetical prote | 957 | 27 | 54.0 | 540 | 2 | S70403 | serine/threonine k |
| 885 | 27 | 54.0 | 412 | 2 | A70839 | probable membrane | 958 | 27 | 54.0 | 564 | 2 | AF2351 | hypothetical prote |
| 886 | 27 | 54.0 | 413 | 2 | T26572 | hypothetical prote | 959 | 27 | 54.0 | 568 | 2 | B86364 | probable membrane |
| 887 | 27 | 54.0 | 421 | 2 | A70962 | hypothetical prote | 960 | 27 | 54.0 | 569 | 2 | AG0998 | streptolysin O pre |
| 888 | 27 | 54.0 | 422 | 2 | F70018 | multiple sugar-bin | 961 | 27 | 54.0 | 571 | 2 | A43507 | hypothetical prote |
| 889 | 27 | 54.0 | 425 | 1 | JH0710 | transcription fact | 962 | 27 | 54.0 | 572 | 2 | B96588 | hypothetical prote |
| 890 | 27 | 54.0 | 425 | 2 | A23703 | ribulose-bisphosph | 963 | 27 | 54.0 | 578 | 1 | BVB5D1 | GCB1 protein - yea |
| 891 | 27 | 54.0 | 425 | 2 | A84849 | probable RING zinc | 964 | 27 | 54.0 | 581 | 2 | T41210 | hypothetical prote |
| 892 | 27 | 54.0 | 426 | 2 | T40610 | probable clathrin | 965 | 27 | 54.0 | 582 | 1 | BNRT3S | myelin-associated |
| 893 | 27 | 54.0 | 426 | 2 | A10287 | conserved hypothet | 966 | 27 | 54.0 | 582 | 2 | T34538 | hypothetical prote |
| 894 | 27 | 54.0 | 426 | 2 | E96581 | hypothetical prote | 967 | 27 | 54.0 | 590 | 2 | C86465 | probable inositol |
| 895 | 27 | 54.0 | 427 | 2 | C87232 | probable integral | 968 | 27 | 54.0 | 590 | 2 | A26638 | homeotic protein D |
| 896 | 27 | 54.0 | 428 | 1 | E38180 | modulation protein | 969 | 27 | 54.0 | 592 | 2 | B83231 | probable short-cha |
| 897 | 27 | 54.0 | 432 | 2 | T23561 | hypothetical prote | 970 | 27 | 54.0 | 593 | 1 | S22984 | catechol oxidase (|
| 898 | 27 | 54.0 | 436 | 2 | S46154 | hypothetical prote | 971 | 27 | 54.0 | 595 | 2 | H69345 | translation initia |
| 899 | 27 | 54.0 | 437 | 2 | S39551 | ribulose-bisphosph | 972 | 27 | 54.0 | 601 | 2 | AF2452 | two-component resp |
| 900 | 27 | 54.0 | 441 | 2 | T10815 | ribulose-bisphosph | 973 | 27 | 54.0 | 603 | 2 | H75272 | probable nucleic a |
| 901 | 27 | 54.0 | 442 | 2 | S19712 | ubiquitin-protein | 974 | 27 | 54.0 | 605 | 2 | G69060 | threonine-tRNA lig |
| 902 | 27 | 54.0 | 442 | 2 | F69042 | signal recognition | 975 | 27 | 54.0 | 610 | 2 | T16761 | hypothetical prote |
| 903 | 27 | 54.0 | 443 | 1 | S29334 | transcription fact | 976 | 27 | 54.0 | 610 | 2 | A28798 | myosin-light-chain |
| 904 | 27 | 54.0 | 445 | 1 | A49447 | transcription fact | 977 | 27 | 54.0 | 618 | 2 | S68450 | apoptosis inhibito |
| 905 | 27 | 54.0 | 445 | 1 | S31224 | transcription fact | 978 | 27 | 54.0 | 619 | 2 | E86466 | protein F23M19.10 |

979 27 54.0 619 2 T03143 R-transactivator p
980 27 54.0 620 2 T52389 hypothetical prote
981 27 54.0 622 2 T51223 hypothetical prote
982 27 54.0 626 1 A61084 myelin-associated
983 27 54.0 626 1 BNR73 myelin-associated
984 27 54.0 627 2 T02610 probable YME1 Atp-
985 27 54.0 628 2 G71565 probable signal pe
986 27 54.0 629 2 A81525 probable peptidogl
987 27 54.0 630 2 J00271 voltage-sensitive
988 27 54.0 630 2 H89056 protein K09H11.4 f
989 27 54.0 630 2 T27991 hypothetical prote
990 27 54.0 630 2 A39344 tumor-associated m
991 27 54.0 631 2 A52257 episialin - mouse
992 27 54.0 633 2 B83478 probable two-compo
993 27 54.0 637 2 B33785 myelin-associated
994 27 54.0 640 2 T25367 hypothetical prote
995 27 54.0 647 2 F95189 threonyl-tRNA synt
996 27 54.0 655 2 T00768 polyadenylate-bind
997 27 54.0 656 1 Q0BET2 UL25 protein - hum
998 27 54.0 657 2 C97113 serine/threonine p
999 27 54.0 657 2 S63459 methylentetrahedr
1000 27 54.0 660 2 G98055 threonine-tRNA lig

ALIGNMENTS

RESULT 1
S19971
Ig kappa chain V region (CD4 mAb clone M-T310 and others) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S19971; S19973
R:Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: S19963
A:Accession: S19971
A:Molecule type: mRNA
A:Residues: 1-112 <WEI>
A:Cross-references: UNIPARC:UPI0000116030; EMBL:X65091; NID:g52288; PIDN:CAA46219.1; PID
A:Experimental source: clone M-T310
A:Accession: S19973
A:Molecule type: mRNA
A:Residues: 1-112 <WEW>
A:Cross-references: UNIPARC:UPI0000116030; EMBL:X65092; NID:g52292; PIDN:CAA46220.1; PID
A:Experimental source: M-T404
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMW>

Query Match 90.0%; Score 45; DB 2; Length 112;
Best Local Similarity 88.9%; Pred. No. 0.17;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQSNEPDPT 9
||||:|||||
Db 93 QQSSEDPPT 101

RESULT 2
PH1226
Ig kappa chain precursor V region (M-T310) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
C:Accession: PH1226
R:Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; Lenz
Gene 121, 271-278, 1992
A:Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and on
A:Reference number: PH1224; MUID:93077041; PMID:1446824
A:Accession: PH1226
A:Molecule type: mRNA
A:Residues: 1-131 <WEI>

A:Cross-references: UNIPARC:UPI00001153EE; GB:S50265; NID:g260765; PIDN:AAB24320.1; PID:
A>Note: this mouse sequence was hybridized and fused with a human constant region gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-131/Product: Ig light chain V region #status predicted <MAT>
F:36-114/Domain: immunoglobulin homology <IMW>

Query Match 90.0%; Score 45; DB 2; Length 131;
Best Local Similarity 88.9%; Pred. No. 0.2;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQSNEPDPT 9
||||:|||||
Db 113 QQSSEDPPT 121

RESULT 3
C38601
Ig kappa chain V region (2B5) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
C:Accession: C38601
R:Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same antigen
A:Reference number: A38601; MUID:91115823; PMID:1703527
A:Accession: C38601
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-65 <GOS>
A:Cross-references: UNIPARC:UPI0000115177; GB:M57980; NID:g196406; PIDN:AAA63361.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 82.0%; Score 41; DB 2; Length 65;
Best Local Similarity 88.9%; Pred. No. 0.55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSNEPDPT 9
||||:|||||
Db 46 QQSNEDPRT 54

RESULT 4
B49442
Ig light chain V region (50.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: B49442
R:Stura, E.A.; Stanfield, R.L.; Fieser, G.G.; Silver, S.; Roguska, M.; Hincapie, L.M.; S
Proteins 14, 499-508, 1992
A:Title: Crystallization, sequence, and preliminary crystallographic data for an antipep
A:Reference number: A49442; MUID:93066166; PMID:1438187
A:Accession: B49442
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-96 <STU>
A:Cross-references: UNIPARC:UPI0000176D6E
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:8-86/Domain: immunoglobulin homology <IMW>

Query Match 80.0%; Score 40; DB 2; Length 96;
Best Local Similarity 88.9%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSNEPDPT 9
||||:|||||
Db 85 QQSNEDPPT 93

RESULT 5

R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
A;Accession: B01937
A;Molecule type: protein
A;Residues: 1-111 <WEI>
A;Cross-references: UNIPROT:P01666; UNIPARC:UPI000002A010
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1:1:1:1 tetramers.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-94/Domain: immunoglobulin homology <IMM>
F;23-92/Disulfide bonds: #status predicted

Query Match 80.0%; Score 40; DB 1; Length 111;
Best Local Similarity 88.9%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSNEPPT 9
Db 93 QQSNEPPT 101
|||||||
|

RESULT 8
KWMSCL
Ig kappa chain V region (CBPC 101) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 09-Jul-2004
C;Accession: A01936
R;McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A;Title: Mechanisms of antibody diversity: multiple genes encode structurally related murine kappa chains.
A;Reference number: A93822; MUID:79012520; PMID:95744
A;Accession: A01936
A;Molecule type: protein
A;Residues: 1-111 <MCK>
A;Cross-references: UNIPROT:P01664; UNIPARC:UPI000002A0PF
C;Comment: This chain was isolated from a myeloma protein.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1:1:1:1 tetramers.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;15-94/Domain: immunoglobulin homology <IMM>
F;23-92/Disulfide bonds: #status predicted

Query Match 80.0%; Score 40; DB 1; Length 111;
Best Local Similarity 88.9%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSNEPPT 9
Db 93 QQSNEPPT 101
|||||||
|

RESULT 9
S09966
Ig kappa chain V-J region (1E10) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C;Accession: S09966
R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Eur. J. Immunol. 20, 771-777, 1990
A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies.
A;Reference number: S09955; MUID:90269328; PMID:2347362
A;Accession: S09966
A;Molecule type: mRNA
A;Residues: 1-111 <REI>
A;Cross-references: UNIPARC:UPI0000115865; EMBL:X51854; NID:G55397; PIDN:CAA36147.1; PFI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-94/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 40; DB 2; Length 111;
Best Local Similarity 88.9%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSNEPDPT 9
Db 93 QQSNEPDPT 101

RESULT 10
KVM543
Ig kappa chain V region (VM201) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C:Accession: A33936
R:Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 86, 4664-4668, 1989
A:Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin gene
A:Reference number: A33936; MUID:89282831; PMID:2471975
A:Accession: A33936
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-111 <ME>
A:Cross-references: UNIPARC:UPI00001148B0; GB:J04575; NID:G623194; PIDN:AAA60448.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-94/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 40; DB 2; Length 111;
Best Local Similarity 88.9%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSNEPDPT 9
Db 93 QQSNEPDPT 101

RESULT 11
S26343
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26343
R:Stark, S.B.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26343
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <STA>
A:Cross-references: UNIPARC:UPI0000115F8A; EMBL:X59207; NID:G52334; PIDN:CAA41917.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-93/Domain: immunoglobulin homology <IMM>

Query Match 78.0%; Score 39; DB 2; Length 107;
Best Local Similarity 88.9%; Pred. No. 2.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSNEPDPT 9
Db 92 QQSNEPDPT 100

RESULT 12
KVM508
Ig kappa chain V region (PC6308) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: C01937; A01937
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978

Query Match 78.0%; Score 39; DB 1; Length 111;
Best Local Similarity 88.9%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSNEPDPT 9
Db 93 QQSNEPDPT 101

RESULT 13
KVM543
Ig kappa chain V region (PC7043) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C:Accession: A01937; S42187; S42194; S42190; S42189; S42188; S42191; S42192
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152; PMID:103003
A:Accession: A01937
A:Molecule type: protein
A:Residues: 1-111 <WEI>
A:Cross-references: UNIPROT:P01665; UNIPARC:UPI000002A100
R:Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec
A:Reference number: S42176; MUID:94009207; PMID:7691608
A:Accession: S42187
A:Molecule type: DNA
A:Residues: 10-99 <MOJ>
A:Cross-references: UNIPARC:UPI000011655C; EMBL:Z25444; NID:G407832; PIDN:CAA80931.1; PI
A:Note: V-kappa-2IE; anti-collagen
A:Accession: S42194
A:Molecule type: DNA
A:Residues: 12-99 <MOV>
A:Cross-references: UNIPARC:UPI000011655E; EMBL:Z25458; NID:G407844; PIDN:CAA80945.1; PI
A:Note: V-kappa-2IE; anti-collagen
A:Accession: S42190
A:Molecule type: DNA
A:Residues: 13-99 <MOF>
A:Cross-references: UNIPARC:UPI0000116562; EMBL:Z25450; NID:G407838; PIDN:CAA80937.1; PI
A:Note: V-kappa-2IE; anti-collagen
A:Accession: S42189
A:Molecule type: DNA
A:Residues: 15-99 <MOA>
A:Cross-references: UNIPARC:UPI0000116560; EMBL:Z25448; NID:G407836; PIDN:CAA80935.1; PI
A:Note: V-kappa-2IE; anti-collagen
A:Accession: S42188
A:Molecule type: DNA
A:Residues: 12-99 <MOZ>
A:Cross-references: UNIPARC:UPI000011655E; EMBL:Z25446; NID:G407834; PIDN:CAA80933.1; PI
A:Note: V-kappa-2IE; anti-collagen
A:Accession: S42191
A:Molecule type: DNA
A:Residues: 10-99 <MOY>
A:Cross-references: UNIPARC:UPI000011655C; EMBL:Z25452; NID:G407840; PIDN:CAA80939.1; PI
A:Note: V-kappa-2IE; anti-collagen
A:Accession: S42192
A:Molecule type: DNA
A:Residues: 10-99 <MOO>

A:Cross-references: UNIPARC:UPI000011655C; EMBL:225454; NID:g407842; PIDN:CAA80941.1; PI
A:Note: V-kappa-21E; anti-collagen
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger multimers.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 78.0%; Score 39; DB 1; Length 111;
Best Local Similarity 88.9%; Pred. No. 2.4; Mismatches 0; Indels 1; Gaps 0;
Matches 8; Conservative 0

QY 1 QQSNEPPT 9
|||||
DB 93 QQSNEPPT 101

RESULT 14
KWSM69
Ig kappa chain V region (PC7769) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: E01937; A01937
R:Wiegert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152; PMID:103003
A:Accession: E01937
A:Molecule type: protein
A:Residues: 1-111 <WEI>
A:Cross-references: UNIPROT:P01669; UNIPARC:UPI000002A104
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger multimers.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 78.0%; Score 39; DB 1; Length 111;
Best Local Similarity 88.9%; Pred. No. 2.4; Mismatches 0; Indels 1; Gaps 0;
Matches 8; Conservative 0

QY 1 QQSNEPPT 9
|||||
DB 93 QQSNEPPT 101

RESULT 15
S42193
Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 07-Oct-1994 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C:Accession: S42193
R:Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with speed of cloning.
A:Reference number: S42176; MUID:94009207; PMID:7691608
A:Accession: S42193
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-81 <MOJ>
A:Cross-references: UNIPARC:UPI0000116566; EMBL:225456; NID:g407846; PIDN:CAA80943.1; PI
A:Note: the authors translated the codon GTT for residue 36 as Ala
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 76.0%; Score 38; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 2.6; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0

QY 1 QQSNEPPT 7
|||||

Db 75 QQSNEPPT 81

RESULT 16
D45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 109) - mouse (C57BL/6J)
C:Species: Mus musculus (house mouse)
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: D45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasci, J.
J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on haemagglutinin of influenza A virus.
A:Reference number: A45722; MUID:93100833; PMID:7677958
A:Accession: D45722
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-111 <SIM>
A:Cross-references: UNIPARC:UPI0000176B43
A:Note: sequence extracted from NCBI backbone (NCBI:120592)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 76.0%; Score 38; DB 2; Length 111;
Best Local Similarity 77.8%; Pred. No. 3.7; Mismatches 1; Indels 0; Gaps 0;
Matches 7; Conservative 1

QY 1 QQSNEPPT 9
|||||
DB 93 QQSNEPPT 101

RESULT 17
S59833
DNA-directed DNA polymerase (EC 2.7.7.7) II chain B - yeast (Saccharomyces cerevisiae)
N:Alternate names: DNA polymerase epsilon chain B; protein P9705.7; protein YPR175W
C:Species: Saccharomyces cerevisiae
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
C:Accession: S59833; A39698
R:Pauley, A.
submitted to the EMBL Data Library, April 1995
A:Description: The sequence of S. cerevisiae cosmid 9705.
A:Reference number: S59829
A:Accession: S59833
A:Molecule type: DNA
A:Residues: 1-692 <PAU>
A:Cross-references: UNIPROT:P24482; UNIPARC:UPI0000052F0B; EMBL:U25842; NID:g786312; PI
R:Araki, H.; Hamatake, R.K.; Johnston, L.H.; Sugino, A.
Proc. Natl. Acad. Sci. U.S.A. 88, 4601-4605, 1991
A:Title: DPB2, the gene encoding DNA polymerase II subunit B, is required for chromosome replication.
A:Reference number: A39698; MUID:91271241; PMID:2052544
A:Accession: A39698
A:Molecule type: DNA
A:Residues: 'MELEAS', 1-460, 'Y', 462-523, 'R', 525-567, 'F', 569-586, 'Q', 588-646, 'I', 648-692
A:Cross-references: UNIPARC:UPI00001691DE; GB:M61710; NID:g171411; PIDN:AAA34576.1; PID
C:Genetics:
A:Gene: SGD:DPB2; MIPS:YPR175W
A:Cross-references: SGD:S0006379; MIPS:YPR175W
A:Map position: 16R
C:Superfamily: DNA polymerase epsilon, subunit B
C:Keywords: DNA binding; heteropentamer; nucleosidyltransferase; nucleus

Query Match 74.0%; Score 37; DB 1; Length 692;
Best Local Similarity 66.7%; Pred. No. 41; Mismatches 2; Indels 0; Gaps 0;
Matches 6; Conservative 2

QY 1 QQSNEPPT 9
|||||
DB 425 QXLNDDPPT 433

RESULT 18
KWSM6

Ig kappa chain precursor V regions (M63, AB22, PC9245, PC4050) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C:Accession: B90412; B90374; B93822; C93204; D93204; PH1078; A01935
R:Burstein, Y.; Schechter, I.
Biochemistry 17, 2392-2400, 1978
A:Title: Primary structures of N-terminal extra peptide segments linked to the variable expression of immunoglobulin genes.
A:Reference number: A90412; MUID:78235887; PMID:981779
A:Contents: M63
A:Accession: B90412
A:Molecule type: protein
A:Residues: 1-35 <BUR>
A:Cross-references: UNIPROT:P01661; UNIPARC:UPI000017371A
R:McKean, D.; Potter, M.; Hood, L.
Biochemistry 12, 760-771, 1973
A:Title: Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains w
A:Reference number: A90374; MUID:73140225; PMID:4691517
A:Contents: M63
A:Accession: B90374
A:Molecule type: protein
A:Residues: 21-46,'Q','48-53','B','55-57','Z','59-86','F','88-131 <MCK>
A:Cross-references: UNIPARC:UPI000017371B
A:Note: this sequence has since been revised in reference A93822
R:McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related mo
A:Reference number: A93822; MUID:79012520; PMID:99744
A:Contents: M63; AB22
A:Accession: B93822
A:Molecule type: protein
A:Residues: 1-53;69-107 <MC2>
A:Cross-references: UNIPARC:UPI000017371C; UNIPARC:UPI000017371D
A:Accession: C93822
A:Molecule type: protein
A:Residues: 21-119,'Y','121-131 <MC3>
A:Cross-references: UNIPARC:UPI000017371C; UNIPARC:UPI000017371D
R:Wiegert, M.; Gattalcan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152; PMID:103003
A:Contents: PC9245; PC4050
A:Accession: C93204
A:Molecule type: protein
A:Residues: 21-119,'Y','121-131 <WE1>
A:Cross-references: UNIPARC:UPI000002A0FD
A:Accession: D93204
A:Molecule type: protein
A:Residues: 21-119,'L',121-123,'A',125-129,'L',131 <WE2>
A:Cross-references: UNIPARC:UPI000002A0FD
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1078
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 21-122 <TIL>
A:Cross-references: UNIPARC:UPI000017371E
A:Experimental source: B cell, strain [NZB x NZM]F1, clone 17p.73
C:Comment: The M63 precursor sequence is shown.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status experimental <SIG>
F:21-131/Domain: Ig kappa chain precursor V region #status experimental <MAT>
F:136-114/Domain: immunoglobulin homology <IMM>
F:143-112/Disulfide bonds: #status predicted

Query Match 72.0%; Score 36; DB 1; Length 131;
Best Local Similarity 77.8%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSNEDEPPT 9
||:|||||
Db 113 QQNNEDEPWT 121

RESULT 19

Ti9840

hypothetical protein C39B10.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T19840

R:White, S.

submitted to the EMBL Data Library, July 1995

A:Reference number: Z19186

A:Accession: T19840

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-435 <WIL>

A:Cross-references: UNIPROT:Q18518; UNIPARC:UPI00008034A; EMBL:Z50027; PIDN:CAA90332.1;

A:Experimental source: Clone C39B10

C:Genetics:

A:Gene: CESP:C39B10.2

A:Map position: X

A:Introns: 17/2; 70/3; 107/2; 156/2; 172/1; 226/1; 269/1; 287/3; 310/1; 351/1

C:Superfamily: acetylcholine receptor

Query Match 72.0%; Score 36; DB 2; Length 435;
Best Local Similarity 77.8%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSNEDEPPT 9
|||||
Db 36 QQSNTREPT 44

RESULT 20

F84921

hypothetical protein At2g47960 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: F84921

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617157

A:Accession: F84921

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-508 <STO>

A:Cross-references: UNIPROT:O82263; UNIPARC:UPI000017A722; GB:AE002093; NID:G3738308; P1

C:Genetics:

A:Gene: At2g47960

A:Map position: 2

Query Match 72.0%; Score 36; DB 2; Length 508;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSNEDEPPT 9
:|||||
Db 241 EDSTEDPPT 249

RESULT 21

A44766

defective chorion-1 fcl25 protein precursor - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004

C:Accession: A44766

R:Waring, G.L.; Hawley, R.J.; Schoenfeld, T.

Dev. Biol. 142, 1-12, 1990
A:Title: Multiple proteins are produced from the dec-1 eggshell gene in Drosophila by al
A:Reference number: A44766; MUID:91032553; PMID:1699826
A:Accession: A44766
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1123 <WAR>
A:Cross-references: UNIPROT:P18169; UNIPARC:UPI0000128F37; GB:M35887; NID:g157181; PID:g
C:Genetics:
A:Gene: FlyBase:dec-1
A:Cross-references: FlyBase:FBgn0000427

Query Match 72.0%; Score 36; DB 2; Length 1123;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSNEDPPT 9
|:|:|:|:|
Db 960 QKSNPNPT 968

RESULT 22
C44766
A:Title: Multiple proteins are produced from the dec-1 eggshell gene in Drosophila by al
A:Reference number: A44766; MUID:91032553; PMID:1699826
A:Accession: C44766
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1589 <WAR>
A:Cross-references: UNIPARC:UPI000017BE86; GB:M35889; NID:g157185; PID:g157186
C:Genetics:
A:Gene: FlyBase:dec-1
A:Cross-references: FlyBase:FBgn0000427

Query Match 72.0%; Score 36; DB 2; Length 1589;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSNEDPPT 9
|:|:|:|:|
Db 960 QKSNPNPT 968

RESULT 23
B38601
A:Title: Multiple proteins are produced from the dec-1 eggshell gene in Drosophila by al
A:Reference number: A38601; MUID:91115823; PMID:1703527
A:Accession: B38601
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-65 <GOS>
A:Cross-references: UNIPARC:UPI0000115176; GB:M57979; NID:g196404; PIDN:AAAG3359.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 70.0%; Score 35; DB 2; Length 65;
Best Local Similarity 87.5%; Pred. No. 7.7;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QSNEDPPT 9
|:|:|:|:|

Db 47 QSNEDPPT 54

RESULT 24

A38601
A:Title: Multiple proteins are produced from the dec-1 eggshell gene in Drosophila by al
A:Reference number: A38601; MUID:91115823; PMID:1703527
A:Accession: A38601
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-93 <GOS>
A:Cross-references: UNIPARC:UPI0000115175; GB:M57979; NID:g196402; PIDN:AAAG3359.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 70.0%; Score 35; DB 2; Length 93;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QSNEDPPT 9
|:|:|:|:|
Db 75 QSNEDPPT 82

RESULT 25

PH1079
A:Title: Multiple proteins are produced from the dec-1 eggshell gene in Drosophila by al
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1079
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-102 <TIL>
A:Cross-references: UNIPARC:UPI00001767CE
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 70.0%; Score 35; DB 2; Length 102;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSNEDPPT 9
|:|:|:|:|
Db 93 QOSKEVPPT 101

RESULT 26

S19972
A:Title: Multiple proteins are produced from the dec-1 eggshell gene in Drosophila by al
A:Reference number: S19972
A:Accession: S19972
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <WEI>

Query Match 70.0%; Score 35; DB 2; Length 102;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSNEDPPT 9
|:|:|:|:|
Db 93 QOSKEVPPT 101

A;Cross-references: UNIPARC:UPI0000116032; EMBL:X65094; NID:g52290; PIDN:CAA46222.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>

Query Match 70.0%; Score 35; DB 2; Length 112;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSNEDPPT 9
|:|:|:|:|
Db 93 QQSSEDPPT 101

RESULT 27
T45859
R2R3-MYB transcription factor - Arabidopsis thaliana
N;Alternate names: protein F3A4.140
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 31-Dec-2004
C;Accession: T45859
R;Bargues, M.; Collado, M.C.; Navarero, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; May
submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23007
A;Accession: T45859
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-301 <BAR>
A;Cross-references: UNIPROT:Q9SN12; UNIPARC:UPI00000A3C92; EMBL:AL132978
A;Experimental source: cultivar Columbia; BAC clone F3A4
C;Genetics:
A;Map position: 3
A;Note: F3A4.140
C;Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology

Query Match 70.0%; Score 35; DB 2; Length 301;
Best Local Similarity 85.7%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SNEPDPT 9
|:|:|:|:|
Db 197 SSEDPT 203

RESULT 28
S71285
myb-related protein, 33.2K - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 31-Dec-2004
C;Accession: S71285
R;Kirik, V.; Baumein, H.
submitted to the EMBL Data Library, September 1995
A;Description: Characterization of two cDNAs encoding MYB-related proteins in Arabidopsi
A;Reference number: S71285
A;Accession: S71285
A;Molecule type: mRNA
A;Residues: 1-304 <KIR>
A;Cross-references: UNIPROT:Q39155; UNIPARC:UPI000009D1EE; EMBL:Z54137; NID:g1263096; PI
C;Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
C;Keywords: DNA binding; duplication
F;1-52/Domain: myb DNA-binding repeat homology <MYB>
F;53-103/Domain: myb DNA-binding repeat homology <MYB2>

Query Match 70.0%; Score 35; DB 1; Length 304;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SNEPDPT 9
|:|:|:|:|
Db 197 SSEDPT 203

RESULT 29

B84668
ethylene-insensitive3-like1 (EIL1) [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: B84668
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: B84668
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-584 <STO>
A;Cross-references: UNIPROT:Q9SLH0; UNIPARC:UPI000000BFC4; GB:AE002093; NID:g3885335; PI
C;Genetics:
A;Gene: At2g27050
A;Map position: 2

Query Match 70.0%; Score 35; DB 2; Length 584;
Best Local Similarity 75.0%; Pred. No. 83;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QSNEDPPT 9
|:|:|:|:|
Db 491 QSNQTPPT 498

RESULT 30
T20353
hypothetical protein D2030.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20353
R;Wilkinson, J.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19261
A;Accession: T20353
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-586 <WIL>
A;Cross-references: UNIPROT:P90788; UNIPARC:UPI0000007FDC1; EMBL:Z73906; PIDN:CAA98115.1;
A;Experimental source: clone D2030
C;Genetics:
A;Gene: CESP:D2030.2
A;Map position: 1
A;Introns: 27/2; 90/1; 224/3; 474/3; 553/2

Query Match 70.0%; Score 35; DB 2; Length 586;
Best Local Similarity 66.7%; Pred. No. 83;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSNEDPPT 9
|:|:|:|:|
Db 223 QQSNNQPPS 231

RESULT 31
T23961
hypothetical protein R06C1.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
C;Accession: T23961
R;Kershaw, J.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19824
A;Accession: T23961
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-597 <WIL>
A;Cross-references: UNIPROT:O62338; UNIPARC:UPI0000164002; EMBL:Z81106; PIDN:CAB03223.1;
A;Experimental source: clone R06C1

C:Genetics:

A:Gene: CESP:R06C1.6

A:Map position: 1

A:Introns: 8/2; 75/2; 141/1; 180/2; 230/2; 288/2; 405/3

Query Match 70.0%; Score 35; DB 2; Length 597;

Best Local Similarity 66.7%; Pred. No. 85;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSNEDPT 9

I: |||||

Db 263 QEDNEDPT 271

RESULT 32

S63208

hypothetical protein YNL242w - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein N1106

C:Species: Saccharomyces cerevisiae

C:Date: 27-Apr-1996 #sequence revision 03-May-1996 #text_change 09-Jul-2004

C:Accession: S63208; S63210; S63187; S67356; S72074

R:Pandolfo, D.; De Antoni, A.; Lanfranchi, G.; Valle, G.

submitted to the Protein Sequence Database, April 1996

A:Reference number: S63188

A:Accession: S63208

A:Molecule type: DNA

A:Residues: 1-1592 <PAN>

A:Cross-references: UNIPROT:P53855; UNIPARC:UPI000005328B; EMBL:Z71518; NID:gl302277; PI

A:Experimental source: strain S288C

R:Salz, J.E.; Baladron, V.; Del Rey, F.

submitted to the Protein Sequence Database, April 1996

A:Reference number: S63210

A:Accession: S63210

A:Molecule type: DNA

A:Residues: 1-277 <SAI>

A:Cross-references: UNIPARC:UPI000017CD0C; EMBL:Z71518; MIPS:YNL242w

A:Experimental source: strain S288C

R:Garcia-Cantalejo, J.M.; Boskovic, J.; Jimenez, A.

submitted to the Protein Sequence Database, April 1996

A:Reference number: S63030

A:Accession: S63187

A:Molecule type: DNA

A:Residues: 278-1304 <GAR>

A:Cross-references: UNIPARC:UPI000017CD0D; EMBL:Z71518; MIPS:YNL242w

A:Experimental source: strain S288C

R:Pandolfo, D.; de Antoni, A.; Lanfranchi, G.; Valle, G.

submitted to the EMBL Data Library, February 1996

A:Description: DNA sequence of cosmid 14-5 from chromosome XIV.

A:Reference number: S67355

A:Accession: S67356

A:Molecule type: DNA

A:Residues: 1-1592 <PAW>

A:Cross-references: UNIPARC:UPI000005328B; EMBL:Z69381; NID:gl183970; PID:e221807; PID:9

R:Pandolfo, D.; de Antoni, A.; Lanfranchi, G.; Valle, G.

Yeast 12, 1071-1076, 1996

A:Title: The DNA sequence of cosmid 14-5 from chromosome XIV reveals 21 open reading fra

A:Reference number: S72073; MUID:97051596; PMID:8896273

A:Accession: S72074

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1592 <PAF>

A:Cross-references: UNIPARC:UPI000005328B; EMBL:Z69381; NID:gl183970; PIDN:CAA93356.1; F

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996

C:Genetics:

A:Gene: SGD:APG2

A:Cross-references: SGD:S0005186

A:Map position: 14L

A>Note: YNL242w

Query Match 70.0%; Score 35; DB 2; Length 1592;

Best Local Similarity 85.7%; Pred. No. 2.5e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNEDPT 7

I: |||||

Db 267 EQSNEDPT 273

RESULT 33

A38432

heparin-binding EGF-like growth factor precursor - human

C:Species: Homo sapiens (man)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: A38432; A37300

R:Higashiyama, S.; Abraham, J.A.; Miller, J.; Fiddes, J.C.; Klagsbrun, M.

Science 251, 936-939, 1991

A:Title: A heparin-binding growth factor secreted by macrophage-like cells that is relat

A:Reference number: A38432; MUID:91157008; PMID:1840698

A:Accession: A38432

A:Molecule type: mRNA

A:Residues: 1-208 <HIG>

A:Cross-references: UNIPROT:Q99075; UNIPARC:UPI0000035E3F; GB:M60278; NID:g183866; PIDN

R:Higashiyama, S.; Lau, K.; Besner, G.E.; Abraham, J.A.; Klagsbrun, M.

J. Biol. Chem. 267, 6205-6212, 1992

A:Title: Structure of heparin-binding EGF-like growth factor. Multiple forms, primary str

A:Reference number: A37300; MUID:92210596; PMID:1556128

A:Accession: A37300

A:Molecule type: protein

A:Residues: 63-74, 'X', 76-84, 'X', 86-148 <HI2>

A:Cross-references: UNIPARC:UPI0000173352

C:Genetics:

A:Gene: GDB:DTR; DTS; HEGFL

A:Cross-references: GDB:I19853; OMIM:126150

A:Map position: 5q23-5q23

C:Superfamily: heparin-binding EGF-like growth factor; EGF homology

C:Keywords: heparin binding; transmembrane protein

F:108-143/Domain: EGF homology <EGF>

Query Match 68.0%; Score 34; DB 1; Length 208;

Best Local Similarity 85.7%; Pred. No. 42;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SNEPDPT 9

I: |||||

Db 38 SNPDPT 44

RESULT 34

JC1409

heparin-binding EGF-like growth factor precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: JC1409

R:Abraham, J.A.; Damm, D.; Bajardi, A.; Miller, J.; Klagsbrun, M.; Ezekowitz, R.A.B.

Biochem. Biophys. Res. Commun. 190, 125-133, 1993

A:Title: Heparin-binding EGF-like growth factor: Characterization of rat and mouse cDNA

A:Reference number: JC1409; MUID:93135756; PMID:7678488

A:Accession: JC1409

A:Molecule type: mRNA

A:Residues: 1-208 <ABR>

A:Cross-references: UNIPROT:Q06175; UNIPARC:UPI0000035E41; GB:L05489; NID:g204289; PIDN

C:Superfamily: heparin-binding EGF-like growth factor; EGF homology

C:Keywords: growth factor; heparin binding; transmembrane protein

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-208/Product: heparin-binding EGF-like growth factor #status predicted <MAT>

F:108-143/Domain: EGF homology <EGF>

F:161-184/Domain: transmembrane #status predicted <TM>

Query Match

Best Local Similarity 68.0%; Score 34; DB 1; Length 208;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SNEPDPT 9

I: |||||

Db 38 SNPDPT 44

```
RESULT 35
JC1410
heparin-binding EGF-like growth factor precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: J01410; J04659
R:Abraham, J.A.; Damm, D.; Bajardi, A.; Miller, J.; Klagsbrun, M.; Ezekowitz, R.A.B.
Biochem. Biophys. Res. Commun. 190, 125-133, 1993
A:Title: Heparin-binding EGF-like growth factor: Characterization of rat and mouse cDNA
A:Reference number: J01409; MUID:93135756; PMID:7678488
A:Accession: J01410
A:Molecule type: mRNA
A:Residues: 1-208 <AR>
A:Cross-references: UNIPROT:Q06186; UNIPARC:UPI0000022373; GB:L07264; NID:g192999; PIDN:
R:Harding, P.A.; Brigstock, D.R.; Shen, L.; Crisman-Combs, M.A.; Besner, G.E.
Gene 169, 291-292, 1996
A:Title: Characterization of the gene encoding murine heparin-binding epidermal growth f
A:Reference number: J04659; MUID:96194822; PMID:8647467
A:Accession: J04659
A:Molecule type: DNA
A:Residues: 1-208 <HAR>
A:Cross-references: UNIPARC:UPI0000022373; GB:U39189
C:Comment: This factor is a member of the epidermal growth factor family. Its binding ac
C:Genetics:
A:Gene: mHB-EGF
A:Introns: 16/1; 74/1; 133/2; 185/2
C:Superfamily: heparin-binding EGF-like growth factor; EGF homology
C:Keywords: growth factor; heparin binding; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-208/Product: heparin-binding EGF-like growth factor #status predicted <MAT>
F:108-143/Domain: EGF homology <EGF>
F:161-184/Domain: transmembrane #status predicted <TM>
```

```
Query Match      68.0%; Score 34; DB 1; Length 208;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 SNEDPPT 9
        |||||
Db      38 SNPDPT 44

RESULT 36
T51678
myb-related transcription factor MYB73 [imported] - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 31-Dec-2004
C:Accession: T51678
R:Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.; J
; Paz-Ares, J.; Weisshaar, B.
Plant J. 16, 263-276, 1998
A:Title: Towards functional characterisation of the members of the R2R3-MYB gene from A
A:Reference number: Z14349; MUID:9839469; PMID:9839469
A:Accession: T51678
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-268 <KRA>
A:Cross-references: UNIPROT:Q9SBF6; UNIPARC:UPI00000A4D20; EMBL:AF062906; PIDN:AAC83628.
A:Experimental source: cultivar Columbia
C:Genetics:
A:Gene: MYB73
A:Map position: IV
C:Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
C:Keywords: transcription factor

Query Match      68.0%; Score 34; DB 2; Length 268;
Best Local Similarity 85.7%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 SNEDPPT 9
        |||||
Db      137 SGEDPPT 143
```

```
RESULT 37
C85440
myb-related protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2004
C:Accession: C85440
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: C85440
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-320 <STO>
A:Cross-references: UNIPROT:O23160; UNIPARC:UPI000009ED18; GB:NC_001268; NID:g7270709; P
C:Genetics:
A:Gene: AT4g37260
A:Map position: 4
C:Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology

Query Match      68.0%; Score 34; DB 2; Length 320;
Best Local Similarity 85.7%; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 SNEDPPT 9
        |||||
Db      189 SGEDPPT 195

RESULT 38
WMBELM
membrane protein LMP-2A - human herpesvirus 4
N:Contains: membrane protein LMP-2B
C:Species: human herpesvirus 4, Epstein-Barr virus
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
C:Accession: A30178; B30178; S00392
R:Sample, J.; Liebowitz, D.; Kieff, E.
J. Virol. 63, 933-937, 1989
A:Title: Two related Epstein-Barr virus membrane proteins are encoded by separate genes.
A:Reference number: A30178; MUID:89095024; PMID:2536113
A:Accession: A30178
A:Molecule type: mRNA
A:Residues: 1-497 <SAM>
A:Cross-references: UNIPROT:P13285; UNIPARC:UPI000000CDBC; GB:M24212; NID:g522186; PIDN:
A:Accession: B30178
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 120-497 <SA2>
A:Cross-references: UNIPARC:UPI000000615B9
R:Laux, G.; Perricaudet, M.; Farrell, P.J.
EMBO J. 7, 769-774, 1988
A:Title: A spliced Epstein-Barr virus gene expressed in immortalized lymphocytes is crea
A:Reference number: S00392; MUID:88283646; PMID:2840285
A:Accession: S00392
A:Molecule type: mRNA
A:Residues: 1-497 <LAU>
A:Cross-references: UNIPARC:UPI000000CDBC; EMBL:Y00835; NID:g59183; PIDN:CAA68762.1; PID
C:Genetics:
A:Gene: terminal
A:Introns: 140/2; 212/1; 245/1; 328/1; 355/1; 412/1; 484/1
C:Superfamily: Epstein-Barr virus membrane protein LMP-2A
C:Keywords: glycoprotein; transmembrane protein
F:120-497/Product: membrane protein LMP-2B #status predicted <LMB>
F:122-141/Domain: transmembrane #status predicted <TMB>
F:150-168/Domain: transmembrane #status predicted <TMB>
F:178-198/Domain: transmembrane #status predicted <TMD>
F:208-235/Domain: transmembrane #status predicted <TMD>
F:242-259/Domain: transmembrane #status predicted <TME>
F:267-288/Domain: transmembrane #status predicted <TMF>
F:300-316/Domain: transmembrane #status predicted <TMG>
```

F:321-339/Domain: transmembrane #status predicted <TMH>
 F:355-373/Domain: transmembrane #status predicted <TMH>
 F:392-411/Domain: transmembrane #status predicted <TMH>
 F:419-443/Domain: transmembrane #status predicted <TMH>
 F:450-470/Domain: transmembrane #status predicted <TMH>
 F:27,320,417/Binding site: carbohydrate (Aen) #status predicted

Query Match 68.0%; Score 34; DB 1; Length 497;
 Best Local Similarity 62.5%; Pred. No. 1.1e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSNEDPPT 8
 DB 50 RESNEEPP 57

RESULT 39
 E90591
 lipoprotein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
 C:Species: Mycoplasma pulmonis
 C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
 C:Accession: E90591
 R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
 Nucleic Acids Res. 29, 2145-2153, 2001
 A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
 A:Reference number: A99512; MUID:21267165; PMID:11353084
 A:Accession: E90591
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-776 <NR>
 A:Cross-references: UNIPROT:Q98PT2; UNIPARC:UPI00000C80DC; GB:AL445566; PID:gl14090052; F
 A:Experimental source: strain UAB CTIP
 C:Genetics:
 A:Gene: MYPV 6370
 A:Genetic code: SGC3

Query Match 68.0%; Score 34; DB 2; Length 776;
 Best Local Similarity 66.7%; Pred. No. 1.7e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QSNEDPPT 9
 DB 147 QRSNEDTFS 155

RESULT 40
 T28431
 variant surface protein 1 homolog A4VAR - malaria parasite (Plasmodium falciparum) (frag
 C:Species: Plasmodium falciparum
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T28431
 R:Smith, J.D.; Kyes, S.; Craig, A.G.; Fagan, T.; Hudson-Taylor, D.; Miller, L.H.; Baruch
 Mol. Biochem. Parasitol. 97, 133-148, 1998
 A:Title: Analysis of adhesive domains from the A4VAR Plasmodium falciparum erythrocyte m
 A:Reference number: Z20486; MUID:99094502; PMID:9879893
 A:Accession: T28431
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-3026 <SMI>
 A:Cross-references: UNIPROT:Q26030; UNIPARC:UPI000007B327; EMBL:L42244; NID:G3540144; PI
 C:Genetics:
 A:Gene: var
 A:Introns: 2906/3

Query Match 68.0%; Score 34; DB 2; Length 3026;
 Best Local Similarity 85.7%; Pred. No. 7.6e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SNEDPPT 9
 DB 298 SNTDPPT 304

RESULT 41
 T02595

hypothetical protein At2g14810 [imported] - Arabidopsis thaliana
 N:Alternate names: hypothetical protein F26C24.5
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
 C:Accession: T02595; G84521
 R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
 submitted to the EMBL Data Library, June 1998
 A:Description: Arabidopsis thaliana chromosome II BAC F26C24 genomic sequence.
 A:Reference number: Z14680
 A:Accession: T02595
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-66 <ROU>
 A:Cross-references: UNIPROT:O80971; UNIPARC:UPI000009E30D; EMBL:AC004705; NID:G3252804;
 A:Experimental source: cultivar Columbia
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.M.;
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: G84521
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-66 <STO>
 A:Cross-references: UNIPARC:UPI000009E30D; GB:AE002093; NID:G3252808; PIDN:AAC24178.1; C
 C:Genetics:
 A:Gene: F26C24.5; At2g14810
 A:Map position: 2
 A:Introns: 45/3

Query Match 66.0%; Score 33; DB 2; Length 66;
 Best Local Similarity 71.4%; Pred. No. 19;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSNEDPPT 8
 DB 33 KSNQDPP 39

RESULT 42
 F87713
 conserved hypothetical protein CC3744 [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C:Accession: F87713
 R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolor
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: F87713
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-169 <STO>
 A:Cross-references: UNIPROT:Q9A222; UNIPARC:UPI00000C7BA9; GB:AE005673; NID:gl3425516;
 C:Genetics:
 A:Gene: CC3744

Query Match 66.0%; Score 33; DB 2; Length 169;
 Best Local Similarity 83.3%; Pred. No. 52;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NEDPPT 9
 DB 116 NDDPPT 121

RESULT 43
 JQ2347

hypothetical 23.6K protein - turkey herpesvirus
N:Alternate names: ORF2 protein
C:Species: turkey herpesvirus
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
C:Accession: JQ2347
R:Zelnik, V.; Darteil, R.; Audonnet, J.C.; Smith, G.D.; Riviere, M.; Paetorek, J.; Ross, J. Gen. Virol. 74, 2151-2162, 1993
A:Title: The complete sequence and gene organization of the short unique region of herpesvirus 23.6K protein
A:Reference number: JQ2346; MUID:94014999; PMID:8409940
A:Accession: JQ2347
A:Molecule type: DNA
A:Residues: 1-209 <ZEL>
A:Cross-references: UNIPROT:Q88519; UNIPARC:UPI00000F790F; EMBL:X68653; NID:9406783; PID:9406783
A:Experimental source: strain FCI26
C:Superfamily: Marek's disease virus minor virion protein

Query Match 66.0%; Score 33; DB 2; Length 209;
Best Local Similarity 71.4%; Pred. No. 66;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSNEDPP 8
|:|:|:|
Db 112 QNNEPP 118

RESULT 44
T51854
RING-H2 finger protein RHF2a [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C:Accession: T51854
R:Jensen, R.B.; Jensen, K.L.; Jespersen, H.M.; Skriver, K. FEBS Lett. 436, 283-7, 1998
A:Title: Widespread occurrence of a highly conserved RING-H2 zinc finger motif in the mouse and Arabidopsis genomes
A:Reference number: T513771; MUID:98452956; PMID:9781696
A:Accession: T51854
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-375 <JEN>
A:Cross-references: UNIPROT:Q9ZT42; UNIPARC:UPI00000AC55E; EMBL:AF079182; PIDN:AAC69856.

Query Match 66.0%; Score 33; DB 2; Length 375;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QSNEDPP 9
|:|:|:|
Db 213 QSNQTP 220

RESULT 45
T45301
homoserine o-acetyltransferase [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
C:Accession: T45301
R:Parkhill, J.; Barrrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, August 1997
A:Reference number: Z22864
A:Accession: T45301
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-382 <PAR>
A:Cross-references: UNIPROT:Q32874; UNIPARC:UPI000012F014; EMBL:Z98271; PIDN:CAB10992.1
A:Experimental source: cosmid B1779
C:Genetics:
A:Note: MLCB1779.11
C:Superfamily: homoserine acetyltransferase

Query Match 66.0%; Score 33; DB 2; Length 382;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QSNEDPPT 9
|:|:|:|
Db 249 QGNEDPAT 256

RESULT 46
S22520
myb-related protein 1 - Arabidopsis thaliana
N:Alternate names: protein Atmyb1
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C:Accession: S22520
R:Shinozaki, K.; Yamaguchi-Shinozaki, K.; Urao, T.; Koizumi, M. Plant Mol. Biol. 19, 493-499, 1992
A:Title: Nucleotide sequence of a gene from Arabidopsis thaliana encoding a myb homology domain protein
A:Reference number: S22520; MUID:92322982; PMID:1623193
A:Accession: S22520
A:Molecule type: DNA
A:Residues: 1-393 <SHI>
A:Cross-references: UNIPROT:Q42575; UNIPARC:UPI000009F710; EMBL:D10936; NID:9217858; PID:9217858
A:Experimental source: strain Columbia
C:Genetics:
A:Gene: myb1
A:Introns: 112/1
C:Superfamily: Arabidopsis myb-related protein 1; myb DNA-binding repeat homology
C:Keywords: DNA binding; duplication; nucleus; transcription regulation
F:50-101/Domain: myb DNA-binding repeat homology <MYB1>
F:102-152/Domain: myb DNA-binding repeat homology <MYB2>

Query Match 66.0%; Score 33; DB 1; Length 393;
Best Local Similarity 55.6%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSNEDPPT 9
:|:|:|:|
Db 232 RQDDKPPT 240

RESULT 47
JC5547
basic helix-loop-helix factor DEC1 - human
C:Species: Homo sapiens (man)
C:Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
C:Accession: JC5547
R:Shen, M.; Kawamoto, T.; Yan, W.; Nakamasu, K.; Tamagami, M.; Koyano, Y.; Noshiro, M.; Biochem. Biophys. Res. Commun. 236, 294-298, 1997
A:Title: Molecular characterization of the novel basic helix-loop-helix protein DEC1 expressed in human cells
A:Reference number: JC5547; MUID:97382424; PMID:9240428
A:Accession: JC5547
A:Molecule type: mRNA
A:Residues: 1-412 <SHE>
A:Cross-references: UNIPROT:O14503; UNIPARC:UPI0000126923; DBJ:AB004066; NID:g2308996;
C:Comment: This protein is involved in the control of cell differentiation in several tissues
F:51-108/Region: helix-loop-helix #status predicted

Query Match 66.0%; Score 33; DB 2; Length 412;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSNEDPPT 9
:|:|:|:|
Db 279 KQSEEPPT 287

RESULT 48
AC1306
carboxy-terminal processing proteinase homolog lmo1851 [imported] - Listeria monocytogenes
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AC1306
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001
 A:Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
 Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
 A:Title: Comparative genomics of *Listeria* species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AC1306
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-496 <GLA>
 A:Cross-references: UNIPROT:Q8Y649; UNIPARC:UPI00005545E; GB:NC_003210; PIDN:CAC99929.1
 A:Experimental source: strain EGD-e
 C:Genetics:
 A:Gene: lmo1851
 C:Superfamily: carboxyl-terminal processing proteinase

Query Match 66.0%; Score 33; DB 2; Length 496;
 Best Local Similarity 75.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSNEDPP 8
 |:|||||
 Db 199 QRSNEDKP 206

RESULT 49

AC1678
 carboxy-terminal processing proteinase homolog lin1965 [imported] - *Listeria innocua* (st
 C:Species: *Listeria innocua*
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AC1678
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
 .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
 Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
 A:Title: Comparative genomics of *Listeria* species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AC1678
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-496 <GLA>
 A:Cross-references: UNIPROT:Q92AF7; UNIPARC:UPI00000CC6F5; GB:AL592022; PIDN:CAC97195.1;
 A:Experimental source: strain Clp11262
 C:Genetics:
 A:Gene: lin1965

Query Match 66.0%; Score 33; DB 2; Length 496;
 Best Local Similarity 75.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSNEDPP 8
 |:|||||
 Db 199 QRSNEDKP 206

RESULT 50

D88536
 acidic protein - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 02-Nov-2001
 C:Accession: D88536
 R:anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A:Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biolog
 A:Reference number: AV5000; MUID:99069613; PMID:9851916
 A:Note: see websites Genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_ele
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A:Accession: D88536
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-705 <STO>
 A:Cross-references: UNIPARC:UPI000017A083; GB:chr_III; PIDN:AAA27898.1; PID:gl56195; GSH

A:Note: putative
 C:Genetics:
 A:Map position: 3

Query Match 66.0%; Score 33; DB 2; Length 705;
 Best Local Similarity 71.4%; Pred. No. 2.4e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QSNEDPP 8
 |:|||||
 Db 290 EQNEDPP 296

Search completed: February 23, 2006, 09:51:20
 Job time : 28.7385 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 09:29:53 ; Search time 77.5385 Seconds
(without alignments)
81.892 Million cell updates/sec

Title: US-10-723-872-20

Perfect score: 50

Sequence: 1 QQSNEDPPT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

1: uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|-------------|
| 1 | 41 | 82.0 | 655 | 2 Q4H3K9 | CIOIN |
| 2 | 40 | 80.0 | 111 | 1 KV3H | MUSCULU |
| 3 | 40 | 80.0 | 111 | 1 KV3L | MUSCULU |
| 4 | 40 | 80.0 | 111 | 1 KV3N | MUSCULU |
| 5 | 40 | 80.0 | 111 | 2 Q81U6 | MUSCULU |
| 6 | 39 | 78.0 | 111 | 1 KV3M | MUSCULU |
| 7 | 39 | 78.0 | 111 | 1 KV3O | MUSCULU |
| 8 | 39 | 78.0 | 111 | 1 KV3Q | MUSCULU |
| 9 | 39 | 78.0 | 380 | 2 Q4Q636 | LEIMA |
| 10 | 39 | 78.0 | 511 | 2 Q5SR29 | CRINE |
| 11 | 39 | 78.0 | 511 | 2 Q5KGF1 | CRINE |
| 12 | 38 | 76.0 | 376 | 2 Q8F526 | LEPIN |
| 13 | 38 | 76.0 | 797 | 2 Q5UQ3 | CANAL |
| 14 | 37 | 74.0 | 111 | 1 KV3J | MUSCULU |
| 15 | 37 | 74.0 | 111 | 1 KV3K | MUSCULU |
| 16 | 37 | 74.0 | 111 | 1 KV3L | MUSCULU |
| 17 | 36 | 72.0 | 101 | 2 Q5DBP2 | SCHJA |
| 18 | 36 | 72.0 | 131 | 1 KV3I | MUSCULU |
| 19 | 36 | 72.0 | 428 | 2 Q5AZV6 | EMENI |
| 20 | 36 | 72.0 | 442 | 2 Q82263 | ARATH |
| 21 | 36 | 72.0 | 443 | 2 Q72LZ6 | LEPIC |
| 22 | 36 | 72.0 | 443 | 2 Q8EYGH | LEPIN |
| 23 | 36 | 72.0 | 460 | 2 Q8S18 | CABEL |
| 24 | 36 | 72.0 | 562 | 2 Q6CF15 | YARLI |
| 25 | 36 | 72.0 | 1208 | 1 DEC11 | DROME |
| 26 | 36 | 72.0 | 1590 | 1 DEC11 | DROME |
| 27 | 35 | 70.0 | 107 | 2 Q7RK78 | PLAYO |
| 28 | 35 | 70.0 | 139 | 2 Q4YR21 | PLAF7 |
| 29 | 35 | 70.0 | 147 | 2 Q81607 | PLAF7 |
| 30 | 35 | 70.0 | 147 | 2 Q4Y6R0 | PLACH |
| 31 | 35 | 70.0 | 267 | 2 Q5AUQ5 | EMENI |

| | | | | | |
|--------|-------------|------|------|----|-----|
| Q5V2W7 | haloarcu | 275 | 70.0 | 35 | 32 |
| Q51CN4 | cytophaga j | 287 | 70.0 | 35 | 33 |
| Q7PY08 | anopheles g | 297 | 70.0 | 35 | 34 |
| Q9N12 | arabidopsis | 301 | 70.0 | 35 | 35 |
| Q39155 | arabidopsis | 304 | 70.0 | 35 | 36 |
| Q49745 | arabidopsis | 304 | 70.0 | 35 | 37 |
| Q560D5 | crine | 315 | 70.0 | 35 | 38 |
| Q4VDG8 | 9STRA | 328 | 70.0 | 35 | 39 |
| Q8BYV6 | mus muscu | 330 | 70.0 | 35 | 40 |
| Q8KPD8 | crine | 334 | 70.0 | 35 | 41 |
| Q7N1A8 | gloeobacter | 430 | 70.0 | 35 | 42 |
| Q62338 | caenorhabdi | 432 | 70.0 | 35 | 43 |
| Q7YTG7 | caenorhabdi | 470 | 70.0 | 35 | 44 |
| Q8H4F4 | eschrichia | 472 | 70.0 | 35 | 45 |
| Q8XR2 | mus muscu | 542 | 70.0 | 35 | 46 |
| Q8CTV2 | mus muscu | 564 | 70.0 | 35 | 47 |
| Q61EX9 | caenorhabdi | 572 | 70.0 | 35 | 48 |
| Q91H0 | arabidopsis | 584 | 70.0 | 35 | 49 |
| P90788 | caenorhabdi | 586 | 70.0 | 35 | 50 |
| Q49280 | tetraodon n | 588 | 70.0 | 35 | 51 |
| Q6165 | xenopus tro | 594 | 70.0 | 35 | 52 |
| Q6P811 | mus muscu | 634 | 70.0 | 35 | 53 |
| Q5151 | mus muscu | 634 | 70.0 | 35 | 54 |
| Q7YV96 | rhodopirell | 770 | 70.0 | 35 | 55 |
| Q4X105 | aspergillus | 917 | 70.0 | 35 | 56 |
| Q6D35 | solanum dem | 943 | 70.0 | 35 | 57 |
| Q7QT13 | giardia lam | 1075 | 70.0 | 35 | 58 |
| P53855 | saccharomyc | 1592 | 70.0 | 35 | 59 |
| Q61ZQ1 | caenorhabdi | 1954 | 70.0 | 35 | 60 |
| Q75JH8 | dictyosteli | 2473 | 70.0 | 35 | 61 |
| Q9F293 | yersinia en | 96 | 68.0 | 34 | 62 |
| Q7X310 | uncultured | 106 | 68.0 | 34 | 63 |
| Q69133 | human herpe | 117 | 68.0 | 34 | 64 |
| Q65550 | human herpe | 118 | 68.0 | 34 | 65 |
| Q65551 | human herpe | 118 | 68.0 | 34 | 66 |
| Q65552 | human herpe | 118 | 68.0 | 34 | 67 |
| Q65553 | human herpe | 118 | 68.0 | 34 | 68 |
| Q65554 | human herpe | 118 | 68.0 | 34 | 69 |
| Q65555 | human herpe | 118 | 68.0 | 34 | 70 |
| Q65556 | human herpe | 118 | 68.0 | 34 | 71 |
| Q65557 | human herpe | 118 | 68.0 | 34 | 72 |
| Q65558 | human herpe | 118 | 68.0 | 34 | 73 |
| Q65559 | human herpe | 118 | 68.0 | 34 | 74 |
| Q65560 | human herpe | 118 | 68.0 | 34 | 75 |
| Q65561 | human herpe | 118 | 68.0 | 34 | 76 |
| Q65562 | human herpe | 118 | 68.0 | 34 | 77 |
| Q65563 | human herpe | 118 | 68.0 | 34 | 78 |
| Q65564 | human herpe | 118 | 68.0 | 34 | 79 |
| Q65565 | human herpe | 118 | 68.0 | 34 | 80 |
| Q65566 | human herpe | 118 | 68.0 | 34 | 81 |
| Q65567 | human herpe | 118 | 68.0 | 34 | 82 |
| Q65568 | human herpe | 118 | 68.0 | 34 | 83 |
| Q65569 | human herpe | 118 | 68.0 | 34 | 84 |
| Q65570 | human herpe | 118 | 68.0 | 34 | 85 |
| Q65571 | human herpe | 118 | 68.0 | 34 | 86 |
| Q65572 | human herpe | 118 | 68.0 | 34 | 87 |
| Q65573 | human herpe | 118 | 68.0 | 34 | 88 |
| Q65574 | human herpe | 118 | 68.0 | 34 | 89 |
| Q65575 | human herpe | 118 | 68.0 | 34 | 90 |
| Q65576 | human herpe | 118 | 68.0 | 34 | 91 |
| Q65577 | human herpe | 118 | 68.0 | 34 | 92 |
| Q65578 | human herpe | 118 | 68.0 | 34 | 93 |
| Q65579 | human herpe | 118 | 68.0 | 34 | 94 |
| Q65580 | human herpe | 118 | 68.0 | 34 | 95 |
| Q65581 | human herpe | 118 | 68.0 | 34 | 96 |
| Q65582 | human herpe | 118 | 68.0 | 34 | 97 |
| Q65583 | human herpe | 118 | 68.0 | 34 | 98 |
| Q65584 | human herpe | 118 | 68.0 | 34 | 99 |
| Q65585 | human herpe | 118 | 68.0 | 34 | 100 |
| Q65586 | human herpe | 118 | 68.0 | 34 | 101 |
| Q65587 | human herpe | 118 | 68.0 | 34 | 102 |
| Q65588 | human herpe | 118 | 68.0 | 34 | 103 |
| Q65589 | human herpe | 118 | 68.0 | 34 | 104 |

| | | | | | | | | | | | | | |
|-----|------|------|------|---|---------------|---------------------|-----|----|------|-------|---|---------------|-----------------------|
| 105 | 34 | 68.0 | 268 | 2 | Q9SBP6_ARATH | Q9ebf6 arabidopsis | 178 | 33 | 56.0 | 426 | 2 | Q5UZ71_HALMA | Q5uz71 haloarcula |
| 106 | 34 | 68.0 | 286 | 2 | Q4T865_TETNG | Q4t865 tetradodon n | 179 | 33 | 66.0 | 428 | 2 | Q7VCF0_PROMA | Q7vcf0 prochloroco |
| 107 | 34 | 68.0 | 300 | 2 | Q4IQ32_GIBZE | Q4iq32 gibberella | 180 | 33 | 66.0 | 434 | 2 | Q8INAS_DROME | Q8inas drosophila |
| 108 | 34 | 68.0 | 320 | 2 | Q23160_ARATH | Q23160 arabidopsis | 181 | 33 | 66.0 | 467 | 2 | Q54RY6_DICDI | Q54ry6 dictyosteli |
| 109 | 34 | 68.0 | 414 | 2 | Q6CKY1_KLULA | Q6ckyl kluyveromyc | 182 | 33 | 66.0 | 468 | 1 | F12AI_BOVIN | P50448 bos taurus |
| 110 | 34 | 68.0 | 417 | 2 | Q5A710_CANAL | Q5a710 candida alb | 183 | 33 | 66.0 | 468 | 1 | F12AI_BOVIN | P50448 bos taurus |
| 111 | 34 | 68.0 | 443 | 2 | Q5V088_HALMA | Q5v088 haloarcula | 184 | 33 | 66.0 | 486 | 2 | Q52786_MAGGR | Q52786 magnaporthe |
| 112 | 34 | 68.0 | 497 | 1 | LMP2_EBV | P13285 epstein-bar | 185 | 33 | 66.0 | 496 | 2 | Q8Y649_LISMO | Q8y649 listeria mo |
| 113 | 34 | 68.0 | 497 | 1 | Q777H4_9GAMA | Q777h4 human herpe | 186 | 33 | 66.0 | 496 | 2 | Q92AF7_LISIN | Q92af7 listeria in |
| 114 | 34 | 68.0 | 502 | 2 | Q5BEK1_BRARE | Q5bek1 brachydanio | 187 | 33 | 66.0 | 529 | 2 | Q59S39_CANAL | Q59s39 candida alb |
| 115 | 34 | 68.0 | 583 | 2 | Q5ABD2_CANAL | Q5abd2 candida alb | 188 | 33 | 66.0 | 539 | 2 | Q7XX03_ORYSA | Q7xx03 oryza sativ |
| 116 | 34 | 68.0 | 652 | 2 | Q8DK85_SYNEL | Q8dk85 synechococc | 189 | 33 | 66.0 | 540 | 2 | Q4P7R9_USTWA | Q4p7r9 ustilago ma |
| 117 | 34 | 68.0 | 654 | 2 | Q4WH51_AS PFU | Q4wh51 aspergillus | 190 | 33 | 66.0 | 557 | 2 | Q8WXD1_HUMAN | Q8wxd1 homo sapien |
| 118 | 34 | 68.0 | 675 | 2 | Q7PGV1_ANOGA | Q7pgv1 anopheles g | 191 | 33 | 66.0 | 565 | 2 | Q7ZTC0_BRARE | Q7ztc0 brachydanio |
| 119 | 34 | 68.0 | 776 | 2 | Q98PT2_MYCPU | Q98pt2 mycoplasma | 192 | 33 | 66.0 | 571 | 2 | Q8X003_NEUCR | Q8x003 neurospora |
| 120 | 34 | 68.0 | 828 | 2 | Q5B953_EMENI | Q5b953 aspergillus | 193 | 33 | 66.0 | 575 | 2 | Q9Y7A8_NEUCR | Q9y7a8 neurospora |
| 121 | 34 | 68.0 | 841 | 2 | Q4WX37_AS PFU | Q4wx37 aspergillus | 194 | 33 | 66.0 | 576 | 2 | Q7RVN7_NEUCR | Q7rvn7 neurospora |
| 122 | 34 | 68.0 | 843 | 2 | Q54GG9_DICDI | Q54gg9 dictyosteli | 195 | 33 | 66.0 | 581 | 2 | Q5TFP2_ANOGA | Q5tfp2 anopheles g |
| 123 | 34 | 68.0 | 857 | 2 | Q4IP90_GIBZE | Q4ipp0 gibberella | 196 | 33 | 66.0 | 592 | 2 | Q610X0_CAEBR | Q610x0 caenorhabdi |
| 124 | 34 | 68.0 | 886 | 2 | Q5B2K3_EMENI | Q5b2k3 aspergillus | 197 | 33 | 66.0 | 600 | 2 | Q9VMX1_DROME | Q9vmx1 drosophila |
| 125 | 34 | 68.0 | 981 | 2 | Q5GQC7_9CAUD | Q5gqc7 bacterioph | 198 | 33 | 66.0 | 612 | 2 | Q8TEN8_HUMAN | Q8ten8 homo sapien |
| 126 | 34 | 68.0 | 1009 | 2 | Q6TMU6_STRCL | Q6tmu6 streptomyce | 199 | 33 | 66.0 | 616 | 1 | YKA4_CAEEL | P34256 caenorhabdi |
| 127 | 34 | 68.0 | 1311 | 2 | Q4QAF3_LEIMA | Q4qaf3 leishmania | 200 | 33 | 66.0 | 649 | 2 | Q6ZPU7_MOUSE | Q6zpu7 mus musculu |
| 128 | 34 | 68.0 | 1430 | 2 | Q6CT88_KLULA | Q6cte8 kluyveromyc | 201 | 33 | 66.0 | 667 | 2 | Q51EG6_ENTHI | Q51eg6 entamoeba h |
| 129 | 34 | 68.0 | 1438 | 2 | Q4WKW7_AS PFU | Q4kwk7 aspergillus | 202 | 33 | 66.0 | 667 | 2 | Q7T2E5_BRARE | Q7t2e5 brachydanio |
| 130 | 34 | 68.0 | 1543 | 2 | Q9W406_DROME | Q9w406 drosophila | 203 | 33 | 66.0 | 668 | 2 | Q75PY4_ORYLA | Q75py4 oryztias lat |
| 131 | 34 | 68.0 | 1633 | 2 | Q5NWD5_AZOSE | Q5nwd5 azoarcus sp | 204 | 33 | 66.0 | 671 | 2 | Q5F3W8_CHICK | Q5f3w8 gallus gall |
| 132 | 34 | 68.0 | 1887 | 2 | Q806Y9_9CLOS | Q806y9 cucumber ye | 205 | 33 | 66.0 | 683 | 2 | Q4X0N6_AS PFU | Q4x0n6 aspergillus |
| 133 | 34 | 68.0 | 2160 | 2 | Q13328_MAGGR | Q13328 magnaporthe | 206 | 33 | 66.0 | 683 | 2 | Q412L0_GIBZE | Q412l0 gibberella |
| 134 | 34 | 68.0 | 2160 | 2 | Q13488_MAGGR | Q13488 magnaporthe | 207 | 33 | 66.0 | 684 | 2 | Q75PV3_ORYLA | Q75pv3 oryztias lat |
| 135 | 34 | 68.0 | 2160 | 2 | Q51J05_MAGGR | Q51j05 magnaporthe | 208 | 33 | 66.0 | 686 | 2 | Q7S0P3_NEUCR | Q7s0p3 neurospora |
| 136 | 34 | 68.0 | 2441 | 2 | Q6VRA8_9CLOS | Q6vra8 beet pseudo | 209 | 33 | 66.0 | 726 | 2 | Q4SL71_TETNG | Q4sl71 tetradodon n |
| 137 | 34 | 68.0 | 2710 | 2 | Q9XZB8_PLAFA | Q9xzb8 plasmodium | 210 | 33 | 66.0 | 803 | 2 | Q6FLS7_CANGA | Q6fls7 candida gla |
| 138 | 34 | 68.0 | 3026 | 2 | Q26030_PLAFA | Q26030 plasmodium | 211 | 33 | 66.0 | 824 | 2 | Q5RAI4_PONPY | Q5rai4 pongo pygma |
| 139 | 34 | 68.0 | 3550 | 2 | Q9JJN2_MOUSE | Q9jjn2 mus musculu | 212 | 33 | 66.0 | 841 | 2 | Q4S813_TETNG | Q4s813 tetradodon n |
| 140 | 33.5 | 67.0 | 872 | 2 | Q7Q559_ANOGA | Q7q559 anopheles g | 213 | 33 | 66.0 | 860 | 2 | Q5B145_EMENI | Q5b145 aspergillus |
| 141 | 33 | 66.0 | 51 | 2 | Q5W2M9_SULIS | Q5w2m9 sulfolobus | 214 | 33 | 66.0 | 872 | 2 | Q8MZFI_DROME | Q8mzf1 drosophila |
| 142 | 33 | 66.0 | 66 | 2 | Q80971_ARATH | Q80971 arabidopsis | 215 | 33 | 66.0 | 872 | 2 | Q8IQI1_DROME | Q8iqi1 drosophila |
| 143 | 33 | 66.0 | 134 | 2 | Q96UR4_COCP0 | Q96ur4 coccidioid | 216 | 33 | 66.0 | 882 | 2 | Q9D4H4_MOUSE | Q9d4h4 mus musculu |
| 144 | 33 | 66.0 | 137 | 2 | Q5YFG5_9VIRU | Q5yfg5 singapore g | 217 | 33 | 66.0 | 905 | 2 | Q7N649_PHOLL | Q7n649 photorhabdu |
| 145 | 33 | 66.0 | 145 | 2 | Q59JUI_CANAL | Q59jui candida alb | 218 | 33 | 66.0 | 906 | 2 | Q63HK7_HUMAN | Q63hk7 homo sapien |
| 146 | 33 | 66.0 | 168 | 2 | Q6ZR29_HUMAN | Q6zr29 homo sapien | 219 | 33 | 66.0 | 911 | 2 | Q7Q5F3_ANOGA | Q7q5f3 anopheles g |
| 147 | 33 | 66.0 | 169 | 2 | Q9A222_CAUCR | Q9a222 caulobacter | 220 | 33 | 66.0 | 913 | 2 | Q8B195_MOUSE | Q8b195 mus musculu |
| 148 | 33 | 66.0 | 190 | 2 | Q52LS8_MOUSE | Q52ls8 mus musculu | 221 | 33 | 66.0 | 925 | 1 | GLHR_ANTEP | P35409 anthopleura |
| 149 | 33 | 66.0 | 196 | 2 | Q5N089_SYNPP6 | Q5n089 synechococc | 222 | 33 | 66.0 | 936 | 2 | Q4P605_USTWA | Q4p605 ustilago ma |
| 150 | 33 | 66.0 | 197 | 2 | Q9CT00_MOUSE | Q9ct00 m mus muscu | 223 | 33 | 66.0 | 956 | 2 | Q81Y63_HUMAN | Q81y63 homo sapien |
| 151 | 33 | 66.0 | 202 | 2 | Q5VKP4_9RHAB | Q5vklp4 irkut virus | 224 | 33 | 66.0 | 979 | 2 | Q91Y11_MOUSE | Q91y11 mus musculu |
| 152 | 33 | 66.0 | 209 | 2 | Q7L62_9ALPH | Q7l62 meleagrid h | 225 | 33 | 66.0 | 985 | 2 | Q6NV83_MOUSE | Q6nv83 mus musculu |
| 153 | 33 | 66.0 | 209 | 2 | Q88519_MEHVL | Q88519 meleagrid h | 226 | 33 | 66.0 | 989 | 2 | Q6CVA2_KLULA | Q6cva2 kluyveromyc |
| 154 | 33 | 66.0 | 236 | 2 | Q6PIH7_HUMAN | Q6pih7 homo sapien | 227 | 33 | 66.0 | 999 | 2 | Q7M114_VIBVY | Q7m114 vibrio vuln |
| 155 | 33 | 66.0 | 236 | 2 | Q4RIN4_TETNG | Q4rin4 tetradodon n | 228 | 33 | 66.0 | 1001 | 2 | Q4S0G2_TETNG | Q4s0g2 tetradodon n |
| 156 | 33 | 66.0 | 249 | 2 | Q4TGS6_TETNG | Q4tgs6 tetradodon n | 229 | 33 | 66.0 | 1027 | 2 | Q9BR70_HUMAN | Q9br70 homo sapien |
| 157 | 33 | 66.0 | 264 | 2 | Q8X218_COCP0 | Q8x218 coccidioid | 230 | 33 | 66.0 | 1028 | 2 | Q15042_HUMAN | Q15042 homo sapien |
| 158 | 33 | 66.0 | 271 | 2 | Q9VU12_DROME | Q9vu12 drosophila | 231 | 33 | 66.0 | 1028 | 2 | Q5R7X2_PONPY | Q5r7x2 pongo pygma |
| 159 | 33 | 66.0 | 283 | 2 | Q7TDM7_9VIRU | Q7tdm7 halovirus h | 232 | 33 | 66.0 | 1029 | 1 | Y2095_RHIME | Q52999 rhizobium m |
| 160 | 33 | 66.0 | 283 | 2 | Q7M6U2_9VIRU | Q7m6u2 halovirus h | 233 | 33 | 66.0 | 1030 | 2 | Q94152_ORYSA | Q94152 oryza sativ |
| 161 | 33 | 66.0 | 323 | 2 | Q9AN04_BRAJA | Q9an04 bradyrhizob | 234 | 33 | 66.0 | 1098 | 2 | Q6PHM6_MOUSE | Q6phm6 mus musculu |
| 162 | 33 | 66.0 | 338 | 2 | Q9CSW7_MOUSE | Q9csw7 m mus muscu | 235 | 33 | 66.0 | 1185 | 2 | Q52FA6_MAGGR | Q52fa6 magnaporthe |
| 163 | 33 | 66.0 | 353 | 2 | Q8GXA8_ARATH | Q8gxa8 arabidopsis | 236 | 33 | 66.0 | 1185 | 2 | Q8DBV4_VIBVU | Q8dbv4 vibrio vuln |
| 164 | 33 | 66.0 | 375 | 2 | Q9ZT42_ARATH | Q9zt42 arabidopsis | 237 | 33 | 66.0 | 1211 | 2 | Q9VSP0_DROME | Q9vsp0 drosophila |
| 165 | 33 | 66.0 | 380 | 1 | SEN2_SCHPO | Q8tfh7 schizosacch | 238 | 33 | 66.0 | 1326 | 1 | FBXW7_DROME | Q9wzf4 drosophila |
| 166 | 33 | 66.0 | 382 | 1 | METX_MYCLE | Q32874 mycobacteri | 239 | 33 | 66.0 | 1455 | 2 | Q81IQ4_PLAFA | Q81iq4 plasmodium |
| 167 | 33 | 66.0 | 383 | 2 | Q4RRX7_TETNG | Q4rrx7 tetradodon n | 240 | 33 | 66.0 | 1876 | 2 | Q9VJF9_DROME | Q9vjf9 drosophila |
| 168 | 33 | 66.0 | 393 | 2 | Q42575_ARATH | Q42575 arabidopsis | 241 | 33 | 66.0 | 2107 | 2 | Q752F6_ASHGO | Q752f6 ashbya goss |
| 169 | 33 | 66.0 | 398 | 2 | Q86DF9_HETGL | Q86df9 heterodera | 242 | 33 | 66.0 | 3013 | 2 | Q6PNC0_MOUSE | Q6pnc0 mus musculu |
| 170 | 33 | 66.0 | 411 | 1 | BHLH2_MOUSE | Q35185 mus musculu | 243 | 33 | 66.0 | 18412 | 2 | Q7ZZ61_BRARE | Q7zz61 brachydanio |
| 171 | 33 | 66.0 | 411 | 1 | BHLH2_RAT | Q35780 rattus norv | 244 | 32 | 64.0 | 55 | 2 | Q8HLP4_9TELE | Q8hlp4 directmoies ar |
| 172 | 33 | 66.0 | 411 | 2 | Q4WTX4_AS PFU | Q4wtx4 aspergillus | 245 | 32 | 64.0 | 55 | 2 | Q8HLQ7_9TELE | Q8hlq7 dictyosteli |
| 173 | 33 | 66.0 | 411 | 2 | Q542A5_MOUSE | Q542a5 m male subm | 246 | 32 | 64.0 | 109 | 2 | Q54T07_DICDI | Q54t07 dictyosteli |
| 174 | 33 | 66.0 | 411 | 2 | Q76J04_RAT | Q76j04 rattus norv | 247 | 32 | 64.0 | 109 | 2 | Q8DJY8_SYNEL | Q8djy8 synechococc |
| 175 | 33 | 66.0 | 412 | 1 | BHLH2_HUMAN | Q14503 homo sapien | 248 | 32 | 64.0 | 126 | 2 | Q8T4Y7_PLAFA | Q8t4y7 plasmodium |
| 176 | 33 | 66.0 | 412 | 2 | Q61B83_HUMAN | Q61b83 homo sapien | 249 | 32 | 64.0 | 136 | 2 | Q8T509_PLAFA | Q8t509 plasmodium |
| 177 | 33 | 66.0 | 412 | 2 | Q5RAI7_PONPY | Q5rai7 pongo pygma | 250 | 32 | 64.0 | 142 | 2 | Q57RK5_SALCH | Q57rk5 salmonella |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|---------------|--------------------|-----|----|------|-----|---|--------------|--------------------|
| 251 | 32 | 64.0 | 142 | 2 | Q5PM25_SALPA | Q5pm25 salmonella | 324 | 32 | 64.0 | 424 | 2 | Q5BBC0_EMENI | Q5bbc0 aspergillus |
| 252 | 32 | 64.0 | 142 | 2 | Q7CQX0_SALTY | Q7cqx0 salmonella | 325 | 32 | 64.0 | 425 | 2 | Q4I315_GIBZE | Q4i315 gibberella |
| 253 | 32 | 64.0 | 142 | 2 | Q8XF53_SALTY | Q8xf53 salmonella | 326 | 32 | 64.0 | 428 | 1 | RSMB_SHEON | Q8ekr0 shewanella |
| 254 | 32 | 64.0 | 145 | 2 | Q7Z209_PLAFA | Q7z209 plaemodium | 327 | 32 | 64.0 | 429 | 2 | Q759K5_ASHGO | Q759k5 ashbya goss |
| 255 | 32 | 64.0 | 148 | 1 | VEGFH_ORFN7 | P52585 orf virus (| 328 | 32 | 64.0 | 431 | 2 | Q82ET0_STRAM | Q82et0 streptomyc |
| 256 | 32 | 64.0 | 157 | 2 | Q5OSQ7_ENTHI | Q5osq7 entamoeba h | 329 | 32 | 64.0 | 440 | 2 | Q8OW26_MOUSE | Q8ow26 mus musculu |
| 257 | 32 | 64.0 | 168 | 2 | Q857R3_9CAUD | Q857r3 mycobacteri | 330 | 32 | 64.0 | 444 | 2 | Q5SVV2_CRYNE | Q5svv2 cryptococcu |
| 258 | 32 | 64.0 | 169 | 2 | Q5TV13_ANOGA | Q5tv13 anopheles g | 331 | 32 | 64.0 | 444 | 2 | Q5KKD7_CRYNE | Q5kkd7 cryptococcu |
| 259 | 32 | 64.0 | 170 | 2 | Q6DEF8_BRARE | Q6def8 brachydanio | 332 | 32 | 64.0 | 446 | 2 | Q8R7H1_PONPY | Q8r7h1 pongo pygma |
| 260 | 32 | 64.0 | 189 | 2 | Q6UF7L3_PLAFA | Q6uf7l3 plaemodium | 333 | 32 | 64.0 | 457 | 2 | Q8IXN4_HUMAN | Q8ixn4 homo sapien |
| 261 | 32 | 64.0 | 192 | 2 | Q6A827_PROAC | Q6a827 propionibac | 334 | 32 | 64.0 | 465 | 2 | Q7S906_NEUCR | Q7s906 neurospora |
| 262 | 32 | 64.0 | 201 | 2 | O10405_BDV | O10405 borna disea | 335 | 32 | 64.0 | 466 | 2 | Q7R492_GALA | Q7r492 giardia lam |
| 263 | 32 | 64.0 | 204 | 2 | Q5LYJ4_MAGGR | Q5lyj4 magnaporthe | 336 | 32 | 64.0 | 479 | 2 | Q15523_HUMAN | Q15523 homo sapien |
| 264 | 32 | 64.0 | 216 | 2 | Q8N4X3_HUMAN | Q8n4x3 homo sapien | 337 | 32 | 64.0 | 483 | 2 | Q6AHY6_HUMAN | Q6ahy6 homo sapien |
| 265 | 32 | 64.0 | 216 | 2 | Q5TH92_HUMAN | Q5th92 homo sapien | 338 | 32 | 64.0 | 510 | 1 | DMP1_BOVIN | Q95120 bos taurus |
| 266 | 32 | 64.0 | 217 | 2 | Q5DZX2_VIBF1 | Q5dxx2 vibrio fisc | 339 | 32 | 64.0 | 513 | 1 | DMP1_HUMAN | Q11316 homo sapien |
| 267 | 32 | 64.0 | 220 | 2 | Q54K17_DICD1 | Q54k17 dictyosteli | 340 | 32 | 64.0 | 535 | 1 | TLB1_BRARE | Q11368 brachydanio |
| 268 | 32 | 64.0 | 230 | 2 | Q6ORU0_CABER | Q6oru0 caenorhabdi | 341 | 32 | 64.0 | 537 | 2 | Q4V8F0_RAT | Q4v8f0 rattus norv |
| 269 | 32 | 64.0 | 240 | 2 | Q821U1_CHICV | Q821u1 chlamydomph | 342 | 32 | 64.0 | 547 | 2 | Q6BQI3_DEBHA | Q6bqi3 debaryomyce |
| 270 | 32 | 64.0 | 248 | 2 | Q7QCZ1_ANOGA | Q7qcz1 anopheles g | 343 | 32 | 64.0 | 569 | 2 | Q9UKB4_HUMAN | Q9ukb4 homo sapien |
| 271 | 32 | 64.0 | 255 | 2 | Q75UQ0_IPOBA | Q75uq0 ipomoea bat | 344 | 32 | 64.0 | 583 | 2 | Q9VZW9_DROME | Q9vzw9 drosophila |
| 272 | 32 | 64.0 | 263 | 2 | Q5GM63_9NEOB | Q5gm63 eleutheroda | 345 | 32 | 64.0 | 585 | 2 | Q60YK9_CABER | Q60yk9 caenorhabdi |
| 273 | 32 | 64.0 | 265 | 2 | Q8SAL3_ORYSA | Q8sal3 oryza sativ | 346 | 32 | 64.0 | 600 | 2 | Q51TH8_MAGGR | Q51th8 magnaporthe |
| 274 | 32 | 64.0 | 272 | 2 | Q994W1_9VIRU | Q994w1 sacbrood vi | 347 | 32 | 64.0 | 600 | 2 | Q96MN4_HUMAN | Q96mn4 homo sapien |
| 275 | 32 | 64.0 | 272 | 2 | Q994W1_9VIRU | Q994w1 sacbrood vi | 348 | 32 | 64.0 | 603 | 1 | HAL4_YEAST | P25333 saccharomyc |
| 276 | 32 | 64.0 | 272 | 2 | Q994W2_9VIRU | Q994w2 sacbrood vi | 349 | 32 | 64.0 | 607 | 2 | Q504U4_HUMAN | Q504u4 homo sapien |
| 277 | 32 | 64.0 | 272 | 2 | Q994W3_9VIRU | Q994w3 sacbrood vi | 350 | 32 | 64.0 | 607 | 2 | Q7QYE5_GIALA | Q7qye5 giardia lam |
| 278 | 32 | 64.0 | 272 | 2 | Q994W4_9VIRU | Q994w4 sacbrood vi | 351 | 32 | 64.0 | 608 | 2 | Q8MT40_DROME | Q8mt40 drosophila |
| 279 | 32 | 64.0 | 272 | 2 | Q994W5_9VIRU | Q994w5 sacbrood vi | 352 | 32 | 64.0 | 608 | 2 | Q968Z5_DROME | Q968z5 drosophila |
| 280 | 32 | 64.0 | 272 | 2 | Q994W6_9VIRU | Q994w6 sacbrood vi | 353 | 32 | 64.0 | 618 | 2 | Q86ZN5_PODAN | Q86zn5 podospira a |
| 281 | 32 | 64.0 | 272 | 2 | Q994W7_9VIRU | Q994w7 sacbrood vi | 354 | 32 | 64.0 | 618 | 2 | Q5SUT0_MOUSE | Q5sut0 mus musculu |
| 282 | 32 | 64.0 | 272 | 2 | Q994W8_9VIRU | Q994w8 sacbrood vi | 355 | 32 | 64.0 | 620 | 2 | Q684M5_PIG | Q684m5 sus scrofa |
| 283 | 32 | 64.0 | 272 | 2 | Q994W9_9VIRU | Q994w9 sacbrood vi | 356 | 32 | 64.0 | 620 | 2 | Q4SHK1_TETNG | Q4shk1 tetraodon n |
| 284 | 32 | 64.0 | 282 | 2 | Q511A3_ENTHI | Q511a3 entamoeba h | 357 | 32 | 64.0 | 623 | 1 | MAK_HUMAN | P20794 homo sapien |
| 285 | 32 | 64.0 | 291 | 2 | Q8SUS0_ENCCU | Q8sus0 encephalito | 358 | 32 | 64.0 | 623 | 2 | Q547D0_HUMAN | Q547d0 homo sapien |
| 286 | 32 | 64.0 | 293 | 2 | Q6S1G4_ORYSA | Q6s1g4 oryza sativ | 359 | 32 | 64.0 | 628 | 2 | Q4Q131_LEIMA | Q4q131 leishmania |
| 287 | 32 | 64.0 | 293 | 2 | Q7TD26_9VIRU | Q7td26 sacbrood vi | 360 | 32 | 64.0 | 631 | 2 | Q44527_CABEL | Q44527 caenorhabdi |
| 288 | 32 | 64.0 | 293 | 2 | Q80JQ9_9VIRU | Q80jq9 sacbrood vi | 361 | 32 | 64.0 | 655 | 1 | EWS_MOUSE | Q61545 mus musculu |
| 289 | 32 | 64.0 | 294 | 2 | Q6AAW6_PROAC | Q6aaw6 propionibac | 362 | 32 | 64.0 | 655 | 2 | Q96FB8_HUMAN | Q96fb8 homo sapien |
| 290 | 32 | 64.0 | 301 | 2 | Q61ZU7_CABER | Q61zu7 caenorhabdi | 363 | 32 | 64.0 | 655 | 2 | Q4R3Q5_MACFA | Q4r3q5 macaca fasc |
| 291 | 32 | 64.0 | 301 | 2 | Q7CUB1_AGRTH | Q7cub1 agrobacteri | 364 | 32 | 64.0 | 655 | 2 | Q9D2P0_MOUSE | Q9d2p0 mus musculu |
| 292 | 32 | 64.0 | 305 | 2 | Q941B3_ARATH | Q941b3 arabidopsis | 365 | 32 | 64.0 | 656 | 1 | EWS_HUMAN | Q01844 mus musculu |
| 293 | 32 | 64.0 | 305 | 2 | Q9FDM1_ARATH | Q9fdm1 arabidopsis | 366 | 32 | 64.0 | 656 | 2 | Q5THL0_HUMAN | Q5thl0 homo sapien |
| 294 | 32 | 64.0 | 310 | 2 | Q4SVF0_TETNG | Q4svf0 tetraodon n | 367 | 32 | 64.0 | 656 | 2 | Q6NVA3_MOUSE | Q6nva3 mus musculu |
| 295 | 32 | 64.0 | 317 | 2 | Q4RM41_RAT | Q4rm41 rattus norv | 368 | 32 | 64.0 | 661 | 2 | Q96MX4_HUMAN | Q96mx4 homo sapien |
| 296 | 32 | 64.0 | 327 | 2 | Q9UYM5_PYRAB | Q9uym5 pyrococcus | 369 | 32 | 64.0 | 661 | 2 | Q5SUS9_MOUSE | Q5sus9 mus musculu |
| 297 | 32 | 64.0 | 331 | 2 | Q61EN3_ORYSA | Q6ien3 oryza sativ | 370 | 32 | 64.0 | 666 | 1 | Y035_MYCPN | P75079 mycoplasma |
| 298 | 32 | 64.0 | 333 | 2 | Q9CRS5_MOUSE | Q9crs5 mus musculu | 371 | 32 | 64.0 | 669 | 2 | Q7R135_GIALA | Q7r135 giardia lam |
| 299 | 32 | 64.0 | 344 | 2 | Q8QLR4_9VIRU | Q8qlr4 rice tungro | 372 | 32 | 64.0 | 680 | 2 | Q51JK7_MAGGR | Q51jk7 magnaporthe |
| 300 | 32 | 64.0 | 348 | 2 | Q8NSD4_CORGL | Q8nsd4 corynebacte | 373 | 32 | 64.0 | 688 | 2 | Q6Y2W8_MAIZE | Q6y2w8 zea mays (m |
| 301 | 32 | 64.0 | 359 | 2 | Q7TWV1_MYCBO | Q7twv1 mycobacteri | 374 | 32 | 64.0 | 689 | 2 | Q6CRN8_KLULA | Q6crn8 kluyveromyc |
| 302 | 32 | 64.0 | 359 | 2 | Q7D5T3_MYCTU | Q7d5t3 mycobacteri | 375 | 32 | 64.0 | 703 | 2 | Q5DU73_9VIRU | Q5du73 rice tungro |
| 303 | 32 | 64.0 | 360 | 2 | Q4JTN7_CORJK | Q4jtn7 corynebacte | 376 | 32 | 64.0 | 703 | 2 | Q5WIL9_9VIRU | Q5wil9 rice tungro |
| 304 | 32 | 64.0 | 362 | 2 | Q6W738_CORGL | Q6w738 corynebacte | 377 | 32 | 64.0 | 718 | 2 | Q7Q6L5_ANOGA | Q7q6l5 anopheles g |
| 305 | 32 | 64.0 | 362 | 2 | Q6NIT4_CORDI | Q6nit4 corynebacte | 378 | 32 | 64.0 | 723 | 2 | Q4QE35_LEIMA | Q4qe35 leishmania |
| 306 | 32 | 64.0 | 366 | 1 | RUVB_RHOA | Q7upg4 rhodopirell | 379 | 32 | 64.0 | 723 | 2 | Q8C2W6_MOUSE | Q8c2w6 mus musculu |
| 307 | 32 | 64.0 | 372 | 2 | Q8FRK5_COREF | Q8frk5 corynebacte | 380 | 32 | 64.0 | 751 | 2 | Q74ZL3_ASHGO | Q74z13 ashbya goss |
| 308 | 32 | 64.0 | 383 | 2 | Q6EDK4_9PASS | Q6edk4 phleippita | 381 | 32 | 64.0 | 761 | 1 | TLB2_BRARE | Q13166 brachydanio |
| 309 | 32 | 64.0 | 384 | 2 | Q6EDJ1_9PASS | Q6edj1 psarisomus | 382 | 32 | 64.0 | 764 | 1 | TLB3_RAT | Q91133 rattus norv |
| 310 | 32 | 64.0 | 384 | 2 | Q6EDM4_9PASS | Q6edm4 neodrepanis | 383 | 32 | 64.0 | 764 | 2 | Q6PRX3_HUMAN | Q6prx3 homo sapien |
| 311 | 32 | 64.0 | 384 | 2 | Q6EDT0_9PASS | Q6edt0 conopopaga | 384 | 32 | 64.0 | 767 | 2 | Q6PRX2_HUMAN | Q6prx2 homo sapien |
| 312 | 32 | 64.0 | 386 | 2 | Q49617_ARATH | Q49617 arabidopsis | 385 | 32 | 64.0 | 767 | 2 | Q6PI57_HUMAN | Q6pi57 homo sapien |
| 313 | 32 | 64.0 | 387 | 2 | Q9SHD8_ARATH | Q9shd8 arabidopsis | 386 | 32 | 64.0 | 771 | 1 | TLB3_MOUSE | Q08122 mus musculu |
| 314 | 32 | 64.0 | 393 | 2 | Q87990_BORBR | Q87990 bordetella | 387 | 32 | 64.0 | 771 | 2 | Q98TH2_BRARE | Q98th2 brachydanio |
| 315 | 32 | 64.0 | 393 | 2 | Q7W251_BORPA | Q7w251 bordetella | 388 | 32 | 64.0 | 772 | 1 | TLB3_HUMAN | Q04726 homo sapien |
| 316 | 32 | 64.0 | 393 | 2 | Q69T30_ORYSA | Q69t30 oryza sativ | 389 | 32 | 64.0 | 782 | 2 | Q6PFP0_MOUSE | Q6pfp0 mus musculu |
| 317 | 32 | 64.0 | 396 | 2 | Q4N2G5_THPGA | Q4n2g5 theileria p | 390 | 32 | 64.0 | 783 | 2 | Q839N9_ENTFA | Q839n9 enterococcu |
| 318 | 32 | 64.0 | 400 | 2 | Q4RRB9_TETNG | Q4rrb9 tetraodon n | 391 | 32 | 64.0 | 787 | 2 | Q7PKS6_ANOGA | Q7pks6 anopheles g |
| 319 | 32 | 64.0 | 405 | 2 | Q7ZWG0_BRARE | Q7zwg0 brachydanio | 392 | 32 | 64.0 | 796 | 2 | Q86NX5_DROME | Q86nx5 drosophila |
| 320 | 32 | 64.0 | 410 | 2 | Q7TNP9_MOUSE | Q7tnp9 mus musculu | 393 | 32 | 64.0 | 808 | 2 | Q7PUW3_ANOGA | Q7puw3 anopheles g |
| 321 | 32 | 64.0 | 416 | 2 | Q4SPX1_TETNG | Q4spx1 tetraodon n | 394 | 32 | 64.0 | 808 | 2 | Q8T5K1_ANOGA | Q8t5k1 anopheles g |
| 322 | 32 | 64.0 | 417 | 2 | Q6HAD5_9ENTR | Q6had5 serratia en | 395 | 32 | 64.0 | 819 | 2 | Q21127_CABEL | Q21127 caenorhabdi |
| 323 | 32 | 64.0 | 420 | 2 | Q9X8Q9_STRCO | Q9x8q9 streptomyc | 396 | 32 | 64.0 | 822 | 2 | Q8IQN2_DROME | Q8iqn2 drosophila |

| | | | | | | | | | | | | | | | | | |
|-----|----|------|------|---|--------|-------|--------|--------------|-----|------|------|------|---|--------|--------|--------|--------------|
| 397 | 32 | 64.0 | 826 | 2 | Q96VU6 | SACCA | Q96VU6 | saccharomyc | 470 | 32 | 64.0 | 1520 | 2 | Q7KBE9 | DROME | Q7KBE9 | drosoophila |
| 398 | 32 | 64.0 | 828 | 2 | Q5B691 | EMENI | Q5B691 | aspergillus | 471 | 32 | 64.0 | 1530 | 2 | Q4ZHU4 | _SSTAP | Q4ZHU4 | staphylococ |
| 399 | 32 | 64.0 | 831 | 2 | Q3BEPI | HUMAN | Q3BEPI | homo sapien | 472 | 32 | 64.0 | 1556 | 2 | Q06554 | YEAST | Q06554 | saccharomyc |
| 400 | 32 | 64.0 | 831 | 2 | Q53EPT | HUMAN | Q53EPT | homo sapien | 473 | 32 | 64.0 | 1558 | 2 | Q06B70 | DEBHA | Q06B70 | debaromyce |
| 401 | 32 | 64.0 | 831 | 2 | Q53X12 | HUMAN | Q53X12 | homo sapien | 474 | 32 | 64.0 | 1576 | 2 | Q01GI3 | CAEBR | Q01GI3 | caenorhabdi |
| 402 | 32 | 64.0 | 831 | 2 | Q0AVM5 | XENLA | Q0AVM5 | xenopus lae | 475 | 32 | 64.0 | 1582 | 2 | Q4Q3H2 | LEIMA | Q4Q3H2 | leishmania |
| 403 | 32 | 64.0 | 832 | 2 | Q6NXX6 | MOUSE | Q6NXX6 | mus musculus | 476 | 32 | 64.0 | 1584 | 1 | UN104 | CAEEL | UN104 | caenorhabdi |
| 404 | 32 | 64.0 | 837 | 1 | VPP1 | HUMAN | Q93050 | h. vacuolar | 477 | 32 | 64.0 | 1594 | 2 | Q55C25 | DICDI | Q55C25 | dictyosteli |
| 405 | 32 | 64.0 | 837 | 1 | VPP1 | PONPY | Q54222 | pongo pygma | 478 | 32 | 64.0 | 1597 | 2 | Q4S0K7 | TETNG | Q4S0K7 | tetraodon n |
| 406 | 32 | 64.0 | 837 | 2 | Q5R5X1 | PONPY | Q5R5X1 | pongo pygma | 479 | 32 | 64.0 | 1598 | 2 | Q60RK8 | CAEBR | Q60RK8 | caenorhabdi |
| 407 | 32 | 64.0 | 837 | 2 | Q5R6N4 | PONPY | Q5R6N4 | pongo pygma | 480 | 32 | 64.0 | 1649 | 2 | Q60K37 | CAEBR | Q60K37 | caenorhabdi |
| 408 | 32 | 64.0 | 838 | 1 | VPP1 | BOVIN | Q29466 | b. vacuolar | 481 | 32 | 64.0 | 1655 | 1 | NU188 | YEAST | NU188 | yeast |
| 409 | 32 | 64.0 | 838 | 1 | VPP1 | RAT | P25286 | r. vacuolar | 482 | 32 | 64.0 | 1716 | 2 | Q99MS7 | MOUSE | Q99MS7 | mus musculus |
| 410 | 32 | 64.0 | 838 | 2 | Q5CZH6 | HUMAN | Q5CZH6 | homo sapien | 483 | 32 | 64.0 | 1742 | 2 | Q5AVP0 | EMENI | Q5AVP0 | aspergillus |
| 411 | 32 | 64.0 | 838 | 2 | Q5I8D0 | CHICK | Q5I8D0 | gallus gall | 484 | 32 | 64.0 | 1766 | 2 | Q4N0J2 | THEPA | Q4N0J2 | theileria p |
| 412 | 32 | 64.0 | 839 | 1 | VPP1 | MOUSE | Q9Z194 | m. vacuolar | 485 | 32 | 64.0 | 1784 | 2 | Q9VES4 | DROME | Q9VES4 | drosoophila |
| 413 | 32 | 64.0 | 859 | 2 | Q9Y2J4 | HUMAN | Q9Y2J4 | homo sapien | 486 | 32 | 64.0 | 1868 | 2 | Q9V7Y0 | DROME | Q9V7Y0 | drosoophila |
| 414 | 32 | 64.0 | 859 | 2 | Q9VUV1 | DROME | Q9VUV1 | drosoophila | 487 | 32 | 64.0 | 1905 | 1 | TAGB | DICDI | TAGB | dictyosteli |
| 415 | 32 | 64.0 | 871 | 2 | Q6CQJ3 | KLULA | Q6CQJ3 | kluyveromyc | 488 | 32 | 64.0 | 1906 | 2 | Q54M83 | DICDI | Q54M83 | dictyosteli |
| 416 | 32 | 64.0 | 871 | 2 | Q99J97 | MOUSE | Q99J97 | mus musculus | 489 | 32 | 64.0 | 1972 | 1 | TF53B | HUMAN | TF53B | homo sapien |
| 417 | 32 | 64.0 | 882 | 2 | Q8MQK2 | DROME | Q8MQK2 | drosoophila | 490 | 32 | 64.0 | 1977 | 1 | Q7Z3U4 | HUMAN | Q7Z3U4 | homo sapien |
| 418 | 32 | 64.0 | 885 | 1 | CHB | SERMA | Q54468 | serratia ma | 491 | 32 | 64.0 | 1984 | 2 | Q4LE46 | HUMAN | Q4LE46 | homo sapien |
| 419 | 32 | 64.0 | 885 | 2 | Q9ZN69 | 9ENTR | Q9ZN69 | enterobacte | 492 | 32 | 64.0 | 2035 | 1 | HCFC1 | HUMAN | HCFC1 | h. host cell |
| 420 | 32 | 64.0 | 889 | 2 | Q4SJ77 | TETNG | Q4SJ77 | tetraodon n | 493 | 32 | 64.0 | 2045 | 1 | HCFC1 | MOUSE | HCFC1 | m. host cell |
| 421 | 32 | 64.0 | 897 | 2 | Q80TC1 | MOUSE | Q80TC1 | mus musculus | 494 | 32 | 64.0 | 2090 | 1 | HCFC1 | MESAU | HCFC1 | m. host cell |
| 422 | 32 | 64.0 | 925 | 2 | Q757X5 | ASHGO | Q757X5 | ashbya goss | 495 | 32 | 64.0 | 3117 | 2 | Q8WY20 | HUMAN | Q8WY20 | homo sapien |
| 423 | 32 | 64.0 | 925 | 2 | Q4UC26 | THEAN | Q4UC26 | theileria a | 496 | 32 | 64.0 | 3117 | 2 | Q5VT06 | HUMAN | Q5VT06 | homo sapien |
| 424 | 32 | 64.0 | 942 | 1 | PKL1 | HUMAN | Q16512 | homo sapien | 497 | 32 | 64.0 | 3278 | 2 | Q4ZHU0 | STAHY | Q4ZHU0 | staphylococ |
| 425 | 32 | 64.0 | 942 | 2 | Q10UV5 | HUMAN | Q81UV5 | homo sapien | 498 | 32 | 64.0 | 5560 | 1 | SPEN | DROME | SPEN | drosoophila |
| 426 | 32 | 64.0 | 943 | 2 | Q02824 | DROME | Q02824 | drosoophila | 499 | 31.5 | 63.0 | 127 | 2 | Q51VM3 | MAGGR | Q51VM3 | magnaporthe |
| 427 | 32 | 64.0 | 950 | 1 | URB1 | USTMA | P40349 | ustilago ma | 500 | 31.5 | 63.0 | 135 | 2 | Q9PAD7 | XYLFA | Q9PAD7 | xyella fas |
| 428 | 32 | 64.0 | 952 | 2 | Q7YU88 | DROME | Q7YU88 | drosoophila | 501 | 31.5 | 63.0 | 1051 | 2 | Q41EP9 | GIBZE | Q41EP9 | gibberella |
| 429 | 32 | 64.0 | 982 | 2 | Q54PH6 | DICDI | Q54PH6 | dictyosteli | 502 | 31 | 62.0 | 30 | 2 | Q7LIF4 | YEAST | Q7LIF4 | saccharomyc |
| 430 | 32 | 64.0 | 1001 | 1 | YON1 | SCHPO | Q9Y824 | schizosacch | 503 | 31 | 62.0 | 53 | 2 | Q9BMS2 | PLAFA | Q9BMS2 | plasmodium |
| 431 | 32 | 64.0 | 1006 | 2 | Q6MRK6 | DROME | Q6MRK6 | drosoophila | 504 | 31 | 62.0 | 59 | 2 | Q7PZ06 | ANOAG | Q7PZ06 | anopheles g |
| 432 | 32 | 64.0 | 1010 | 2 | Q9GNT4 | LEIMA | Q9GNT4 | leishmania | 505 | 31 | 62.0 | 63 | 2 | Q8VT57 | STRMU | Q8VT57 | streptococ |
| 433 | 32 | 64.0 | 1017 | 2 | Q54VU5 | DICDI | Q54VU5 | dictyosteli | 506 | 31 | 62.0 | 90 | 2 | Q8XK2 | CAEEL | Q8XK2 | caenorhabdi |
| 434 | 32 | 64.0 | 1026 | 2 | Q5TH93 | HUMAN | Q5TH93 | homo sapien | 507 | 31 | 62.0 | 100 | 2 | Q8EM67 | OCEIH | Q8EM67 | oceanobacil |
| 435 | 32 | 64.0 | 1026 | 2 | Q86V48 | HUMAN | Q86V48 | homo sapien | 508 | 31 | 62.0 | 101 | 2 | Q5CDD0 | CRYHO | Q5CDD0 | cryptospori |
| 436 | 32 | 64.0 | 1029 | 2 | Q6NRK0 | XENLA | Q6NRK0 | xenopus lae | 509 | 31 | 62.0 | 104 | 2 | Q01569 | CAEEL | Q01569 | caenorhabdi |
| 437 | 32 | 64.0 | 1034 | 2 | Q9W3X2 | DROME | Q9W3X2 | drosoophila | 510 | 31 | 62.0 | 109 | 2 | Q9N0W5 | RABIT | Q9N0W5 | oryctolagus |
| 438 | 32 | 64.0 | 1038 | 2 | Q54MW3 | DICDI | Q54MW3 | dictyosteli | 511 | 31 | 62.0 | 110 | 2 | Q6FAU0 | ACIAD | Q6FAU0 | acinetobact |
| 439 | 32 | 64.0 | 1046 | 2 | Q8TEH1 | HUMAN | Q8TEH1 | homo sapien | 512 | 31 | 62.0 | 111 | 2 | Q8T518 | PLAFA | Q8T518 | plasmodium |
| 440 | 32 | 64.0 | 1084 | 2 | Q4PPR3 | USTMA | Q4PPR3 | ustilago ma | 513 | 31 | 62.0 | 113 | 2 | Q6CTC5 | KLULA | Q6CTC5 | kluyveromyc |
| 441 | 32 | 64.0 | 1084 | 2 | Q86A87 | DICDI | Q86A87 | dictyosteli | 514 | 31 | 62.0 | 116 | 2 | Q59LJ3 | CANAL | Q59LJ3 | candida alb |
| 442 | 32 | 64.0 | 1087 | 2 | Q9BMG3 | LEIDO | Q9BMG3 | leishmania | 515 | 31 | 62.0 | 116 | 2 | Q95W60 | PLAFA | Q95W60 | plasmodium |
| 443 | 32 | 64.0 | 1099 | 2 | Q4Q0J9 | LEIMA | Q4Q0J9 | leishmania | 516 | 31 | 62.0 | 120 | 2 | Q59LJ0 | CANAL | Q59LJ0 | candida alb |
| 444 | 32 | 64.0 | 1111 | 2 | Q6CON0 | YARLI | Q6CON0 | yarrowia li | 517 | 31 | 62.0 | 122 | 2 | Q77193 | PLAFA | Q77193 | plasmodium |
| 445 | 32 | 64.0 | 1112 | 2 | Q55V8 | DICDI | Q55V8 | dictyosteli | 518 | 31 | 62.0 | 125 | 2 | Q86R66 | PLAFA | Q86R66 | plasmodium |
| 446 | 32 | 64.0 | 1114 | 2 | Q4SVU4 | TETNG | Q4SVU4 | tetraodon n | 519 | 31 | 62.0 | 127 | 2 | Q9HSR1 | HALSA | Q9HSR1 | halobacteri |
| 447 | 32 | 64.0 | 1115 | 2 | Q9C5K1 | ARATH | Q9C5K1 | arabidopsis | 520 | 31 | 62.0 | 127 | 2 | Q8T586 | PLAFA | Q8T586 | plasmodium |
| 448 | 32 | 64.0 | 1116 | 2 | Q9FPT1 | ARATH | Q9FPT1 | arabidopsis | 521 | 31 | 62.0 | 130 | 2 | Q9XZ88 | PLAFA | Q9XZ88 | plasmodium |
| 449 | 32 | 64.0 | 1126 | 2 | Q9FG10 | ARATH | Q9FG10 | arabidopsis | 522 | 31 | 62.0 | 131 | 2 | Q86822 | PLAFA | Q86822 | plasmodium |
| 450 | 32 | 64.0 | 1139 | 2 | Q54Z39 | DICDI | Q54Z39 | dictyosteli | 523 | 31 | 62.0 | 132 | 2 | Q6ZV53 | HUMAN | Q6ZV53 | homo sapien |
| 451 | 32 | 64.0 | 1163 | 2 | Q84714 | CHLTR | Q84714 | chlamydia t | 524 | 31 | 62.0 | 133 | 2 | Q6PIM9 | HUMAN | Q6PIM9 | homo sapien |
| 452 | 32 | 64.0 | 1181 | 2 | Q9PLJ6 | CHLMU | Q9PLJ6 | chlamydia m | 525 | 31 | 62.0 | 137 | 2 | Q8FRB5 | COREF | Q8FRB5 | corynebacte |
| 453 | 32 | 64.0 | 1188 | 2 | Q57Z65 | 9TRYP | Q57Z65 | trypanosoma | 526 | 31 | 62.0 | 139 | 2 | Q7Z222 | PLAFA | Q7Z222 | plasmodium |
| 454 | 32 | 64.0 | 1259 | 2 | Q9W061 | DROME | Q9W061 | drosoophila | 527 | 31 | 62.0 | 141 | 2 | Q4ZMU4 | PSESY | Q4ZMU4 | pseudomonas |
| 455 | 32 | 64.0 | 1261 | 2 | Q96685 | DROME | Q96685 | drosoophila | 528 | 31 | 62.0 | 143 | 2 | Q9XZ87 | PLAFA | Q9XZ87 | plasmodium |
| 456 | 32 | 64.0 | 1280 | 2 | Q95RC8 | DROME | Q95RC8 | drosoophila | 529 | 31 | 62.0 | 144 | 2 | Q5A5U3 | CANAL | Q5A5U3 | candida alb |
| 457 | 32 | 64.0 | 1307 | 2 | Q8GY37 | ARATH | Q8GY37 | arabidopsis | 530 | 31 | 62.0 | 144 | 2 | Q9H657 | HUMAN | Q9H657 | homo sapien |
| 458 | 32 | 64.0 | 1307 | 2 | Q9S710 | ARATH | Q9S710 | arabidopsis | 531 | 31 | 62.0 | 147 | 2 | Q6S8Q9 | PLAFA | Q6S8Q9 | plasmodium |
| 459 | 32 | 64.0 | 1327 | 2 | Q51VX4 | MAGGR | Q51VX4 | magnaporthe | 532 | 31 | 62.0 | 151 | 2 | Q6S827 | PLAFA | Q6S827 | plasmodium |
| 460 | 32 | 64.0 | 1402 | 2 | Q7KREB | DROME | Q7KREB | drosoophila | 533 | 31 | 62.0 | 153 | 2 | Q69YW1 | HUMAN | Q69YW1 | homo sapien |
| 461 | 32 | 64.0 | 1420 | 1 | SGN2 | YEAST | P38931 | saccharomyc | 534 | 31 | 62.0 | 156 | 2 | Q9VB41 | DROME | Q9VB41 | drosoophila |
| 462 | 32 | 64.0 | 1423 | 2 | Q754I4 | ASHGO | Q754I4 | ashbya goss | 535 | 31 | 62.0 | 157 | 2 | Q5BAW8 | EMENI | Q5BAW8 | aspergillus |
| 463 | 32 | 64.0 | 1431 | 1 | H8XAP | HUMAN | Q95T23 | homo sapien | 536 | 31 | 62.0 | 157 | 2 | Q5JZB7 | HUMAN | Q5JZB7 | homo sapien |
| 464 | 32 | 64.0 | 1450 | 1 | SUREJ | STRPU | Q86227 | strongyloce | 537 | 31 | 62.0 | 157 | 2 | Q47853 | ENTAG | Q47853 | enterobacte |
| 465 | 32 | 64.0 | 1465 | 2 | Q8C0Q1 | MOUSE | Q8C0Q1 | mus musculus | 538 | 31 | 62.0 | 157 | 2 | Q47853 | ENTAG | Q47853 | enterobacte |
| 466 | 32 | 64.0 | 1467 | 2 | Q4T699 | TETNG | Q4T699 | tetraodon n | 539 | 31 | 62.0 | 159 | 2 | Q47853 | ENTAG | Q47853 | enterobacte |
| 467 | 32 | 64.0 | 1491 | 2 | Q8VI43 | RAT | Q8VI43 | rattus norv | 540 | 31 | 62.0 | 161 | 2 | Q5CQ16 | CRYPV | Q5CQ16 | cryptospori |
| 468 | 32 | 64.0 | 1508 | 2 | Q7QWD3 | GIALA | Q7QWD3 | giardia lam | 541 | 31 | 62.0 | 166 | 2 | Q52559 | AMYMD | Q52559 | amycolatops |
| 469 | 32 | 64.0 | 1516 | 2 | Q61ZP0 | CAEBR | Q61ZP0 | caenorhabdi | 542 | 31 | 62.0 | 169 | 1 | RGS2 | _CAEEL | RGS2 | caenorhabdi |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|---------------|---------------------|-----|----|------|-----|---|--------------|--------------------|
| 543 | 31 | 62.0 | 169 | 2 | Q8L1K2_ORYSA | Q8L1K2 oryza sativ | 616 | 31 | 62.0 | 323 | 2 | Q77LY8_9NUCL | Q77LY8 helicoverpa |
| 544 | 31 | 62.0 | 172 | 2 | Q78C16_NEURCP | Q78C16 neurospora | 617 | 31 | 62.0 | 323 | 2 | Q99H22_9NUCL | Q99H22 helicoverpa |
| 545 | 31 | 62.0 | 174 | 2 | Q9M6L2_SORBI | Q9M6L2 sorghum bic | 618 | 31 | 62.0 | 327 | 2 | Q5SWC6_HUMAN | Q5SWC6 homo sapien |
| 546 | 31 | 62.0 | 175 | 2 | Q45UD5_TETNG | Q45UD5 tetraodon n | 619 | 31 | 62.0 | 328 | 2 | Q55FS3_DICDI | Q55FS3 dictyosteli |
| 547 | 31 | 62.0 | 181 | 2 | Q9TVK0_CAEEL | Q9TVK0 caenorhabdi | 620 | 31 | 62.0 | 329 | 2 | Q4PC67_USTMA | Q4PC67 usilago ma |
| 548 | 31 | 62.0 | 182 | 2 | Q6REQ6_9NOCA | Q6REQ6 rhodococcus | 621 | 31 | 62.0 | 330 | 2 | Q89QS3_BRAJA | Q89QS3 bradyrhizob |
| 549 | 31 | 62.0 | 183 | 2 | Q75WN4_RHOSR | Q75WN4 rhodococcus | 622 | 31 | 62.0 | 333 | 2 | Q9U8W4_EPTBU | Q9U8W4 eptaretus |
| 550 | 31 | 62.0 | 184 | 2 | Q9U7K2_PLAFA | Q9U7K2 plasmodium | 623 | 31 | 62.0 | 335 | 2 | Q615B5_ORYSA | Q615B5 oryza sativ |
| 551 | 31 | 62.0 | 184 | 2 | Q4QH60_LEIMA | Q4QH60 leishmania | 624 | 31 | 62.0 | 338 | 2 | Q7RZT6_NEURC | Q7RZT6 neurospora |
| 552 | 31 | 62.0 | 188 | 2 | Q5ST14_BRACM | Q5ST14 brassica ca | 625 | 31 | 62.0 | 338 | 2 | Q7S603_NEURC | Q7S603 neurospora |
| 553 | 31 | 62.0 | 196 | 2 | Q9C9M6_ARATH | Q9C9M6 arabidopsis | 626 | 31 | 62.0 | 339 | 2 | Q75FY2_LEPIC | Q75FY2 leptospira |
| 554 | 31 | 62.0 | 197 | 2 | Q54K69_DICDI | Q54K69 dictyosteli | 627 | 31 | 62.0 | 339 | 2 | Q8EX24_LAPIN | Q8EX24 leptospira |
| 555 | 31 | 62.0 | 199 | 1 | ULI4_VZVD | P09295 varicella-z | 628 | 31 | 62.0 | 347 | 2 | Q9ES19_RAT | Q9ES19 rattus norv |
| 556 | 31 | 62.0 | 199 | 2 | Q6QCL0_HV3 | Q6QCL0 human herpe | 629 | 31 | 62.0 | 349 | 1 | ATF4_MOUSE | ATF4 mus musculu |
| 557 | 31 | 62.0 | 200 | 2 | Q5XZ39_BORGA | Q5XZ39 borrelia ga | 630 | 31 | 62.0 | 349 | 2 | Q5U4B2_MOUSE | Q5U4B2 mus musculu |
| 558 | 31 | 62.0 | 202 | 1 | CD3E_FELCA | Q51R11 felis silve | 631 | 31 | 62.0 | 350 | 2 | Q8CF69_MOUSE | Q8CF69 mus musculu |
| 559 | 31 | 62.0 | 211 | 2 | Q41G77_GIBZE | Q41G77 gibberella | 632 | 31 | 62.0 | 355 | 2 | Q8ZJ49_YERPE | Q8ZJ49 yersinia pe |
| 560 | 31 | 62.0 | 214 | 2 | Q5R8V5_PONPY | Q5R8V5 pongo pygma | 633 | 31 | 62.0 | 355 | 2 | Q66FKC_YERPS | Q66FKC yersinia ps |
| 561 | 31 | 62.0 | 215 | 1 | VIF_HVZNZ | P05901 human immun | 634 | 31 | 62.0 | 356 | 2 | Q8D1F9_YERPE | Q8D1F9 yersinia pe |
| 562 | 31 | 62.0 | 216 | 2 | Q6ZDW4_ORYSA | Q6ZDW4 oryza sativ | 635 | 31 | 62.0 | 359 | 2 | Q8D1F9_YERPE | Q8D1F9 yersinia pe |
| 563 | 31 | 62.0 | 216 | 2 | Q7Y047_ORYSA | Q7Y047 oryza sativ | 636 | 31 | 62.0 | 370 | 2 | Q921X0_MOUSE | Q921X0 mus musculu |
| 564 | 31 | 62.0 | 218 | 2 | Q9LS09_ARATH | Q9LS09 arabidopsis | 637 | 31 | 62.0 | 371 | 2 | Q5YKX8_NOCFA | Q5YKX8 nocardia fa |
| 565 | 31 | 62.0 | 219 | 2 | Q7SAM3_NEURC | Q7SAM3 neurospora | 638 | 31 | 62.0 | 373 | 2 | Q8T8S0_DROME | Q8T8S0 drosophila |
| 566 | 31 | 62.0 | 223 | 2 | Q73WX8_MYCPA | Q73WX8 mycobacteri | 639 | 31 | 62.0 | 373 | 2 | Q9V686_DROME | Q9V686 drosophila |
| 567 | 31 | 62.0 | 226 | 2 | Q4NIE6_9MTC | Q4NIE6 arthrobacte | 640 | 31 | 62.0 | 374 | 2 | Q4LHH4_9BURK | Q4LHH4 burkholderi |
| 568 | 31 | 62.0 | 227 | 2 | Q4GZ97_9TRYP | Q4GZ97 trypanosoma | 641 | 31 | 62.0 | 380 | 2 | Q7QNF2_ANOGA | Q7QNF2 anopheles g |
| 569 | 31 | 62.0 | 230 | 2 | Q5P6D9_AZOSE | Q5P6D9 azoarcus sp | 642 | 31 | 62.0 | 381 | 2 | Q61328_MOUSE | Q61328 mus musculu |
| 570 | 31 | 62.0 | 242 | 2 | Q6FUN4_CANGA | Q6FUN4 candida gla | 643 | 31 | 62.0 | 381 | 2 | Q63095_RAT | Q63095 rattus norv |
| 571 | 31 | 62.0 | 247 | 2 | Q5JZB8_HUMAN | Q5JZB8 homo sapien | 644 | 31 | 62.0 | 388 | 2 | Q51FU0_ENTHI | Q51FU0 antamoeba h |
| 572 | 31 | 62.0 | 253 | 2 | Q4HC11_9DEIO | Q4HC11 deinococcus | 645 | 31 | 62.0 | 388 | 2 | Q4SXX3_TETNG | Q4SXX3 tetraodon n |
| 573 | 31 | 62.0 | 258 | 1 | SPIN2_HUMAN | Q9BP22 homo sapien | 646 | 31 | 62.0 | 390 | 2 | Q9FW03_ARATH | Q9FW03 arabidopsis |
| 574 | 31 | 62.0 | 258 | 1 | SPIN2_PONPY | Q9BP22 pongo pygma | 647 | 31 | 62.0 | 392 | 2 | Q9VFY2_DROME | Q9VFY2 drosophila |
| 575 | 31 | 62.0 | 259 | 1 | SPIN3_HUMAN | Q99865 homo sapien | 648 | 31 | 62.0 | 396 | 2 | Q75824_HUMAN | Q75824 homo sapien |
| 576 | 31 | 62.0 | 259 | 2 | Q9U7K1_PLAFA | Q9U7K1 plasmodium | 649 | 31 | 62.0 | 398 | 2 | Q4R914_MACFA | Q4R914 macaca fasc |
| 577 | 31 | 62.0 | 260 | 2 | Q7XCM6_ORYSA | Q7XCM6 oryza sativ | 650 | 31 | 62.0 | 404 | 2 | Q7QRV2_GIALA | Q7QRV2 giardia lam |
| 578 | 31 | 62.0 | 260 | 2 | Q7FRJ7_ORYSA | Q7FRJ7 oryza sativ | 651 | 31 | 62.0 | 406 | 2 | Q8RMI1_PETHY | Q8RMI1 petunia hyb |
| 579 | 31 | 62.0 | 263 | 2 | Q7QCC4_EIMTE | Q7QCC4 eimeria ten | 652 | 31 | 62.0 | 408 | 2 | Q4N219_THEPA | Q4N219 theileria p |
| 580 | 31 | 62.0 | 263 | 2 | Q794G7_MOUSE | Q794G7 mus musculu | 653 | 31 | 62.0 | 411 | 2 | Q5AY67_ENEMI | Q5AY67 aspergillus |
| 581 | 31 | 62.0 | 264 | 2 | Q4WD12_ASPPU | Q4WD12 aspergillus | 654 | 31 | 62.0 | 413 | 2 | Q5Z9H6_ORYSA | Q5Z9H6 oryza sativ |
| 582 | 31 | 62.0 | 265 | 2 | Q8C6H2_MOUSE | Q8C6H2 mus musculu | 655 | 31 | 62.0 | 417 | 1 | SOXC_RHOSG | SOXC rhodococcus |
| 583 | 31 | 62.0 | 266 | 2 | Q7TFSA_RHOM6 | Q7TFSA rhesus cyto | 656 | 31 | 62.0 | 417 | 2 | Q86LZ4_DICDI | Q86LZ4 dictyosteli |
| 584 | 31 | 62.0 | 267 | 2 | Q91966_ORENI | Q91966 oreochromis | 657 | 31 | 62.0 | 417 | 2 | Q84F40_NOCGL | Q84F40 nocardia gl |
| 585 | 31 | 62.0 | 268 | 2 | Q7QCCD2_EIMTE | Q7QCCD2 eimeria ten | 658 | 31 | 62.0 | 417 | 2 | Q64F46_9ACTO | Q64F46 gordonia al |
| 586 | 31 | 62.0 | 268 | 2 | Q82CQ4_STRAW | Q82CQ4 streptomyce | 659 | 31 | 62.0 | 417 | 2 | Q56G99_9RHIZ | Q56G99 agrobacteri |
| 587 | 31 | 62.0 | 270 | 2 | Q7QCD3_EIMTE | Q7QCD3 eimeria ten | 660 | 31 | 62.0 | 417 | 2 | Q6WNP1_9NOCA | Q6WNP1 rhodococcus |
| 588 | 31 | 62.0 | 270 | 2 | Q6P7R6_RAT | Q6P7R6 rattus norv | 661 | 31 | 62.0 | 417 | 2 | Q7WZT8_RHOER | Q7WZT8 rhodococcus |
| 589 | 31 | 62.0 | 271 | 2 | Q52E22_MAGGR | Q52E22 magnaporthe | 662 | 31 | 62.0 | 417 | 2 | Q5U772_9NOCA | Q5U772 rhodococcus |
| 590 | 31 | 62.0 | 271 | 2 | Q6L5F0_ORYSA | Q6L5F0 oryza sativ | 663 | 31 | 62.0 | 417 | 2 | Q64F43_RHOER | Q64F43 rhodococcus |
| 591 | 31 | 62.0 | 271 | 2 | Q6R993_MAIZE | Q6R993 zea mays (m | 664 | 31 | 62.0 | 417 | 2 | Q7QWTO_9NOCA | Q7QWTO rhodococcus |
| 592 | 31 | 62.0 | 277 | 1 | J11_HCMVA | P09711 human cytom | 665 | 31 | 62.0 | 417 | 2 | Q4PPA1_BREBE | Q4PPA1 brevibacill |
| 593 | 31 | 62.0 | 278 | 2 | Q5SWC8_HUMAN | Q5SWC8 homo sapien | 666 | 31 | 62.0 | 417 | 2 | Q4PPA7_ACIDE | Q4PPA7 acidovorax |
| 594 | 31 | 62.0 | 280 | 2 | Q6NU74_XENLA | Q6NU74 xenopus lae | 667 | 31 | 62.0 | 418 | 2 | Q61IM1_DROME | Q61IM1 drosophila |
| 595 | 31 | 62.0 | 282 | 2 | Q7PEY9_ANOGA | Q7PEY9 anopheles g | 668 | 31 | 62.0 | 426 | 2 | Q7PZG2_ANOGA | Q7PZG2 anopheles g |
| 596 | 31 | 62.0 | 282 | 2 | Q818P9_ANOGA | Q818P9 anopheles g | 669 | 31 | 62.0 | 427 | 2 | Q9SEZ9_ARATH | Q9SEZ9 arabidopsis |
| 597 | 31 | 62.0 | 282 | 2 | Q48628_PRUAR | Q48628 prunus arme | 670 | 31 | 62.0 | 429 | 2 | Q5ZBJO_ORYSA | Q5ZBJO oryza sativ |
| 598 | 31 | 62.0 | 282 | 2 | Q61688_MOUSE | Q61688 mus musculu | 671 | 31 | 62.0 | 429 | 2 | Q6D2U9_ERWCT | Q6D2U9 erwinia car |
| 599 | 31 | 62.0 | 283 | 2 | Q5QMC1_ORYSA | Q5QMC1 oryza sativ | 672 | 31 | 62.0 | 431 | 2 | Q4U9V1_THEAN | Q4U9V1 theileria a |
| 600 | 31 | 62.0 | 286 | 2 | Q57WB3_9TRYP | Q57WB3 trypanosoma | 673 | 31 | 62.0 | 431 | 2 | Q9X116_CAEEL | Q9X116 caenorhabdi |
| 601 | 31 | 62.0 | 288 | 2 | Q51CNC_9FLAO | Q51CNC chryseobact | 674 | 31 | 62.0 | 445 | 2 | Q5SES5_DICDI | Q5SES5 dictyosteli |
| 602 | 31 | 62.0 | 296 | 2 | P90333_PRANA | P90333 praomys nat | 675 | 31 | 62.0 | 447 | 1 | GASR_HUMAN | GASR homo sapien |
| 603 | 31 | 62.0 | 297 | 1 | YMY9_YEAST | Q03161 saccharomyc | 676 | 31 | 62.0 | 447 | 1 | Q16144_HUMAN | Q16144 homo sapien |
| 604 | 31 | 62.0 | 302 | 1 | Q4LGG1_9BURK | Q4LGG1 burkholderi | 677 | 31 | 62.0 | 447 | 2 | Q92492_HUMAN | Q92492 homo sapien |
| 605 | 31 | 62.0 | 303 | 1 | GP49A_MOUSE | Q61450 mus musculu | 678 | 31 | 62.0 | 447 | 2 | Q5NVG7_PONPY | Q5NVG7 pongo pygma |
| 606 | 31 | 62.0 | 303 | 2 | Q642G5_RAT | Q642G6 rattus norv | 679 | 31 | 62.0 | 450 | 1 | GASR_PRANA | GASR praomys nat |
| 607 | 31 | 62.0 | 303 | 2 | Q549E3_MOUSE | Q549E3 mus musculu | 680 | 31 | 62.0 | 450 | 2 | Q4QB08_LEIMA | Q4QB08 leishmania |
| 608 | 31 | 62.0 | 307 | 2 | Q4XRA7_PLACH | Q4XRA7 plasmodium | 681 | 31 | 62.0 | 450 | 2 | P89005_PRANA | P89005 praomys nat |
| 609 | 31 | 62.0 | 309 | 1 | YLZ9_CAEEL | P34414 caenorhabdi | 682 | 31 | 62.0 | 451 | 2 | Q5NBF4_ORYSA | Q5NBF4 oryza sativ |
| 610 | 31 | 62.0 | 311 | 2 | Q5CYX3_CRYPV | Q5CYX3 cryptospori | 683 | 31 | 62.0 | 451 | 2 | Q8BX13_MOUSE | Q8BX13 mus musculu |
| 611 | 31 | 62.0 | 316 | 2 | P89000_PRANA | P89000 praomys nat | 684 | 31 | 62.0 | 452 | 1 | Q8BX13_MOUSE | Q8BX13 mus musculu |
| 612 | 31 | 62.0 | 319 | 2 | Q8TL90_METAC | Q8TL90 methanosarc | 685 | 31 | 62.0 | 452 | 1 | GASR_RAT | GASR rattus norv |
| 613 | 31 | 62.0 | 321 | 1 | PGUB_BOVIN | P79119 bos taurus | 686 | 31 | 62.0 | 452 | 1 | GASR_CANFA | GASR canis famill |
| 614 | 31 | 62.0 | 322 | 1 | Q7YTC2_SACKO | Q7YTC2 saccoglouse | 687 | 31 | 62.0 | 453 | 1 | GASR_MOUSE | GASR mus musculu |
| 615 | 31 | 62.0 | 323 | 2 | Q77K94_9NUCL | Q77K94 helicoverpa | 688 | 31 | 62.0 | 453 | 2 | Q8BKf6_MOUSE | Q8BKf6 mus musculu |

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|-----|----|------|-----|---|--------------|--------|--------------|
| 689 | 31 | 62.0 | 454 | 1 | GASR_BOVIN | P79266 | bos taurus |
| 690 | 31 | 62.0 | 454 | 2 | Q8AYG3_RAT | Q6ayg3 | rattus norv |
| 691 | 31 | 62.0 | 455 | 1 | DHX15_STRPU | O17438 | strongyloce |
| 692 | 31 | 62.0 | 460 | 2 | Q6P2P0_HUMAN | Q6p2p0 | homo sapien |
| 693 | 31 | 62.0 | 461 | 2 | Q5F4C3_CHICK | Q5fc43 | gallus gall |
| 694 | 31 | 62.0 | 467 | 1 | HSLU_STAPQ | Q8cph0 | staphylococ |
| 695 | 31 | 62.0 | 467 | 1 | HSLU_STABQ | Q5hpt8 | staphylococ |
| 696 | 31 | 62.0 | 469 | 2 | QZV74_BRARE | Q7zv74 | brachydanio |
| 697 | 31 | 62.0 | 476 | 1 | REN3A_HUMAN | Q9hlj1 | homo sapien |
| 698 | 31 | 62.0 | 477 | 2 | Q9S8M2_BRAJA | Q89sm2 | bradyrhizob |
| 699 | 31 | 62.0 | 480 | 2 | Q6U5H3_ROSCH | Q6u5h3 | rosa hybrid |
| 700 | 31 | 62.0 | 483 | 2 | Q9ZW36_ARATH | Q9zw36 | arabidopsis |
| 701 | 31 | 62.0 | 488 | 2 | Q91GT6_HVH8 | Q91gt6 | human herpe |
| 702 | 31 | 62.0 | 489 | 2 | Q91GT7_HVH8 | Q91gt7 | human herpe |
| 703 | 31 | 62.0 | 489 | 2 | Q91GT8_HVH8 | Q91gt8 | human herpe |
| 704 | 31 | 62.0 | 489 | 2 | Q91GT4_HVH8 | Q91gt4 | human herpe |
| 705 | 31 | 62.0 | 489 | 2 | Q91GT5_HVH8 | Q91gt5 | human herpe |
| 706 | 31 | 62.0 | 489 | 2 | Q91GT6_HVH8 | Q91gt6 | human herpe |
| 707 | 31 | 62.0 | 489 | 2 | Q91GT7_HVH8 | Q91gt7 | human herpe |
| 708 | 31 | 62.0 | 489 | 2 | Q91GT8_HVH8 | Q91gt8 | human herpe |
| 709 | 31 | 62.0 | 489 | 2 | Q9Q69_HVH8 | Q9qr69 | human herpe |
| 710 | 31 | 62.0 | 489 | 2 | Q9WNA8_HVH8 | Q9wna8 | human herpe |
| 711 | 31 | 62.0 | 490 | 2 | Q6OS68_CAEBR | Q6os68 | caenorhabdi |
| 712 | 31 | 62.0 | 490 | 2 | Q7QFC7_ANOGA | Q7qfc7 | anopheles g |
| 713 | 31 | 62.0 | 490 | 2 | Q83NC8_ORYSA | Q5nc8 | oryza sativ |
| 714 | 31 | 62.0 | 492 | 2 | Q9XK15_CAEBL | Q9xx15 | caenorhabdi |
| 715 | 31 | 62.0 | 493 | 1 | OC90_HUMAN | Q2509 | homo sapien |
| 716 | 31 | 62.0 | 493 | 2 | Q7QYQ7_GIALA | Q7qyq7 | giardia lam |
| 717 | 31 | 62.0 | 495 | 2 | Q7Q126_9HIV1 | Q7q126 | human immun |
| 718 | 31 | 62.0 | 496 | 2 | Q8UB83_ARATH | Q8au83 | arabidopsis |
| 719 | 31 | 62.0 | 501 | 2 | Q9XEE7_ARATH | Q9xee7 | arabidopsis |
| 720 | 31 | 62.0 | 503 | 2 | Q9SL44_ORYSA | Q691a4 | oryza sativ |
| 721 | 31 | 62.0 | 508 | 2 | Q5SSC2_CRYNE | Q5sec2 | cryptococcu |
| 722 | 31 | 62.0 | 508 | 2 | Q5KGR9_CRYNE | Q5kgr9 | cryptococcu |
| 723 | 31 | 62.0 | 508 | 2 | Q6TGV8_BRARE | Q6tgv8 | brachydanio |
| 724 | 31 | 62.0 | 509 | 1 | AVT5_YEAST | P38176 | saccharomyc |
| 725 | 31 | 62.0 | 509 | 2 | Q8BZK3_DEBHA | Q6bzk3 | debaromyce |
| 726 | 31 | 62.0 | 509 | 2 | Q6GVH3_CHICK | Q6gvh3 | gallus gall |
| 727 | 31 | 62.0 | 515 | 2 | Q5SSJ6_HUMAN | Q5ssj6 | homo sapien |
| 728 | 31 | 62.0 | 516 | 2 | Q96LC6_HUMAN | Q96lc6 | homo sapien |
| 729 | 31 | 62.0 | 516 | 2 | Q9H647_HUMAN | Q9h647 | homo sapien |
| 730 | 31 | 62.0 | 516 | 2 | Q9NYK7_HUMAN | Q9nyk7 | homo sapien |
| 731 | 31 | 62.0 | 516 | 2 | Q45133_CAEBL | Q45133 | caenorhabdi |
| 732 | 31 | 62.0 | 516 | 2 | Q8C911_MOUSE | Q8c911 | mus musculus |
| 733 | 31 | 62.0 | 518 | 1 | MSFD2_MOUSE | Q9cwp6 | mus musculus |
| 734 | 31 | 62.0 | 524 | 2 | Q5JPN5_HUMAN | Q5jpn5 | homo sapien |
| 735 | 31 | 62.0 | 527 | 2 | Q52F89_MAGGR | Q52f89 | magnaporthe |
| 736 | 31 | 62.0 | 528 | 2 | Q92PR1_RHIME | Q92pr1 | rhizobium m |
| 737 | 31 | 62.0 | 530 | 1 | MATP_HUMAN | Q9umx9 | homo sapien |
| 738 | 31 | 62.0 | 531 | 2 | Q5B8P7_EMENI | Q5b8p7 | aspergillus |
| 739 | 31 | 62.0 | 532 | 2 | Q55T77_CRYNE | Q55t77 | cryptococcu |
| 740 | 31 | 62.0 | 532 | 2 | Q8CEL7_MOUSE | Q8cel7 | mus musculus |
| 741 | 31 | 62.0 | 539 | 1 | P4H42_CAEBL | Q20065 | caenorhabdi |
| 742 | 31 | 62.0 | 541 | 2 | Q4WGH5_ASPFU | Q4wgh9 | aspergillus |
| 743 | 31 | 62.0 | 546 | 2 | Q418E2_GIBZE | Q418e2 | gibberella |
| 744 | 31 | 62.0 | 547 | 2 | Q7SE72_NEUCR | Q7se72 | neurospora |
| 745 | 31 | 62.0 | 548 | 2 | Q82A20_STRAW | Q82a20 | streptomyce |
| 746 | 31 | 62.0 | 551 | 2 | Q7SAI6_NEUCR | Q7sai6 | brachydanio |
| 747 | 31 | 62.0 | 551 | 2 | Q4V9P4_BRARE | Q4v9p4 | brachydanio |
| 748 | 31 | 62.0 | 553 | 2 | Q5SSJ5_HUMAN | Q5ssj5 | homo sapien |
| 749 | 31 | 62.0 | 553 | 2 | Q8BT17_MOUSE | Q8bt17 | mus musculus |
| 750 | 31 | 62.0 | 554 | 2 | Q9UHY0_HUMAN | Q9uhy0 | homo sapien |
| 751 | 31 | 62.0 | 554 | 2 | Q8VE06_MOUSE | Q8ve06 | mus musculus |
| 752 | 31 | 62.0 | 554 | 2 | Q9DB11_MOUSE | Q9db11 | mus musculus |
| 753 | 31 | 62.0 | 556 | 2 | Q9FFK3_ARATH | Q9ffk3 | arabidopsis |
| 754 | 31 | 62.0 | 558 | 2 | Q4CQH4_HUMAN | Q4cqh4 | homo sapien |
| 755 | 31 | 62.0 | 559 | 2 | Q8CCT6_RUTRU | Q5cct6 | rutilus rut |
| 756 | 31 | 62.0 | 560 | 2 | Q5XXP1_9TELE | Q5xxp1 | pinephales |
| 757 | 31 | 62.0 | 564 | 2 | Q90WV1_CARAU | Q90wv1 | carassius a |
| 758 | 31 | 62.0 | 565 | 2 | Q5NKI4_9TELE | Q5nki4 | andidia ba |
| 759 | 31 | 62.0 | 567 | 2 | Q4MPW2_BACCE | Q4mpw2 | bacillus ce |
| 760 | 31 | 62.0 | 567 | 2 | Q73EW1_BACCI | Q73ew1 | bacillus ce |
| 761 | 31 | 62.0 | 568 | 2 | Q4T9T3_TETNG | Q4t9t3 | tetraodon n |

| | | | | | | | |
|-----|----|------|-----|---|------------------|--------|--------------|
| 762 | 31 | 62.0 | 578 | 2 | Q5GH23_HUMAN | Q5gh23 | homo sapien |
| 763 | 31 | 62.0 | 579 | 1 | YTHD2_HUMAN | Q9ysa9 | homo sapien |
| 764 | 31 | 62.0 | 579 | 2 | Q5VSZ9_HUMAN | Q5vsz9 | homo sapien |
| 765 | 31 | 62.0 | 579 | 2 | Q4R5D9_MACFA | Q4r5d9 | macaca fasc |
| 766 | 31 | 62.0 | 579 | 2 | Q8K325_MOUSE | Q8k325 | mus musculus |
| 767 | 31 | 62.0 | 579 | 2 | Q91Y77_MOUSE | Q91yt7 | m high gluc |
| 768 | 31 | 62.0 | 585 | 2 | Q4PDT1_USTWA | Q4pdt1 | ustilago ma |
| 769 | 31 | 62.0 | 587 | 2 | Q528Y5_MAGGR | Q528y5 | magnaporthe |
| 770 | 31 | 62.0 | 587 | 2 | Q8MZV0_HALCO | Q8mzv0 | halictis co |
| 771 | 31 | 62.0 | 588 | 2 | Q8COM4_MOUSE | Q8com4 | mus musculus |
| 772 | 31 | 62.0 | 591 | 2 | Q5KJ64_CRYNE | Q5kj64 | cryptococcu |
| 773 | 31 | 62.0 | 591 | 2 | Q18627_CAEBL | Q18627 | caenorhabdi |
| 774 | 31 | 62.0 | 594 | 2 | Q8DBG4_MOUSE | Q8dbg4 | mus musculus |
| 775 | 31 | 62.0 | 594 | 2 | Q8BMB6_MOUSE | Q8bmb6 | mus musculus |
| 776 | 31 | 62.0 | 594 | 2 | Q9EQI9_MOUSE | Q9eqi9 | mus musculus |
| 777 | 31 | 62.0 | 594 | 2 | Q8BHG8_MOUSE | Q8bhg8 | m mus muscu |
| 778 | 31 | 62.0 | 596 | 2 | Q52GA7_MAGGR | Q52ga7 | magnaporthe |
| 779 | 31 | 62.0 | 597 | 2 | Q7X914_ORYSA | Q7x914 | oryza sativ |
| 780 | 31 | 62.0 | 597 | 2 | Q8R0V3_MOUSE | Q8rov3 | mus musculus |
| 781 | 31 | 62.0 | 598 | 2 | Q5RE01_PONPY | Q5re01 | pongo pygma |
| 782 | 31 | 62.0 | 599 | 2 | Q5KQ81_CRYPTOC | Q5kq81 | cryptococcu |
| 783 | 31 | 62.0 | 599 | 2 | Q9P216_GVXN | Q9p216 | xestia c-ni |
| 784 | 31 | 62.0 | 601 | 2 | Q6FU91_CANGA | Q6fu91 | candida gla |
| 785 | 31 | 62.0 | 603 | 2 | Q89234_PPARA | Q89234 | human parai |
| 786 | 31 | 62.0 | 604 | 2 | Q4ZNX9_PSESY | Q4znx9 | pseudomonas |
| 787 | 31 | 62.0 | 607 | 2 | Q7FA04_ORYSA | Q7fa04 | oryza sativ |
| 788 | 31 | 62.0 | 610 | 2 | Q8NB00_HUMAN | Q8nb00 | homo sapien |
| 789 | 31 | 62.0 | 613 | 2 | Q4P856_USTWA | Q4p856 | ustilago ma |
| 790 | 31 | 62.0 | 620 | 2 | Q19807_CAEBL | Q19807 | caenorhabdi |
| 791 | 31 | 62.0 | 623 | 2 | Q27560_DICDI | Q27560 | dictyosteli |
| 792 | 31 | 62.0 | 623 | 2 | Q7YSW8_DICDI | Q7ysw8 | dictyosteli |
| 793 | 31 | 62.0 | 624 | 2 | Q4SMS4_TETNG | Q4sms4 | tetraodon n |
| 794 | 31 | 62.0 | 634 | 2 | Q4H210_CIOIN | Q4h210 | ciona intes |
| 795 | 31 | 62.0 | 635 | 2 | Q53RS3_HUMAN | Q53rs3 | homo sapien |
| 796 | 31 | 62.0 | 636 | 2 | Q7Z1D2_PLACH | Q7z1d2 | plasmodium |
| 797 | 31 | 62.0 | 640 | 2 | Q8BQ19_MOUSE | Q8bq19 | mus musculus |
| 798 | 31 | 62.0 | 643 | 1 | VP40_ERV2 | P52369 | equine herp |
| 799 | 31 | 62.0 | 644 | 2 | Q8WZX0_NEUCR | Q8wzx0 | neurospora |
| 800 | 31 | 62.0 | 647 | 2 | Q9P469_NEUCR | Q9p469 | neurospora |
| 801 | 31 | 62.0 | 648 | 2 | Q45038_SCHJA | Q45038 | schistosoma |
| 802 | 31 | 62.0 | 649 | 2 | Q9V884_ROME | Q9v884 | drosophila |
| 803 | 31 | 62.0 | 652 | 2 | Q85056_ATKINONEL | Q85056 | atkinsonell |
| 804 | 31 | 62.0 | 661 | 2 | Q21394_CAEBL | Q21394 | caenorhabdi |
| 805 | 31 | 62.0 | 678 | 2 | Q8Z025_ANASP | Q8z025 | anabaena sp |
| 806 | 31 | 62.0 | 680 | 2 | Q4YNV2_PLABE | Q4ynv2 | plasmodium |
| 807 | 31 | 62.0 | 697 | 2 | Q5AWA8_EMENI | Q5awa8 | aspergillus |
| 808 | 31 | 62.0 | 700 | 2 | Q8NIU2_NEUCR | Q8niu2 | neurospora |
| 809 | 31 | 62.0 | 702 | 2 | Q95215_CAEBL | Q95215 | caenorhabdi |
| 810 | 31 | 62.0 | 703 | 2 | Q98650_9VIRU | Q98650 | rice tungro |
| 811 | 31 | 62.0 | 704 | 2 | Q5AH44_CANAL | Q5ah44 | candida alb |
| 812 | 31 | 62.0 | 718 | 1 | CBK1_KLULA | P31034 | kluyveromyc |
| 813 | 31 | 62.0 | 718 | 2 | Q5JPN6_HUMAN | Q5jpn6 | homo sapien |
| 814 | 31 | 62.0 | 718 | 2 | Q8HXH0_MACFA | Q8hxo0 | macaca fasc |
| 815 | 31 | 62.0 | 720 | 2 | Q59P39_CANAL | Q59p39 | candida alb |
| 816 | 31 | 62.0 | 720 | 2 | Q6TLM5_AERHY | Q6tlm5 | aeromonas h |
| 817 | 31 | 62.0 | 724 | 2 | Q8LP12_CAPAN | Q8lp12 | capsicum an |
| 818 | 31 | 62.0 | 724 | 2 | Q93XM4_CAPAN | Q93xm4 | capsicum an |
| 819 | 31 | 62.0 | 726 | 2 | Q9LZQ9_ARATH | Q9lzh9 | arabidopsis |
| 820 | 31 | 62.0 | 728 | 2 | Q05812_YEAST | Q05812 | saccharomyc |
| 821 | 31 | 62.0 | 729 | 1 | DHX15_ARATH | Q28899 | arabidopsis |
| 822 | 31 | 62.0 | 732 | 2 | Q5L1X1_MAGGR | Q5l1x1 | magnaporthe |
| 823 | 31 | 62.0 | 737 | 2 | Q861X1_DICDI | Q86ix1 | dictyosteli |
| 824 | 31 | 62.0 | 747 | 1 | GR1PE_RAT | Q50007 | rattus norv |
| 825 | 31 | 62.0 | 751 | 2 | Q68AN0_PSOFE | Q68an0 | psophocarpu |
| 826 | 31 | 62.0 | 756 | 2 | Q5UMW7_CRYNE | Q5umw7 | cryptococcu |
| 827 | 31 | 62.0 | 756 | 2 | Q5KHR7_CRYNE | Q5khr7 | cryptococcu |
| 828 | 31 | 62.0 | 757 | 2 | Q23501_CAEBL | Q23501 | caenorhabdi |
| 829 | 31 | 62.0 | 757 | 2 | Q6VXA8_ORYSA | Q6vxa8 | oryza sativ |
| 830 | 31 | 62.0 | 759 | 2 | Q6CCF1_YARLI | Q6ccf1 | yarrowia li |
| 831 | 31 | 62.0 | 764 | 2 | Q68B10_9APIC | Q68b10 | plasmodium |
| 832 | 31 | 62.0 | 764 | 2 | Q60QM4_CAEBR | Q60qm4 | caenorhabdi |
| 833 | 31 | 62.0 | 768 | 2 | Q6CI00_YARLI | Q6ci00 | yarrowia li |
| 834 | 31 | 62.0 | 769 | 2 | Q50TW0_ENTHI | Q50tw0 | entamoeba h |

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|-----|----|------|------|---|----------------|--------------------|-----|----|------|------|---|----------------|--------------------|
| 835 | 31 | 62.0 | 771 | 2 | Q54IN8_DICTDI | Q54IN8 dictyosteli | 908 | 31 | 62.0 | 1153 | 2 | Q8MQW5_DROME | Q8mqw5 drosophila |
| 836 | 31 | 62.0 | 771 | 2 | Q87LW2_VIBPA | Q87lw2 vibrio para | 909 | 31 | 62.0 | 1170 | 2 | Q16587_CAEBL | Q16587 caenorhabdi |
| 837 | 31 | 62.0 | 776 | 2 | Q41BX2_GIBZE | Q41bx2 gibberella | 910 | 31 | 62.0 | 1189 | 2 | Q95R60_DROME | Q95r60 drosophila |
| 838 | 31 | 62.0 | 780 | 2 | Q794H1_ANOGA | Q794h1 anopheles g | 911 | 31 | 62.0 | 1189 | 2 | Q9V7N3_DROME | Q9v7n3 drosophila |
| 839 | 31 | 62.0 | 783 | 2 | Q51UX6_MAGGR | Q51ux6 magnaporthe | 912 | 31 | 62.0 | 1192 | 2 | Q81KU3_PLAF7 | Q81ku3 plasmodium |
| 840 | 31 | 62.0 | 829 | 2 | Q60H58_BRARE | Q60h58 brachydanio | 913 | 31 | 62.0 | 1199 | 2 | Q56301_9BETA | Q56301 human herpe |
| 841 | 31 | 62.0 | 834 | 2 | Q9VE75_DROME | Q9ve75 drosophila | 914 | 31 | 62.0 | 1212 | 2 | Q86AF2_DICTDI | Q86af2 dictyosteli |
| 842 | 31 | 62.0 | 843 | 2 | Q7RBH9_PLAYO | Q7rbh9 plasmodium | 915 | 31 | 62.0 | 1213 | 1 | SMRC2_MOUSE | Q86dg5 mus musculu |
| 843 | 31 | 62.0 | 852 | 2 | Q96QU3_HUMAN | Q96qu3 homo sapien | 916 | 31 | 62.0 | 1220 | 2 | Q5A319_CANAL | Q5a319 candida alb |
| 844 | 31 | 62.0 | 853 | 2 | Q96RS0_HUMAN | Q96rs0 homo sapien | 917 | 31 | 62.0 | 1246 | 2 | Q12276_YEAST | Q12276 saccharomyc |
| 845 | 31 | 62.0 | 853 | 2 | Q8RTD9_HUMAN | Q8rtd9 homo sapien | 918 | 31 | 62.0 | 1256 | 2 | Q54RH9_DICTDI | Q54rh9 dictyosteli |
| 846 | 31 | 62.0 | 857 | 1 | APPL1_SCHPO | Q9p7e8 schizosacch | 919 | 31 | 62.0 | 1259 | 2 | Q7KT76_DROME | Q7kt76 drosophila |
| 847 | 31 | 62.0 | 867 | 2 | Q7XPL3_ORYSA | Q7xp13 oryza sativ | 920 | 31 | 62.0 | 1262 | 2 | Q60988_DROME | Q60988 mus musculu |
| 848 | 31 | 62.0 | 874 | 2 | Q60H57_BRACHD | Q60h57 brachydanio | 921 | 31 | 62.0 | 1288 | 2 | Q75522_ASHGO | Q75522 ashbya goss |
| 849 | 31 | 62.0 | 890 | 1 | KI20A_HUMAN | Q55235 homo sapien | 922 | 31 | 62.0 | 1300 | 2 | Q8MLP1_DROME | Q8mlp1 drosophila |
| 850 | 31 | 62.0 | 893 | 2 | Q68D55_HUMAN | Q68d55 homo sapien | 923 | 31 | 62.0 | 1338 | 2 | Q9V416_DROME | Q9v416 drosophila |
| 851 | 31 | 62.0 | 905 | 1 | VPP1_CAEL | Q30628 caenorhabdi | 924 | 31 | 62.0 | 1342 | 2 | Q7YZB2_DROME | Q7yzb2 drosophila |
| 852 | 31 | 62.0 | 905 | 2 | Q6CN39_KULUA | Q6cn39 kluyveromyc | 925 | 31 | 62.0 | 1342 | 2 | Q59E61_DROME | Q59e61 drosophila |
| 853 | 31 | 62.0 | 911 | 2 | Q5ALR7_CANAL | Q5alr7 candida alb | 926 | 31 | 62.0 | 1344 | 2 | Q7QBK8_ANOGA | Q7qb8 anopheles g |
| 854 | 31 | 62.0 | 914 | 1 | AZF1_YEAST | P41696 saccharomyc | 927 | 31 | 62.0 | 1355 | 2 | Q8T6G6_DICTDI | Q8t6g6 dictyosteli |
| 855 | 31 | 62.0 | 915 | 2 | Q4QL82_HAB18 | Q4ql82 haemophilus | 928 | 31 | 62.0 | 1359 | 2 | Q5B1R6_EMENI | Q5b1r6 aspergillus |
| 856 | 31 | 62.0 | 923 | 2 | Q5AM66_CANAL | Q5am66 candida alb | 929 | 31 | 62.0 | 1385 | 2 | Q81R66_DICTDI | Q81r6 dictyosteli |
| 857 | 31 | 62.0 | 928 | 2 | Q5U4A1_XENLA | Q5u4a1 xenopus lae | 930 | 31 | 62.0 | 1399 | 2 | Q6CUN4_KULUA | Q6cun4 kluyveromyc |
| 858 | 31 | 62.0 | 929 | 1 | PCDGP_HUMAN | Q9y5g1 homo sapien | 931 | 31 | 62.0 | 1423 | 2 | Q4QIK1_LEIMA | Q4qik1 leishmania |
| 859 | 31 | 62.0 | 936 | 2 | Q99N13_MOUSE | Q99n13 mus musculu | 932 | 31 | 62.0 | 1431 | 2 | Q7TPJ1_RAT | Q7tpj1 rattus norv |
| 860 | 31 | 62.0 | 942 | 2 | Q96611_DICTDI | Q96611 dictyosteli | 933 | 31 | 62.0 | 1449 | 2 | Q9ZVFO_ARATH | Q9zvfo arabidopsis |
| 861 | 31 | 62.0 | 942 | 2 | Q80VK7_MOUSE | Q80vk7 mus musculu | 934 | 31 | 62.0 | 1451 | 2 | Q8IM56_PLAF7 | Q8im56 plasmodium |
| 862 | 31 | 62.0 | 945 | 2 | Q6X8F1_ORYSA | Q6x8f1 oryza sativ | 935 | 31 | 62.0 | 1505 | 2 | Q54VU4_DICTDI | Q54vu4 dictyosteli |
| 863 | 31 | 62.0 | 945 | 2 | Q948G6_ORYSA | Q948g6 oryza sativ | 936 | 31 | 62.0 | 1520 | 2 | Q55E24_DICTDI | Q55e24 dictyosteli |
| 864 | 31 | 62.0 | 945 | 2 | Q9FLM6_ARATH | Q9flm6 arabidopsis | 937 | 31 | 62.0 | 1537 | 2 | Q9VAI2_DROME | Q9vai2 drosophila |
| 865 | 31 | 62.0 | 947 | 2 | Q52522_NOCFA | Q52522 nocardia fa | 938 | 31 | 62.0 | 1538 | 2 | Q6QU66_DROME | Q6qu66 drosophila |
| 866 | 31 | 62.0 | 948 | 2 | Q60H60_BRARE | Q60h60 brachydanio | 939 | 31 | 62.0 | 1551 | 2 | Q8IS13_DICTDI | Q8is13 dictyosteli |
| 867 | 31 | 62.0 | 948 | 2 | Q59222_BRARE | Q59222 brachydanio | 940 | 31 | 62.0 | 1557 | 2 | Q44FF3_DICTDI | Q44ff3 dictyosteli |
| 868 | 31 | 62.0 | 951 | 2 | Q61BY2_CAEBR | Q61by2 caenorhabdi | 941 | 31 | 62.0 | 1561 | 2 | Q55X03_CRYNE | Q55x03 cryptococcu |
| 869 | 31 | 62.0 | 957 | 2 | Q7PQN4_ANOGA | Q7pqn4 anopheles g | 942 | 31 | 62.0 | 1568 | 2 | Q16858_MICPR | Q16858 microciona |
| 870 | 31 | 62.0 | 963 | 2 | Q5XQP8_9SACH | Q5xqp8 saccharomyc | 943 | 31 | 62.0 | 1597 | 2 | Q6DUR4_RAT | Q6dur4 rattus norv |
| 871 | 31 | 62.0 | 964 | 2 | Q8NFP1_HUMAN | Q8nfp1 homo sapien | 944 | 31 | 62.0 | 1608 | 2 | Q5KMX9_CRYNE | Q5kmx9 cryptococcu |
| 872 | 31 | 62.0 | 966 | 2 | Q7PAP6_RICCN | Q7pap6 corynebacte | 945 | 31 | 62.0 | 1608 | 2 | Q95VA5_DROYA | Q95va5 drosophila |
| 873 | 31 | 62.0 | 966 | 2 | Q92JC3_RICCN | Q92jc3 rickettsia | 946 | 31 | 62.0 | 1608 | 2 | Q54VR7_DICTDI | Q54vr7 dictyosteli |
| 874 | 31 | 62.0 | 966 | 2 | Q60H59_BRARE | Q60h59 brachydanio | 947 | 31 | 62.0 | 1638 | 2 | Q6A049_MOUSE | Q6a049 mus musculu |
| 875 | 31 | 62.0 | 967 | 2 | Q4RM23_TETNG | Q4rm23 tetradon n | 948 | 31 | 62.0 | 1644 | 2 | Q41LG3_GIBZE | Q41lg3 gibberella |
| 876 | 31 | 62.0 | 971 | 1 | GMIP_MOUSE | Q6p9g2 mus musculu | 949 | 31 | 62.0 | 1674 | 2 | Q61L95_CAEBR | Q61l95 caenorhabdi |
| 877 | 31 | 62.0 | 971 | 2 | Q6M621_CORGL | Q6m621 corynebacte | 950 | 31 | 62.0 | 1703 | 2 | Q9W179_DROSOPH | Q9w179 drosophila |
| 878 | 31 | 62.0 | 978 | 2 | Q4Q463_LEIMA | Q4q463 leishmania | 951 | 31 | 62.0 | 1761 | 2 | Q54RR9_DICTDI | Q54rr9 dictyosteli |
| 879 | 31 | 62.0 | 979 | 2 | Q4WJPI_ASPFU | Q4wjpi aspergillus | 952 | 31 | 62.0 | 1779 | 2 | Q59IU2_SAMCY | Q59iu2 sania cynth |
| 880 | 31 | 62.0 | 983 | 2 | Q8NDX5_HUMAN | Q8ndx5 homo sapien | 953 | 31 | 62.0 | 1799 | 2 | Q9BPP6_SAMCR | Q9bpb6 sania cynth |
| 881 | 31 | 62.0 | 983 | 2 | Q8NFT7_HUMAN | Q8nft7 homo sapien | 954 | 31 | 62.0 | 1784 | 2 | Q9CDB1_MYCLE | Q9cdb1 mycobacteri |
| 882 | 31 | 62.0 | 989 | 1 | PTP3_DICTDI | P54637 dictyosteli | 955 | 31 | 62.0 | 1799 | 2 | Q51GB4_ENTHI | Q51gb4 entamoeba h |
| 883 | 31 | 62.0 | 990 | 2 | Q815C6_PLAF7 | Q815c6 plasmodium | 956 | 31 | 62.0 | 1919 | 2 | Q60293_HUMAN | Q60293 homo sapien |
| 884 | 31 | 62.0 | 990 | 2 | Q54SY3_DICTDI | Q54sy3 dictyosteli | 957 | 31 | 62.0 | 1962 | 2 | Q7S784_NEUCR | Q7s784 neurospora |
| 885 | 31 | 62.0 | 991 | 2 | Q5RG20_BRARE | Q5rg20 brachydanio | 958 | 31 | 62.0 | 1966 | 2 | Q9NHX6_DROME | Q9nhx6 drosophila |
| 886 | 31 | 62.0 | 995 | 1 | FOG1_MOUSE | Q35615 mus musculu | 959 | 31 | 62.0 | 1966 | 2 | Q81Q46_DROME | Q81qa6 drosophila |
| 887 | 31 | 62.0 | 1001 | 2 | Q4F4X8_USTMA | Q4f4x8 ustilago ma | 960 | 31 | 62.0 | 1985 | 2 | Q9VSK5_DROME | Q9vks5 drosophila |
| 888 | 31 | 62.0 | 1004 | 2 | Q9V3H9_DROME | Q9v3h9 drosophila | 961 | 31 | 62.0 | 1985 | 2 | Q8T9N4_DROME | Q8t9n4 drosophila |
| 889 | 31 | 62.0 | 1006 | 2 | Q500Y6_DROME | Q500y6 drosophila | 962 | 31 | 62.0 | 1985 | 2 | Q7KU48_DROME | Q7ku48 drosophila |
| 890 | 31 | 62.0 | 1006 | 1 | DDEF2_HUMAN | Q43150 homo sapien | 963 | 31 | 62.0 | 1986 | 2 | Q4WU47_ASPFU | Q4wu47 aspergillus |
| 891 | 31 | 62.0 | 1014 | 2 | Q510E1_ENTHI | Q510e1 entamoeba h | 964 | 31 | 62.0 | 1988 | 2 | Q86BH2_DROME | Q86bh2 drosophila |
| 892 | 31 | 62.0 | 1026 | 2 | Q55SV8_CRYNE | Q55sv8 cryptococcu | 965 | 31 | 62.0 | 2000 | 2 | Q41WX4_9BURK | Q41wx4 burkholderi |
| 893 | 31 | 62.0 | 1028 | 2 | Q7S6J5_NEUCR | Q7s6j5 neurospora | 966 | 31 | 62.0 | 2035 | 1 | GRIP6_MOUSE | Q6gyp7 mus musculu |
| 894 | 31 | 62.0 | 1047 | 2 | Q4S3H4_TETNG | Q4s3h4 tetradon n | 967 | 31 | 62.0 | 2036 | 1 | GRIP6_HUMAN | Q6gyq0 homo sapien |
| 895 | 31 | 62.0 | 1051 | 2 | Q54QC7_DICTDI | Q54qc7 dictyosteli | 968 | 31 | 62.0 | 2087 | 2 | Q8MXL2_LEIMA | Q8mxl2 leishmania |
| 896 | 31 | 62.0 | 1051 | 2 | Q8RSV1_RAT | Q8rsv1 rattus norv | 969 | 31 | 62.0 | 2123 | 2 | Q59U97_DICTDI | Q59u97 dictyosteli |
| 897 | 31 | 62.0 | 1068 | 2 | Q8R4U7_MOUSE | Q8r4u7 mus musculu | 970 | 31 | 62.0 | 2123 | 2 | Q55P68_DICTDI | Q55p68 dictyosteli |
| 898 | 31 | 62.0 | 1093 | 2 | Q8SD16_9CAUD | Q8sd16 pseudomonas | 971 | 31 | 62.0 | 2162 | 2 | Q81EV1_PLAF7 | Q81ev1 plasmodium |
| 899 | 31 | 62.0 | 1094 | 2 | Q8C7U6_MOUSE | Q8c7u6 mus musculu | 972 | 31 | 62.0 | 2162 | 2 | Q4Q795_LEIMA | Q4q795 leishmania |
| 900 | 31 | 62.0 | 1108 | 2 | Q8T148_DICTDI | Q8t148 dictyosteli | 973 | 31 | 62.0 | 2199 | 2 | Q96296_PLAF7 | Q96296 plasmodium |
| 901 | 31 | 62.0 | 1117 | 2 | Q9VK50_DROME | Q9vk50 drosophila | 974 | 31 | 62.0 | 2207 | 2 | Q81495_PLAF7 | Q81495 plasmodium |
| 902 | 31 | 62.0 | 1121 | 2 | Q9NJ94_DROSOPH | Q9nj94 drosophila | 975 | 31 | 62.0 | 2256 | 2 | Q81515_PLAF7 | Q81515 plasmodium |
| 903 | 31 | 62.0 | 1129 | 2 | Q6P4K6_XENTR | Q6p4k6 xenopus tro | 976 | 31 | 62.0 | 2308 | 2 | Q9W2U7_DROME | Q9w2u7 drosophila |
| 904 | 31 | 62.0 | 1131 | 2 | Q853A4_9CAUD | Q853a4 mycobacteri | 977 | 31 | 62.0 | 2351 | 2 | Q9VT00_DROME | Q9vt00 drosophila |
| 905 | 31 | 62.0 | 1134 | 2 | Q4EPK7_USTMA | Q4epk7 ustilago ma | 978 | 31 | 62.0 | 2368 | 2 | Q4S4K5_TETNG | Q4s4k5 tetradon n |
| 906 | 31 | 62.0 | 1138 | 2 | Q95VA3_DROYA | Q95va3 drosophila | 979 | 31 | 62.0 | 2405 | 2 | Q5T1R5_HUMAN | Q5t1r5 homo sapien |
| 907 | 31 | 62.0 | 1153 | 2 | Q756W8_ASHGO | Q756w8 ashbya goss | 980 | 31 | 62.0 | 2406 | 2 | Q9BZS0_HUMAN | Q9bzs0 homo sapien |

981 31 62.0 2406 2 Q5TLR4 homo sapien
 982 31 62.0 2414 2 Q9HCL7 homo sapien
 983 31 62.0 2429 2 Q5BB54 aspergillus
 984 31 62.0 2475 2 Q4WN65 aspergillus
 985 31 62.0 2813 2 Q8WXQ6 homo sapien
 986 31 62.0 2813 2 Q96JP6 homo sapien
 987 31 62.0 2817 2 Q96P79 homo sapien
 988 31 62.0 3005 1 ZFH2_DROME
 989 31 62.0 3018 2 Q81KQ6 PLAF7
 990 31 62.0 3147 2 Q4RXM3 TETNG
 991 31 62.0 3149 1 TRGU_EBV
 992 31 62.0 3149 2 Q777G4 9GAMA
 993 31 62.0 3160 1 FREM2_MOUSE
 994 31 62.0 3169 1 FREM2_HUMAN
 995 31 62.0 3179 2 Q8V2A4 9GAMA
 996 31 62.0 3210 2 Q6C216 YARLI
 997 31 62.0 3471 1 POLG_RTSVT
 998 31 62.0 3712 1 ACVS_CEPAC
 999 31 62.0 3812 2 Q4RLC8 TETNG
 1000 31 62.0 3888 2 Q51X35 magnaporthe

ALIGNMENTS

RESULT 1
 Q4H3K9_CIOIN PRELIMINARY; PRT; 655 AA.
 AC Q4H3K9;
 DT 13-SEP-2005 (TRENBLrel. 31, Created)
 DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
 DE Transcription factor protein.
 GN Name=Ci-ets/pointed1;
 OS Ciona intestinalis.
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
 OC Phlebobranchia; Cionidae; Ciona.
 OX NCBI_TaxID=7719;
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15269171; DOI=10.1242/dev.01270;
 RA Imai K.S., Hino K., Yagi K., Satoh N., Satou Y.;
 RT "Genomewide surveys of developmentally relevant genes in Ciona
 intestinalis.";
 RL Development 131:4047-4058(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=12736827; DOI=10.1007/s00427-003-0330-z;
 RA Satou Y., Satoh N.;
 RT "Genomewide surveys of developmentally relevant genes in Ciona
 intestinalis.";
 RL Dev. Genes Evol. 213:211-212(2003).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Satou Y.;
 RT "Expressed genes in Ciona intestinalis.";
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB210413; BAE06418.1; -; mRNA.
 SQ SEQUENCE 655 AA; 72268 MW; 9959DDB73E0D61B7 CRC64;

Query Match 82.0%; Score 41; DB 2; Length 655;
 Best Local Similarity 88.9%; Pred. No. 59;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSNEDPPT 9
 |||||
 Db 268 QOSNEMPT 276

RESULT 2
 KV3H_MOUSE
 ID KV3H_MOUSE STANDARD; PRT; 111 AA.
 AC P01660;

DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig kappa chain V-III region PC 3741/TEPC 111.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP PROTEIN SEQUENCE (PC 3741).
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatnaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 diversity.";
 RL Nature 276:785-790(1978).
 RN [2]
 RP PROTEIN SEQUENCE (TEPC 111).
 RX MEDLINE=79012520; PubMed=99744;
 RA McKean D.J., Bell M., Potter M.;
 RT "Mechanisms of antibody diversity: multiple genes encode structurally
 related mouse kappa variable regions.";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
 CC -1- MISCELLANEOUS: The PC 3741 and TEPC 111 sequences are identical.
 CC -----
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 CC -----
 CC PIR; A93204; KVM537.
 DR HSSP; P01665; 1QNZ.
 DR Ensembl; ENSMUSG0000060064; Mus musculus.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; Ig-Like; 1.
 DR Direct protein sequencing; Immunoglobulin domain;
 KW Immunoglobulin V region.
 FT REGION 1 23 Framework-1.
 FT REGION 24 38 Complementarity-determining-1.
 FT REGION 39 53 Framework-2.
 FT REGION 54 60 Complementarity-determining-2.
 FT REGION 61 92 Framework-3.
 FT REGION 93 101 Complementarity-determining-3.
 FT REGION 102 111 Framework-4.
 FT DISULFID 23 92 By similarity.
 FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;
 Query Match 80.0%; Score 40; DB 1; Length 111;
 Best Local Similarity 88.9%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 QOSNEDPPT 9
 |||||
 Db 93 QOSNEDPPT 101
 RESULT 3
 KV3L_MOUSE
 ID KV3L_MOUSE STANDARD; PRT; 111 AA.
 AC P01664;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig kappa chain V-III region CBPC 101.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;


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Db          92 QQSNEDPYT 100

RESULT 6
KV3M_MOUSE
ID_KV3M_MOUSE STANDARD; PRT; 111 AA.
AC P01655;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE IG kappa chain V-III region PC 7043.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 10-99.
RX MEDLINE=94003207; PubMed=7691608;
RA Mo J.A., Bona C.A., Holmdahl R.;
RT "Variable region gene selection of immunoglobulin G-expressing B cells
RT with specificity for a defined epitope on type II collagen.";
RL Eur. J. Immunol. 23:2503-2510(1993).
RN [3]
RP STRUCTURE BY NMR OF 1-111.
RX MEDLINE=20264305; PubMed=10801487; DOI=10.1016/S0969-2126(00)00119-2;
RA Tugarinov V., Zvi A., Levy R., Hayek Y., Matsushita S., Anglister J.;
RT "NMR structure of an anti-gp120 antibody complex with a V3 peptide
RT reveals a surface important for co-receptor binding.";
RL Structure 8:385-395(2000).
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; Z25444; CRA80931.1; -; mRNA.
DR EMBL; Z25446; CRA80933.1; -; mRNA.
DR EMBL; Z25448; CRA80935.1; -; mRNA.
DR EMBL; Z25450; CRA80937.1; -; mRNA.
DR EMBL; Z25452; CRA80939.1; -; mRNA.
DR EMBL; Z25454; CRA80941.1; -; mRNA.
DR EMBL; Z25458; CRA80945.1; -; mRNA.
DR PIR; A01937; KVM543.
DR PDB; 1QNZ; NMR; L=1-111.
DR Ensembl; ENSMUSG00000053225; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 38
FT REGION 39 53
FT REGION 54 60
FT REGION 61 92
FT REGION 93 101
FT REGION 102 111
FT DISULFID 23 92
FT NON_TER 111
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;
Query Match 78.0%; Score 39; DB 1; Length 111;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          1 QQSNEDPPT 9
Db          93 QQSNEDPPT 101

RESULT 7
KV3Q_MOUSE
ID_KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01667;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE IG kappa chain V-III region PC 6308.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
CC -----
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CC -----
DR PIR; C01937; KVM508.
DR HSSP; P01665; 1QNZ.
DR SMR; P01667; 1-111.
DR Ensembl; ENSMUSG00000053225; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 38
FT REGION 39 53
FT REGION 54 60
FT REGION 61 92
FT REGION 93 101
FT REGION 102 111
FT DISULFID 23 92
FT NON_TER 111
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;
Query Match 78.0%; Score 39; DB 1; Length 111;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          1 QQSNEDPPT 9
Db          93 QQSNEDPPT 101

RESULT 8
KV3Q_MOUSE
ID_KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE IG kappa chain V-III region PC 7769.
OS Mus musculus (Mouse).
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
CC -----
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CC -----
DR EMBL; Z25444; CRA80931.1; -; mRNA.
DR EMBL; Z25446; CRA80933.1; -; mRNA.
DR EMBL; Z25448; CRA80935.1; -; mRNA.
DR EMBL; Z25450; CRA80937.1; -; mRNA.
DR EMBL; Z25452; CRA80939.1; -; mRNA.
DR EMBL; Z25454; CRA80941.1; -; mRNA.
DR EMBL; Z25458; CRA80945.1; -; mRNA.
DR PIR; A01937; KVM543.
DR PDB; 1QNZ; NMR; L=1-111.
DR Ensembl; ENSMUSG00000053225; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 38
FT REGION 39 53
FT REGION 54 60
FT REGION 61 92
FT REGION 93 101
FT REGION 102 111
FT DISULFID 23 92
FT NON_TER 111
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;
Query Match 78.0%; Score 39; DB 1; Length 111;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1] _____
 RP PROTEIN SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity.";
 RL Nature 276:785-790(1978).
 CC -----
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 CC -----
 CC PIR; E01937; KMS59.
 DR HSP; P01665; IQN2.
 DR SMR; P01669; 1-111.
 DR Ensembl; ENSMUSG0000053225; Mus musculus.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin domain;
 KW Immunoglobulin V region.
 FT REGION 1 23
 FT REGION 24 38
 FT REGION 39 53
 FT REGION 54 60
 FT REGION 61 92
 FT REGION 93 101
 FT REGION 102 111
 FT DISULFID 23 92
 FT NON_TER 111 111
 FT SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;
 Query Match 78.0%; Score 39; DB 1; Length 111;
 Best Local Similarity 88.9%; Pred. No. 19;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 QOSNEDPPT 9
 DB 93 QOSNEDPWT 101
 RESULT 9
 Q4Q636 LEIMA
 ID Q4Q636 LEIMA PRELIMINARY; PRT; 380 AA.
 AC Q4Q636;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE 3,2-trans-enoyl-CoA isomerase, mitochondrial, putative
 DE (EC 5.3.3.8).
 GN ORFNames=LmjF31.2250;
 OS Leishmania major.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1] _____
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Friedlin;
 RA Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,
 RA Smith D., Collins M., Foster N., Harris D., Oliver K., O'Neil S.,
 RA Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.;
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CT005268; CAJ08414.1; -; Genomic_DNA.
 KW Isomerase.
 SQ SEQUENCE 380 AA; 42876 MW; 3D7DA5DC8D7B531C CRC64;
 Query Match 78.0%; Score 39; DB 2; Length 380;
 Best Local Similarity 87.5%; Pred. No. 76;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 QOSNEDPPT 8
 DB 11 QASNEDPPT 18
 RESULT 10
 Q5SRZ9 CRYNE
 ID Q5SRZ9 CRYNE PRELIMINARY; PRT; 511 AA.
 AC Q5SRZ9;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=CNEB3830;
 OS Cryptococcus neoformans var. neoformans B-3501A.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
 OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
 OX NCBI_TaxID=283643;
 RN [1] _____
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B-3501A;
 RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
 RA Wickes B.L., Fu J., Davis R.W.;
 RT "Cryptococcus neoformans serotype D sequencing";
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; AA0100028; EAL20462.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 511 AA; 56762 MW; 21468107971233BD CRC64;
 Query Match 78.0%; Score 39; DB 2; Length 511;
 Best Local Similarity 87.5%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 QOSNEDPPT 8
 DB 229 QQFNEDPPT 236
 RESULT 11
 Q5KGF1 CRYNE
 ID Q5KGF1 CRYNE PRELIMINARY; PRT; 511 AA.
 AC Q5KGF1;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Expressed protein.
 GN ORFNames=CNE03840;
 OS Cryptococcus neoformans var. neoformans JEC21.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
 OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
 OX NCBI_TaxID=214684;
 RN [1] _____
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=JEC21;
 RA Loftus B., Amedeo P., Roncaglia P., Vamathevan J., Utterback T.,
 RA Van Aken S., Fraser C.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 RN [2] _____
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=JEC21;
 RX PubMed=15653466; DOI=10.1126/science.1103773;
 RA Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,
 RA Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
 RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
 RA D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,
 RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,
 RA Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E.,

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RA Mathewson C.A., Mitchell T.G., Perteau M., Riggs F.R., Salzberg S.L.,
RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
RA Suh B.B., Tenney A., Uterback T.R., Wickes B.L., Wortman J.R.,
RA Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,
RA Fraser C.M., Hyman R.W.;
RT "The genome of the basidiomycetous yeast and human pathogen
RT Cryptococcus neoformans.";
RL Science 307:1321-1324(2005).
DR EMBL; AE017345; AAW43670.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 511 AA; 56762 MW; 21468107971233BD CRC64;

Query Match 78.0%; Score 39; DB 2; Length 511;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSNEPPP 8
Db 229 QQFNEDPP 236

RESULT 12
Q8F526 LEPIN
ID Q8F526 LEPIN PRELIMINARY; PRT; 376 AA.
AC Q8F526
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=LA1861;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-O., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Girona I., Somerville R.L., Wen Y.-W., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
RT interrogans revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).
DR EMBL; AE011360; AAN49060.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR000379; Serestr.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 376 AA; 42295 MW; 3BD6B83967FF3971 CRC64;

Query Match 76.0%; Score 38; DB 2; Length 376;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSNEPPP 9
Db 102 QEKNSDPPT 110

RESULT 13
Q59UO3 CANAL
ID Q59UO3 CANAL PRELIMINARY; PRT; 797 AA.
AC Q59UO3
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Hypothetical protein MNR2.
GN Name=MNR2; ORFNames=CaO19.13112, CaO19.5667;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
```

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OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S., Magee P.T.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of Candida albicans.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RA Dungan J., Luo A., Newport G., Ian C.-Y., Iijima C., Adegbola O.,
RA Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W.,
RA Jones T., Scherer S., Agabian N.;
RT "Annotation of the Genome of Candida albicans.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AACQ01000129; EAK94231.1; -; Genomic_DNA.
DR EMBL; AACQ01000128; EAK94278.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 797 AA; 90614 MW; 5F9B1DBSF4559746 CRC64;

Query Match 76.0%; Score 38; DB 2; Length 797;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQSNEPPP 9
Db 82 QKSNKDPSP 90

RESULT 14
KV3J MOUSE
ID KV3J MOUSE STANDARD; PRT; 111 AA.
AC P01662;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region ABPC 22/PC 9245.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE (ABPC 22).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
RN [2]
RP PROTEIN SEQUENCE (PC 9245).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
CC -1- MISCELLANEOUS: The ABPC22 and PC9241 sequences are identical.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC HSSP; P01665; 10NZ.
DR SMR; P01662; 1-111.
DR Ensembl; ENSMUSG00000060064; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
```

DR SMART; SM00406; IGV; 1.
 KW PROSITE; PS50835; IG_LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin domain;
 KW Immunoglobulin V region.
 FT REGION 1 23
 FT REGION 24 38
 FT REGION 39 53
 FT REGION 54 60
 FT REGION 61 92
 FT REGION 93 101
 FT REGION 102 111
 FT DISULFID 23 92
 FT NON_TER 111
 SQ SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;

Query Match 74.0%; Score 37; DB 1; Length 111;
 Best Local Similarity 77.8%; Pred. No. 45;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QOSNEDPPT 9
 ||:|||||
 Db 93 QQNEDPVT 101

RESULT 15
 ID KV3K MOUSE STANDARD; PRT; 111 AA.
 AC P01663;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 10-MAY-2005 (Rel. 47, Last annotation update)
 DE IG kappa chain V-III region PC 4050.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of Genetic Information may produce immunoglobulin
 RT diversity";
 RL Nature 276:785-790 (1978).
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC removed.
 CC -----
 DR HSP; P01665; 1QNZ.
 DR SMR; P01663; 1-111.
 DR Ensembl; ENSMUSG000000060064; Mus musculus.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin domain;
 KW Immunoglobulin V region.
 FT REGION 1 23
 FT REGION 24 38
 FT REGION 39 53
 FT REGION 54 60
 FT REGION 61 92
 FT REGION 93 101
 FT REGION 102 111
 FT DISULFID 23 92
 FT NON_TER 111
 SQ SEQUENCE 111 AA; 12005 MW; 39D87619313453CB CRC64;
 Query Match 74.0%; Score 37; DB 1; Length 111;
 Best Local Similarity 77.8%; Pred. No. 45;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QOSNEDPPT 9
 ||:|||||
 Db 93 QQNEDPVT 101
 RESULT 16
 ID DPB2 YEAST STANDARD; PRT; 692 AA.
 AC P24482; Q06622;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE DNA polymerase epsilon subunit B (EC 2.7.7.7) (DNA polymerase II
 DE subunit B).
 DE Name=DPB2; OrderedLocustNames=YPR175W; ORFNames=P9705.7;
 GN Saccharomyces cerevisiae (Baker's yeast).
 OS Saccharomycetes cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=YH48;
 RX MEDLINE=91271241; PubMed=2052544;
 RA Araki H., Hamatake R.K., Johnston L.H., Sugino A.;
 RT "DPB2, the gene encoding DNA polymerase II subunit B, is required for
 RT chromosome replication in Saccharomyces cerevisiae.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:4601-4605 (1991).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=S288c / AB972;
 RX MEDLINE=97313271; PubMed=9169875;
 RA Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge W.,
 RA Araujo R., Aparicio A., Barrell B.G., Badcock K., Bense V., J.M.,
 RA Botstein D., Bowman S., Brueckner M., Carpenter J., Cherry J.M.,
 RA Chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,
 RA Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,
 RA Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,
 RA Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.W.,
 RA Hunnicke-Smith S., Hyman R.W., Johnston M., Kalman S., Kleine K.,
 RA Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,
 RA Marathe R., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D.,
 RA Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D.,
 RA Petel F.X., Pohl T.M., Purnelle B., Rajandream M.A., Reckmann S.,
 RA Rieger M., Riles L., Roberts D., Schaefer M., Scharfe M., Scherens B.,
 RA Schramm S., Schroeder M., Sdicu A.-M., Tettein H., Urrestarazu L.A.,
 RA Ushinsky S., Vierendeels F., Vissers S., Voss H., Walsh S.V.,
 RA Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E., Zhong W.-W.,
 RA Zollner A., Vo D.H., Hani J.;
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
 RL Nature 387:103-105 (1997).
 CC -!- FUNCTION: DNA polymerase II participates in chromosomal DNA
 CC replication. DPB2 is essential for cell growth. May have a role in
 CC DNA synthesis.
 CC -!- CATALYTIC ACTIVITY: Deoxynucleoside triphosphate + DNA(n) =
 CC diphosphate + DNA(n+1).
 CC -!- SUBUNIT: Consists of five subunits (200 kDa, 80 kDa, 34 kDa, 30
 CC kDa, and 29 kDa).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- MISCELLANEOUS: In eukaryotes there are five DNA polymerases:
 CC alpha, beta, gamma, delta, and epsilon which are responsible for
 CC different reactions of DNA synthesis.
 CC -!- SIMILARITY: Belongs to the DNA polymerase epsilon subunit B
 CC family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; M61710; AAA34576.1; ALT_INIT; Genomic_DNA.

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DR EMBL; U25842; AAB68109.1; -; Genomic_DNA.
DR PIR; S59833; S59833.
DR IntAct; P24482; -.
DR GenOnline; 144440; -.
DR EMBL; YPR175W; Saccharomyces cerevisiae.
DR SGB; S00006379; DPB2.
DR GO; GO:0005737; Cytoplasm; IDA.
DR GO; GO:0008622; C:epsilon DNA polymerase complex; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0005657; C:replication fork; TAS.
DR GO; GO:0003893; F:epsilon DNA polymerase activity; TAS.
DR GO; GO:0006273; P:lagging strand elongation; TAS.
DR GO; GO:0006272; P:leading strand elongation; TAS.
DR GO; GO:0006298; P:mismatch repair; TAS.
DR GO; GO:0006289; P:nucleotide-excision repair; TAS.
DR InterPro; IPR007185; DNA_pol_E_B.
DR PANTHER; PTHR12708; DNA_pol_E_B; 3.
DR Pfam; PF04042; DNA_pol_E_B_1.
KW Complete proteome; DNA replication; DNA-binding;
KW DNA-directed DNA polymerase; Nuclear protein; Nucleotidyltransferase;
KW Transferrase.
FT CONFLICT 461 461 F -> Y (in Ref. 1).
FT CONFLICT 524 524 K -> R (in Ref. 1).
FT CONFLICT 568 568 V -> F (in Ref. 1).
FT CONFLICT 587 587 E -> Q (in Ref. 1).
FT CONFLICT 647 647 T -> I (in Ref. 1).
SQ SEQUENCE 692 AA; 78704 MW; 5C01647BD2B6A39A CRC64;
Query Match 74.0%; Score 37; DB 1; Length 692;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QQSNEPPT 9
Db 425 QKLNDDPPT 433
RESULT 17
Q5DBP2_SCHJA Q5DBP2_SCHJA PRELIMINARY; PRT; 101 AA.
AC Q5DBP2;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Han Z.;
RT "The full-length cDNA sequences of Schistosoma japonicum genes.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY815032; AAW26764.1; -; mRNA.
KW Hypothetical protein.
SQ SEQUENCE 101 AA; 11265 MW; 0596177A437D46BC CRC64;
Query Match 72.0%; Score 36; DB 2; Length 101;
Best Local Similarity 75.0%; Pred. No. 63;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QQSNEPPT 8
Db 91 QRNRDPP 98
RESULT 18
KV3I_MOUSE
ID KV3I_MOUSE STANDARD; PRT; 131 AA.
AC P01661;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
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DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region MOPC 63 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE OF 1-35.
RX MEDLINE=78235887; PubMed=981179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to the
variable and constant regions of immunoglobulin light chain
precursors: implications on the organization and controlled expression
of immunoglobulin genes.";
RL Biochemistry 17:2392-2400(1978).
RN [2]
RP PROTEIN SEQUENCE OF 21-131.
RX MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.B.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
kappa chains with limited sequence differences.";
RL Biochemistry 12:760-771(1973).
RN [3]
RP SEQUENCE REVISION.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -----
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removed.
CC -----
DR PIR; B90412; KYMSM6.
DR HSPP; P01665; 1QNZ.
DR SMR; P01661; 21-131.
DR EMBL; ENSMUSG0000060064; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 131 Ig kappa chain V-III region MOPC 63.
FT REGION 21 43 Framework-1.
FT REGION 44 58 Complementarity-determining-1.
FT REGION 59 73 Framework-2.
FT REGION 74 80 Complementarity-determining-2.
FT REGION 81 112 Complementarity-determining-3.
FT REGION 113 121 Complementarity-determining-3.
FT REGION 122 131 Framework-4.
FT DISULFID 43 112 By similarity.
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;
Query Match 72.0%; Score 36; DB 1; Length 131;
Best Local Similarity 77.8%; Pred. No. 84;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QQSNEPPT 9
Db 113 QQNEDPPT 121
RESULT 19
Q5AZV6_EMENI
ID Q5AZV6_EMENI PRELIMINARY; PRT; 428 AA.
AC Q5AZV6;
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DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=AN6174.2;
 OS Aspergillus nidulans FGSC A4.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eutotiales; Trichocomaceae; Emericella.
 OX NCBI_TaxID=227321;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FGSC A4;
 RA Birren B., Nussbaum C., Abouelleil A., Allen N., Anderson S.,
 RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
 RA Boukhalter B., Butler J., Calvo S.E., Camatata J., Chang J.,
 RA Choepl Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
 RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
 RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
 RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
 RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
 RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
 RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
 RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
 RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
 RA Rachupka A., Ramaamy U., Raymond C., Retta R., Rise C., Rogov P.,
 RA Roman J., Schauer S., Schnupack R., Seaman S., Severy P., Smirnov S.,
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
 RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
 RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
 RA Lander E.;
 RT "Genome Sequence of Aspergillus nidulans.";
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBSJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBSJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AACD01000105; EAA57960.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 428 AA; 46924 MW; 18CFD56508F8787 CRC64;

 Query Match 72.0%; Score 36; DB 2; Length 428;
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 Qy 1 QOSNEDPPP 8
 Db 203 QOSNEDPPP 210

 RESULT 20
 ID 082263 ARATH PRELIMINARY; PRT; 442 AA.
 AC 082263; Q944K4;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Expressed protein (Hypothetical protein At2g47960)
 DE (At2g47960/T9J23.10).
 GN Name=At2g47960;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
 RA Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBSJ databases.
 RN [2]

RP NUCLEOTIDE SEQUENCE.
 RA Town C.D., Kaul S.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBSJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
 RA Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.,
 RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
 RA Fraser C.M., Venter J.C.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBSJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
 RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBSJ databases.
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBSJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
 RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
 RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
 RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; AC005309; AAC3650.2; -; Genomic_DNA.
 DR EMBL; AC006072; AAM15133.1; -; mRNA.
 DR EMBL; AY074352; AAL67048.1; -; mRNA.
 DR EMBL; AF428334; AAL16264.1; -; mRNA.
 DR EMBL; AY113973; AAM45021.1; -; mRNA.
 DR PIR; F84921; F84921.
 DR InterPro; IPR010378; DUF974.
 DR Pfam; PF06159; DUF974; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 442 AA; 49290 MW; D6E987FA3D95BE30 CRC64;

 Query Match 72.0%; Score 36; DB 2; Length 442;
 Best Local Similarity 66.7%; Pred. No. 3.4e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

 Qy 1 QOSNEDPPP 9
 Db 246 EDSTEDPPP 254

 RESULT 21
 Q72LZ6 LEPIC
 ID Q72LZ6 LEPIC PRELIMINARY; PRT; 443 AA.
 AC Q72LZ6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Phosphodiesterase.
 GN Name=phod; OrderedLocName=IIC13397;
 OS Leptosira interrogans (serogroup Icterohaemorrhagiae / serovar
 OS Copenhageni).

OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
 OX NCBI_TaxID=44275;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Fiocruz L1-130;
 RX PubMed=15028702; DOI=10.1128/JB.186.7.2164-2172.2004;
 RA Nascimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B.,
 RA Ho P.L., Haake D.A., Verjovski-Almeida S., Hartskeerl R.A.,
 RA Marques M.V., Oliveira M.C., Menck C.F.M., Leite L.C.C., Carrer H.,
 RA Coutinho L.L., Degraive W.M., Dellagostin O.A., El-Dorri H.,
 RA Ferro E.S., Ferro M.I.T., Furlan L.R., Gamberini M., Giglioti E.A.,
 RA Goes-Neto A., Goldman G.H., Goldman M.H.S., Harakava R.,
 RA Jeronimo S.M.B., Junqueira-de-Azevedo J.L.M., Kimura E.T.,
 RA Kuramae E.E., Lemos E.G.M., Lemos M.V.F., Marino C.L., Nunes L.R.,
 RA de Oliveira R.C., Pereira G.G., Reis M.S., Schriefer A.,
 RA Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A.,
 RA Canargo L.E.A., Kitajima J.P., Setubal J.C., Van Sluys M.A.;
 RA "Comparative genomics of two Leptospira interrogans serovars reveals
 RT novel insights into physiology and pathogenesis.";
 RL J. Bacteriol. 186:2164-2172(2004).
 DR EMBL; AB017300; AAS71937.1; -; Genomic_DNA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR001952; Alk phosphatase.
 DR InterPro; IPR000413; Integrin_alpha.
 DR Pfam; PF00245; Alk_phosphatase; 1.
 DR PROSITE; PS00242; INTEGRIN_ALPHA; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 443 AA; 51548 MW; D8A13873080C33CC CRC64;
 Query Match 72.0%; Score 36; DB 2; Length 443;
 Best Local Similarity 85.7%; Pred. No. 3.4e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SNEDPPT 9
 Db 127 SNEDPPS 133
 RESULT 22
 Q8EYGS LEPIN PRELIMINARY; PRT; 443 AA.
 AC Q8EYGS
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Phosphodiesterase/alkaline phosphatase D (EC 3.1.3.1).
 GN OrderedLocustNames=LA4246;
 OS Leptospira interrogans.
 OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
 OX NCBI_TaxID=173;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=56501 / Serogroup Icterohaemorrhagiae / Serovar lai;
 RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
 RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
 RA Zhang J.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
 RA Jiang Y.-Y., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
 RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
 RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
 RA Saint Girons I., Sonerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
 RA Xu J.-G., Zhao G.-P.;
 RT "Unique physiological and pathogenic features of Leptospira
 RT interrogans revealed by whole-genome sequencing.";
 RL Nature 422:888-893(2003).
 DR EMBL; AB011577; AAN51444.1; -; Genomic_DNA.
 DR GO; GO:0004035; P:alkaline phosphatase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR001952; Alk_phosphatase.
 DR InterPro; IPR000413; Integrin_alpha.
 DR Pfam; PF00245; Alk_phosphatase; 1.
 DR PROSITE; PS00242; INTEGRIN_ALPHA; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 443 AA; 51489 MW; 89B4A7D462327F50 CRC64;

Query Match 72.0%; Score 36; DB 2; Length 443;
 Best Local Similarity 85.7%; Pred. No. 3.4e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SNEDPPT 9
 Db 127 SNEDPPS 133
 RESULT 23
 Q18518 CAEEL PRELIMINARY; PRT; 460 AA.
 ID Q18518
 AC Q18518
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein C39B10.2.
 GN ORFNames=C39B10.2;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Longons to the ligand-gated ionic channel (TC 1.A.9)
 CC family.
 DR EMBL; Z50027; CAA90332.3; -; Genomic_DNA.
 DR PIR; T19840; T19840.
 DR Ensembl; C39B10.2; Caenorhabditis elegans.
 DR WormBase; WBGene00008022; C39B10.2.
 DR WormPep; C39B10.2; CE36632.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0045211; C:postsynaptic membrane; IEA.
 DR GO; GO:0005230; F:extracellular ligand-gated ion channel acti. .; IEA.
 DR GO; GO:0004890; F:GABA-A receptor activity; IEA.
 DR GO; GO:0005216; F:ion channel activity; IEA.
 DR GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
 DR GO; GO:0006811; P:ion transport; IEA.
 DR InterPro; IPR006028; GABAA_recept.
 DR InterPro; IPR006029; Neu channel memb.
 DR InterPro; IPR006202; Neu channel memb.
 DR InterPro; IPR006201; Neur_channel.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00253; GABAAREC3PTR.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMs; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUOTR_ION_CHANNEL; 1.
 KW Complete proteome; Hypothetical protein; Ion transport; Ionic channel;
 KW Postsynaptic membrane; Transmembrane; Transport.
 SQ SEQUENCE 460 AA; 52798 MW; 9C4E95B292E86409 CRC64;
 Query Match 72.0%; Score 36; DB 2; Length 460;
 Best Local Similarity 77.8%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QQSNEPPT 9
 Db 36 QQSNTREPT 44
 RESULT 24
 Q6CF15 YARLI PRELIMINARY; PRT; 562 AA.
 ID Q6CF15
 AC Q6CF15

DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Similarities with tr|Q9UVF6 Yarrowia lipolytica Pal2 protein.
 GN OrderedLocusNames=YALI0B06710g;
 OS Yarrowia lipolytica (Candida lipolytica).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Dipodascaceae; Yarrowia.
 OX NCBI_TaxID=4952;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=15229592; DOI=10.1038/nature02579;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
 RA Goffard N., Franchin L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
 RA Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.-P., Straub M.-L., Suleau A.,
 RA Swennen D., Tekia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
 RA Wincker P., Souciet J.-L.;
 RT "Genome evolution in yeasts.";
 RT Nature 430:35-44(2004).
 DR EMBL; CH382128; CAG82808.1; -; Genomic_DNA.
 KW Complete proteome.
 SQ SEQUENCE 562 AA; 61494 MW; F3F69CECE74CDBD0 CRC64;

 Query Match 72.0%; Score 36; DB 2; Length 562;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 4 NEDPPT 9
 Db 547 NEDPPT 552

 RESULT 25
 DEC11 DROME STANDARD; PRT; 1208 AA.
 AC P18169; Q8IRP1;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Defective chorion-1 protein, FC125 isoform precursor.
 GN Name=dec-1; ORFNames=CG2175;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE, AND ALTERNATIVE SPLICING.
 RX MEDLINE=91032553; PubMed=1699826;
 RA Waring G.L., Hawley R.J., Schoenfeld T.;
 RT "Multiple proteins are produced from the dec-1 eggshell gene in
 RT Drosophila by alternative RNA splicing and proteolytic cleavage
 RT events.";
 RL Dev. Biol. 142:1-12(1990).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celisniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Efannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delecher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasner K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hoston D., Houston K.A., Howland T.J., Wei M.-H., Ibegwegu C.,
 RA Jalali M., Kalush F., Karp G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Massarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RT Science 287:2185-2195(2000).
 RN [3]
 RP GENOME REANNOTATION, AND ALTERNATIVE SPLICING.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celisniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";
 RN Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [4]
 RP FUNCTION, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
 RX MEDLINE=88243015; PubMed=3378704;
 RA Hawley R.J., Waring G.L.;
 RT "Cloning and analysis of the dec-1 female-sterile locus, a gene
 RT required for proper assembly of the Drosophila eggshell.";
 RL Genes Dev. 2:341-349(1988).
 CC -!- FUNCTION: Required for proper assembly of the eggshell.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=FC125;
 CC IsoId=P18169-1; Sequence=Displayed;
 CC Name=FC106;
 CC IsoId=P18170-1; Sequence=External;
 CC Name=FC177;
 CC IsoId=P18171-1; Sequence=External;
 CC -!- DEVELOPMENTAL STAGE: Expression peaks at embryonic stage 10A, is
 CC slightly reduced by stage 10B, and undetected in stage 11.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; M35887; AAA28446.1; -; mRNA.
 CC EMBL; AE003442; AAN09215.1; -; Genomic_DNA.
 DR

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DR PIR; A44766; A44766.
DR Ensembl; CG2175; Drosophila melanogaster.
DR FlyBase; FBgn000427; dec-1.
DR GO; GO:0042600; C:chorion; IDA.
DR GO; GO:0005576; C:structural constituent of chorion (sensu In. .); IMP.
DR GO; GO:0005213; F:structural constituent of chorion (sensu In. .); IMP.
DR GO; GO:0007306; P:insect chorion formation; IMP.
DR InterPro; IPR006720; DEC-1_C.
DR InterPro; IPR006719; DEC-1_N.
DR InterPro; IPR006718; DEC-1_REPEAT.
DR Pfam; PF04624; DEC-1; 12.
DR Pfam; PF04626; DEC-1_C; 1.
DR Pfam; PF04625; DEC-1_N; 1.
KW Alternative splicing; Chorion; Repeat; Signal.
FT SIGNAL 1 19
FT CHAIN 20 1208
FT REPEAT 493 518
FT REPEAT 519 544
FT REPEAT 545 570
FT REPEAT 571 596
FT REPEAT 597 622
FT REPEAT 623 652
FT REPEAT 653 680
FT REPEAT 681 696
FT REPEAT 697 720
FT REPEAT 721 733
FT REPEAT 734 758
FT REPEAT 759 788
FT REGION 493 788
FT Gln, Met-rich
FT A -> V (in Ref. 1).
FT C -> E (in Ref. 1).
FT D -> H (in Ref. 1).
FT A -> T (in Ref. 1).
FT PENEGRHKVDALGVGNKKSKSAPP -> AGRRRH
FT RQASRCPSRQQAQEVQVGVGA (in Ref. 1).
FT QRPVQSYGTSYGG -> SVNRFRVTEQATAE (in Ref. 1).
FT CONFLICT 888 901
FT CONFLICT 1208 AA; 137444 MW; 2D8D140756FFDEE CRC64;
SQ SEQUENCE 1208 AA; 137444 MW; 2D8D140756FFDEE CRC64;

Query Match 72.0%; Score 36; DB 1; Length 1208;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QQSNEPPT 9
Db 960 QKSNSNPPT 968
|::|::|::|
|::|::|::|

RESULT 26
DEC13 DROME STANDARD; PRT; 1590 AA.
AC P18171; Q9W3P3;
DT 01-NOV-1990 (Rel. 16, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Defective chorion-1 protein, FC177 isoform precursor.
GN Name=dec-1; ORFNames=CG2175;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
[1]
RN NUCLEOTIDE SEQUENCE, AND ALTERNATIVE SPLICING.
RX MEDLINE=91032553; PubMed=1699826;
RA Waring G.L., Hawley R.J., Schoenfeld T.;
RT "Multiple proteins are produced from the dec-1 eggshell gene in
RT Drosophila by alternative RNA splicing and proteolytic cleavage
RT events."
RL Dev. Biol. 142:1-12(1990).
[2]

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RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Evansgelieta C.C., Ferraz C., Ferreira S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Garg N.S., Gelbart W.M., Glasser K.,
RA Foele C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski W.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
[3]
RN GENOME REANNOTATION, AND ALTERNATIVE SPLICING.
RP MEDLINE=2426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
[4]
RN FUNCTION, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RP MEDLINE=88243015; PubMed=3378704;
RA Hawley R.J., Waring G.L.;
RT "Cloning and analysis of the dec-1 female-sterile locus, a gene
RT required for proper assembly of the Drosophila eggshell."
RL Genes Dev. 2:341-349(1988).
CC -!- FUNCTION: Required for proper assembly of the eggshell.
CC -!- INTERACTION:
CC Q8T8S1:CG13322; NbExp=1; IntAct=EBI-101563, EBI-89202;
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Name=FC177;
CC Event=Alternative splicing; Named isoforms=3;
CC Name=FC177;
CC IsoId=P18171-1; Sequence=Displayed;
CC Name=FC106;
CC IsoId=P18170-1; Sequence=External;
CC Name=FC125;
CC IsoId=P18169-1; Sequence=External;

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CC -!- DEVELOPMENTAL STAGE: Expressed during embryonic stage 11.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; M35889; AAA28448.1; -; mRNA.
CC EMBL; AB003442; AAF46278.2; -; Genomic_DNA.
CC IntAct; P18171; -.
CC Ensembl; CG2175; Drosophila melanogaster.
CC FlyBase; FBgn0000427; dec-1.
CC GO; GO:0042600; C:chorion; IDA.
CC GO; GO:0005576; C:extracellular region; IDA.
CC GO; GO:0005213; F:structural constituent of chorion (sensu In. . .; IMP.
CC GO; GO:0007306; P:insect chorion formation; IMP.
CC InterPro; IPR006720; DEC-1_C.
CC InterPro; IPR006719; DEC-1_N.
CC InterPro; IPR006718; DEC-1_REPEAT.
CC Pfam; PF04624; DEC-1; 12.
CC Pfam; PF04626; DEC-1_C; 1.
CC Pfam; PF04625; DEC-1_N; 1.
CC Alternative splicing; Chorion; Repeat; Signal.
KW SIGNAL 1 19 Potential.
FT CHAIN 20 1590 Defective chorion-1 protein, FC177
FT REPEAT 493 518 isoform.
FT REPEAT 519 544 1.
FT REPEAT 545 570 2.
FT REPEAT 571 596 3.
FT REPEAT 597 622 4.
FT REPEAT 623 652 5.
FT REPEAT 653 680 6 (approximate).
FT REPEAT 681 696 7 (approximate).
FT REPEAT 697 720 8 (approximate).
FT REPEAT 721 733 9 (approximate).
FT REPEAT 734 758 10 (approximate).
FT REPEAT 759 788 11 (approximate).
FT REGION 493 788 12 X 26 AA approximate tandem repeats,
FT Glu, Met-rich
FT CONFLICT 17 17 A -> V (in Ref. 1).
FT CONFLICT 219 219 R -> E (in Ref. 1).
FT CONFLICT 347 347 D -> H (in Ref. 1).
FT CONFLICT 382 382 A -> T (in Ref. 1).
FT CONFLICT 847 877 PENEETARKVDALGVGNKRYKSKSAPP -> AGERRH
FT RQAQRCPCGSWQQAEVQVQAA (in Ref. 1).
FT CONFLICT 888 901 QRFPVQSYGTSTGG -> SVRFVRTEQTAE (in Ref.
FT 1).
FT CONFLICT 995 995 R -> Q (in Ref. 1).
FT CONFLICT 1051 1052 SV -> C (in Ref. 1).
FT CONFLICT 1296 1296 Q -> P (in Ref. 1).
FT CONFLICT 1299 1299 E -> D (in Ref. 1).
FT SEQUENCE 1590 AA; 179188 MW; F78F36B465D1D790 CRC64;

Query Match 72.0%; Score 36; DB 1; Length 1590;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSNDPPT 9
Db 960 QKSNSNPPT 968

RESULT 27
Q7RK78 PLAYO
ID Q7RK78 PLAYO PRELIMINARY; PRT; 107 AA.
AC Q7RK78;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative ubiquitin-conjugating enzyme (fragment).
GN Name=PY03025;

Query Match 72.0%; Score 36; DB 1; Length 1590;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSNDPPT 9
Db 960 QKSNSNPPT 968

RESULT 28
Q4YR21 PLABE
ID Q4YR21 PLABE PRELIMINARY; PRT; 139 AA.
AC Q4YR21;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Ubiquitin-conjugating enzyme e2, putative (fragment).
GN ORFNames=PB000336.03.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bertman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.I., Rajadream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RA "A comprehensive survey of the Plasmodium life cycle by genomic,

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OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perte M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallow S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman M.J.,
RA Carucci D.J.;
RA "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519 (2002).
CC -!- CATALYTIC ACTIVITY: ATP + ubiquitin + protein lysine = AMP +
CC diphosphate + protein N-ubiquityllysine.
CC -!- PATHWAY: Ubiquitin conjugation; second step.
CC -!- SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AABL01000856; EAA22551.1; -; Genomic_DNA.
CC HSP; P52490; 1JAT.
CC SMR; Q7RK78; 1-106.
CC GO; GO:0016874; F:Ligase activity; IEA.
CC GO; GO:0004840; F:ubiquitin conjugating enzyme activity; IEA.
CC GO; GO:0006512; P:ubiquitin cycle; IEA.
CC InterPro; IPR000608; UBO-conjugat_E2.
CC Pfam; PF00179; UQ_con; 1.
CC Prodom; PD000461; UBO_conjugat; 1.
CC PROSITE; PS00183; UBIQUITIN_CONJUGAT_1; 1.
CC PROSITE; PS0127; UBIQUITIN_CONJUGAT_2; 1.
KW Ligase; Ubl conjugation pathway.
FT NON_TER 1
FT NON_TER 107
FT SEQUENCE 107 AA; 11811 MW; ED9F62F412B49B99 CRC64;

Query Match 70.0%; Score 35; DB 2; Length 107;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSNDPPT 9
Db 3 QDLNKPPT 11

RESULT 29
Q4YR21 PLABE
ID Q4YR21 PLABE PRELIMINARY; PRT; 139 AA.
AC Q4YR21;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Ubiquitin-conjugating enzyme e2, putative (fragment).
GN ORFNames=PB000336.03.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Bertman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.I., Rajadream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RA "A comprehensive survey of the Plasmodium life cycle by genomic,

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RT transscriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- CATALYTIC ACTIVITY: ATP + ubiquitin + protein lysine = AMP +
CC diphosphate + protein N-ubiquityllysine.
CC -!- PATHWAY: Ubiquitin conjugation; second step.
CC -!- SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family.
DR EMBL; CAAT101002860; CAH99536.1; -; Genomic_DNA.
DR InterPro; IPR000608; UBQ-conjugat_E2.
DR Pfam; PF001179; UQ_con; 1.
DR ProDom; PD000461; UBQ_conjugat; 1.
DR SMART; SM00212; UBCC; 1.
DR PROSITE; PS00183; UBIQUITIN_CONJUGAT_1; 1.
DR PROSITE; PS0127; UBIQUITIN_CONJUGAT_2; 1.
KW Ligase; Ub1 conjugation pathway.
FT NON TER 1
SQ SEQUENCE 139 AA; 15597 MW; 5DE03B5E857E8C43 CRC64;

Query Match 70.0%; Score 35; DB 2; Length 139;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSNEDPPT 9
Db | | | | |
3 QDLNKPPT 11

RESULT 29
Q81607_PLAF7
ID Q81607; PLAF7 PRELIMINARY; PRT; 147 AA.
AC Q81607;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ubiquitin-conjugating enzyme e2, putative.
GN ORFNames=PF010190w;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22255705; PubMed=12369864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow J., Suh B., Peterson J., Angiuoli S.,
RA Pertea M., Allen J., Selengut J.J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Vaidya A.B.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.G.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:496-511(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Hyman R.W., Fung E., Conway A., Kurdi O., Mao J., Miranda M.,
RA Nakao B., Rowley D., Tamaki T., Wang F., Davis R.W.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + ubiquitin + protein lysine = AMP +
CC diphosphate + protein N-ubiquityllysine.
CC -!- PATHWAY: Ubiquitin conjugation; second step.
CC -!- SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family.
DR EMBL; AE014844; AAN36127.1; -; Genomic_DNA.
DR HSSP; P15731; 1QCQ.
DR SMR; Q81607; 1-146.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0004840; F:ubiquitin conjugating enzyme activity; IEA.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR000608; UBQ-conjugat_E2.
DR Pfam; PF00179; UQ_con; 1.

DR ProDom; PD000461; UBQ_conjugat; 1.
DR SMART; SM00212; UBCC; 1.
DR PROSITE; PS00183; UBIQUITIN_CONJUGAT_1; 1.
DR PROSITE; PS0127; UBIQUITIN_CONJUGAT_2; 1.
KW Ligase; Ub1 conjugation pathway.
FT NON TER 1
SQ SEQUENCE 147 AA; 16539 MW; 233FBD5A8481B085 CRC64;

Query Match 70.0%; Score 35; DB 2; Length 147;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSNEDPPT 9
Db | | | | |
11 QDLNKPPT 19

RESULT 30
Q4Y6R0_PLACH
ID Q4Y6R0_PLACH PRELIMINARY; PRT; 147 AA.
AC Q4Y6R0;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Ubiquitin-conjugating enzyme e2, putative.
GN ORFNames=PC000554.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- CATALYTIC ACTIVITY: ATP + ubiquitin + protein lysine = AMP +
CC diphosphate + protein N-ubiquityllysine.
CC -!- PATHWAY: Ubiquitin conjugation; second step.
CC -!- SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family.
DR EMBL; CAAJ01000592; CAH75150.1; -; Genomic_DNA.
DR InterPro; IPR000608; UBQ-conjugat_E2.
DR Pfam; PF001179; UQ_con; 1.
DR ProDom; PD000461; UBQ_conjugat; 1.
DR SMART; SM00212; UBCC; 1.
DR PROSITE; PS00183; UBIQUITIN_CONJUGAT_1; 1.
DR PROSITE; PS0127; UBIQUITIN_CONJUGAT_2; 1.
KW Ligase; Ub1 conjugation pathway.
SQ SEQUENCE 147 AA; 16539 MW; 233FBD5A8481B085 CRC64;

Query Match 70.0%; Score 35; DB 2; Length 147;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSNEDPPT 9
Db | | | | |
11 QDLNKPPT 19

RESULT 31
Q5AUQ5_EMENI
ID Q5AUQ5_EMENI PRELIMINARY; PRT; 267 AA.
AC Q5AUQ5;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Predicted protein.
```

GN ORFNames=AN7975.2;
 OS Aspergillus nidulans FGSC A4.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Emericella.
 OX NCBI_TaxID=227321;
 RN [1]_NCBI_TaxID=227321;
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FGSC A4;
 RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
 RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
 RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
 RA Chospel Y., Collymore A., Cook A., Cooke P., Corum B., Dearrellano K.,
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
 RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
 RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
 RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
 RA Kellis C., Landers T., Levine R., Lindblad-Toh K., Liu G., Iml A.,
 RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
 RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
 RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
 RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
 RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
 RA Roman J., Schauer S., Schupack R., Seaman S., Severy P., Smirnov S.,
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
 RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
 RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
 RA Lander E.;
 RT "Genome Sequence of Aspergillus nidulans";
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AACD01000135; EAA59629.1; -; Genomic DNA.
 SQ SEQUENCE 267 AA; 30232 MW; 5841E7EB112B77BB CRC64;

Query Match 70.0%; Score 35; DB 2; Length 267;
 Best Local Similarity 66.7%; Pred. No. 2.9e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSNEDPPT 9
 | | | | |
 Db 136 QSSNESPPS 144

RESULT 32
 Q5V2W7 HALMA
 ID Q5V2W7 HALMA PRELIMINARY; PRT; 275 AA.
 AC Q5V2W7;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Molybdenum cofactor biosynthesis protein.
 GN Name=moaE; OrderedLocNames=mrnA1186;
 OS Haloarcula marismortui (Haloaracterium marismortui).
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Haloarcula.
 OX NCBI_TaxID=2238;
 RN [1]_NCBI_TaxID=2238;
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 43049;
 EX PubMed=15520287; DOI=10.1101/gr.2700304;
 RA Balliga N.S., Bonneau R., Facciotti M.T., Pan M., Glusman G.,
 RA Deutsch E.W., Shannon P., Chiu Y., Weng R.S., Gan R.R., Hung P.,
 RA Date S.V., Marcotte E., Hood L., Ng W.V.;
 RT "Genome sequence of Haloarcula marismortui: a halophilic archaeon from
 the Dead Sea";
 RL Genome Res. 14:2221-2234(2004).
 DR EMBL; AY596297; AAV46135.1; -; Genomic DNA.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0006777; P:Mo-molybdopterin cofactor biosynthesis; IEA.

DR InterPro; IPR003448; Mb_biosynth_MoaE.
 DR InterPro; IPR004435; MoB reg.
 DR PANTHER; PTHR10311; Mb_biosynth_MoaE; 1.
 DR Pfam; PF02391; MoaE; 1.
 DR Pfam; PF03205; MoBB; 1.
 DR TIGRPFAMs; TIGR00176; moBB; 1.
 KW Complete proteome.
 SQ SEQUENCE 275 AA; 30435 MW; 32546495775A07BB CRC64;

Query Match 70.0%; Score 35; DB 2; Length 275;
 Best Local Similarity 66.7%; Pred. No. 3e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSNEDPPT 9
 | | | | |
 Db 174 QSGPEDPPT 182

RESULT 33
 Q5ICN4 CYTJO
 ID Q5ICN4 CYTJO PRELIMINARY; PRT; 287 AA.
 AC Q5ICN4;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE RpoD.
 GN Name=rpoD;
 OS Cytophaga johnsonae.
 OC Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
 OC Flavobacteriaceae; Flavobacterium.
 OX NCBI_TaxID=986;
 RN [1]_NCBI_TaxID=986;
 RP NUCLEOTIDE SEQUENCE.
 RA Vingadassalom D., Kolb A., Mayer C., Rybkin T., Collatz B.,
 RA Podglajen I.;
 RT "An unusual primary sigma factor in the Bacteroidetes phylum";
 RL Mol. Microbiol. 56:888-902(2005).
 DR EMBL; AY781293; AAW50927.1; -; Genomic DNA.
 DR GO; GO:0016987; P:sigma factor activity; IEA.
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0006352; P:transcription initiation; IEA.
 DR InterPro; IPR009042; Sigma70_r1.2.
 DR InterPro; IPR007627; Sigma70_r2.
 DR InterPro; IPR007624; Sigma70_r3.
 DR InterPro; IPR007630; Sigma70_r4.
 DR InterPro; IPR00943; Sigma70.
 DR InterPro; IPR011991; Wing_Hlx_DNA_bd.
 DR Pfam; PF00140; Sigma70_r1.2; 1.
 DR Pfam; PF04542; Sigma70_r2; 1.
 DR Pfam; PF04539; Sigma70_r3; 1.
 DR Pfam; PF04545; Sigma70_r4; 1.
 DR PRINTS; PR00046; SIGMA70FCT.
 KW DNA-directed RNA polymerase; Nucleotidyltransferase; Sigma factor;
 KW Transferase.
 SQ SEQUENCE 287 AA; 32916 MW; 106DDA6228A55FDE CRC64;

Query Match 70.0%; Score 35; DB 2; Length 287;
 Best Local Similarity 66.7%; Pred. No. 3.2e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSNEDPPT 9
 | | | | |
 Db 146 EQSNERPPS 154

RESULT 34
 Q7PY08 ANOGA
 ID Q7PY08 ANOGA PRELIMINARY; PRT; 297 AA.
 AC Q7PY08;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

```
DE ENSANGP00000011561 (Fragment).
GN ORFNames=ENSANGG00000009072;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008987; EAA00827.1; -; Genomic_DNA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0017137; F:Rab GTPase binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006886; F:intracellular protein transport; IEA.
DR InterPro; IPR010911; Rab binding.
DR InterPro; IPR000306; Znf FYVE.
DR PROSITE; PS0916; RABBD_1.
DR PROSITE; PS0178; ZF FYVE; 1.
FT NON TER 297
SQ SEQUENCE 297 AA; 33344 MW; ED430BD36548B941 CRC64;

Query Match 70.0%; Score 35; DB 2; Length 297;
Best Local Similarity 66.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOSNEDPPT 9
Db 188 QYSQDPPT 196

RESULT 35
Q9SN12_ARATH
ID Q9SN12_ARATH PRELIMINARY; PRT; 301 AA.
AC Q9SN12;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE R2R3-MYB transcription factor (At3G50060/F3A4_140).
GN Name=F3A4_140; ORFNames=At3G50060;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Barques M., Collado M.C., Navarro P., Terol J., Perez-Alonso M.,
RA Meves H.W., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
[3]
RP NUCLEOTIDE SEQUENCE.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
[4]
RP NUCLEOTIDE SEQUENCE.
RA Kim C.J., Chen H., Cheuk R., Shinn P., Banh J., Bowser L.,
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RA Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
[5]
RN NUCLEOTIDE SEQUENCE.
RP Qu L., Gu H.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AL132978; CAB62114.1; -; Genomic_DNA.
DR EMBL; AF424588; AAL11582.1; -; mRNA.
DR EMBL; AY151958; AAS10068.1; -; mRNA.
DR EMBL; AY124828; AAM70537.1; -; mRNA.
DR PIR; T45859; T45859.
DR HSP; P01104; I18A.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0045449; F:regulation of transcription; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR001005; Myb DNA bd.
DR Pfam; PF00249; Myb DNA-binding; 2.
DR SMART; SM00717; SANT; 2. UNKNOWN_1.
DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
DR PROSITE; PS00334; MYB_2; 2.
DR PROSITE; PS00090; MYB_3; 2.
KW Nuclear protein; Repeat.
SQ SEQUENCE 301 AA; 33111 MW; 9CCD5863E9D06DEC CRC64;

Query Match 70.0%; Score 35; DB 2; Length 301;
Best Local Similarity 85.7%; Pred. No. 3.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SNEDPPT 9
Db 197 SSDDPPT 203

RESULT 36
Q39155_ARATH
ID Q39155_ARATH PRELIMINARY; PRT; 304 AA.
AC Q39155;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MYB-related protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Landsberg erecta; TISSUE=Silique;
RX MEDLINE=983417; PubMed=9678577; DOI=10.1023/A:1006011002499;
RA Kirik V., Kolle K., Misera S., Baumlein H.;
RT "Two novel MYB homologues with changed expression in late
RT embryogenesis-defective Arabidopsis mutants.";
RL Plant Mol. Biol. 37; 819-827(1998). (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear
DR EMBL; Z54137; CAA90810.1; -; mRNA.
DR PIR; S71285; S71285.
DR HSP; P01104; I18A.
DR TRANSFAC; T02590; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0045449; F:regulation of transcription; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR001005; Myb DNA bd.
DR Pfam; PF00249; Myb DNA-binding; 2.
DR SMART; SM00717; SANT; 2.
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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B-3501A;
RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
RW Wickes B.L., Fu J., Davis R.W.;
RT "Cryptococcus neoformans serotype D sequencing";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AA0Y01000001; EAL23658.1; -; Genomic_DNA.
DR GO; GO:0000785; C:chromatin; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003682; F:chromatin binding; IEA.
DR GO; GO:0006333; P:chromatin assembly or disassembly; IEA.
KW Hypothetical protein; Nuclear protein.
SQ SEQUENCE 315 AA; 36950 MW; 4863F2C56366D68E CRC64;

Query Match 70.0%; Score 35; DB 2; Length 315;
Best Local Similarity 55.8%; Pred.No. 3.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps

Qy 1 QQSNEPPT 9
Db 207 EGEDEPPT 215
:::|||||

RESULT 39
Q4VDG8_9STRA PRELIMINARY; PRT; 328 AA.
AC Q4VDG8_9STRA PRELIMINARY; PRT; 328 AA.
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Putative methylene tetrahydrofolate dehydrogenase.
GN Name:MTD;
OS Hyaloperonospora parasitica.
OC Eukaryota; stramenopiles; Oomycetes; Peronosporales; Peronosporaceae;
OC Hyaloperonospora.
OX NCBI_TaxID=123356;
RN 11
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Emoy2;
RX PubMed=15894715;
RA Rehmany A.P., Gordon A., Rose L.E., Allen R.L., Armstrong M.R.,
RW Whisson S.C., Kamoun S., Tyler B.M., Birch P.R., Beynon J.L.;
RT "Differential Recognition of Highly Divergent Downy Mildew Avirulence
RT Gene Alleles by RPP1 Resistance Genes from Two Arabidopsis Lines.";
RL Plant Cell 17:1839-1850(2005).
DR EMBL; AY973541; XAY5908.1; -; Genomic DNA.
SQ SEQUENCE 328 AA; 36445 MW; B7D65FA4A589D330 CRC64;

Query Match 70.0%; Score 35; DB 2; Length 328;
Best Local Similarity 85.7%; Pred.No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps

Qy 1 QQSNEPPT 7
Db 91 QQANEDP 97
:::|||||

RESULT 40
QB8YY6_MOUSE
ID QB8YY6_MOUSE PRELIMINARY; PRT; 330 AA.
AC QB8YY6_MOUSE PRELIMINARY; PRT; 330 AA.
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Mus musculus 6 days neonate skin cDNA, RIKEN full-length enriched
DE library, clone:A030004P03 product:similar to OVARC1001010
DE PROTEIN.
GN Name=4933434L15Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=92279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN (2)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN (3)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN (4)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN (5)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto S., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Iehikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN (6)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK037169; BAC29731.1; -, mRNA.
DR Ensembl; ENSMUSG0000028018; Mus musculus.
DR MGI; MGI:1914803; 4933434L15Rik.
SQ SEQUENCE 330 AA; 36862 MW; 0132B96F9DB16212 CRC64;

Query Match 70.08; Score 35; DB 2; Length 330;
Best Local Similarity 66.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSNEPPT 9
Db 164 QESSEHPPT 172
|:|:|
|:|:|

RESULT 41
Q5KPD8 CRYNE PRELIMINARY; PRT; 334 AA.
AC Q5KPD8;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORENAMES=CNA03150;
OS Cryptococcus neoformans var. neoformans JEC21.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=214684;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JEC21;
RA Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,
RA Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
RA D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,
RA Huang J.C., Janbon G., Jones S.J.M., Krzywinski M.I., Kwon-Chung J.K.,
RA Lengeler K.B., Maiti R., Marra M.A., Marra R.E., Mathewson C.A.,
RA Mitchell T.G., Pertea M., Riggs F.R., Salzberg S.L., Shvartsbeyn A.,
RA Schein J.E., Shin H., Specht C.A., Suh B., Tenney A., Utterback T.,
RA Wickes B.L., Wye N.H., Kronstad J., Lodge J.K., Heitman J.,
RA Davis R.W., Fraser C.M., Hyman R.W.;
RT "The genome and transcriptome of Cryptococcus neoformans, a
RT basidiomycete fungal pathogen of humans.";
RL Science 0:0-0(2005).
RN (2)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JEC21;
RA Loftus B., Amedeo P., Roncaglia P., Vamathevan J., Utterback T.,
RA Van Aken S., Fraser C.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN (3)
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=JEC21;
RX PubMed=15653466; DOI=10.1126/science.1103773;
RA Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
RA D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,
RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,
RA Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E.,
RA Mathewson C.A., Mitchell T.G., Pertea M., Riggs F.R., Salzberg S.L.,
RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
RA Suh B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,
RA Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,
RA Fraser C.M., Hyman R.W.;
RT "The genome of the basidiomycetous yeast and human pathogen
RT Cryptococcus neoformans.";


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RL Science 307:1321-1324(2005).
DR EMBL; AA017341; AAW40937.1; -; Genomic_DNA.
DR GO; GO:0000785; C:chromatin; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003682; F:chromatin binding; IEA.
DR GO; GO:0006333; P:chromatin assembly or disassembly; IEA.
DR InterPro; IPR000953; Chromo.
DR Pfam; PF00385; Chromo; 1.
DR SMART; SM00298; CHROMO; 1.
DR PROSITE; PS0013; CHROMO 2; 1.
KW Complete proteome; Hypothetical protein; Nuclear protein.
SQ SEQUENCE 334 AA; 39200 MW; E1E20A7092538F15 CRC64;

Query Match 70.0%; Score 35; DB 2; Length 334;
Best Local Similarity 55.6%; Pred. No. 3.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSNEDPPT 9
   :::|||||
Db 229 EGGEDPPT 237

RESULT 42
ID HEMI_GLOVI STANDARD; PRT; 430 AA.
AC Q7NLA8;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Glutamyl-tRNA reductase (EC 1.2.1.70) (GluTr).
GN Name=hema; OrderedLocusNames=gir1218;
OS Gloeobacter violaceus.
OC Bacteria; Cyanobacteria; Gloeobacteriales; Gloeobacter.
OX NCBI_TaxID=33072;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=PCC 7421;
RX MEDLINE=22977040; PubMed=14621292;
RA Nakamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya T.,
RA Sasamoto S., Watanabe A., Kawashina K., Kishida Y., Kiyokawa C.,
RA Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of Gloeobacter violaceus PCC 7421, a
RT cyanobacterium that lacks thylakoids.";
RL DNA Res. 10:137-145(2003).
CC -!- CATALYTIC ACTIVITY: L-glutamate 1-semialdehyde + NADP(+) +
CC tRNA(Glu) = L-glutamyl-tRNA(Glu) + NADPH.
CC -!- PATHWAY: Porphyrin biosynthesis by the C5 pathway; first step.
CC Involved in chlorophyll biosynthesis.
CC -!- SIMILARITY: Belongs to the glutamyl-tRNA reductase family.
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use as long as its content is in no way modified and this statement is not
removed.
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DR EMBL; BA000045; BAC89159.1; -; Genomic_DNA.
DR HAVAP; MF_00087; -; 1.
DR InterPro; IPR000343; GluTr.
DR InterPro; IPR006151; Shikimate DH.
DR InterPro; IPR000594; Thif_NAD_FAD_bd.
DR Pfam; PF00745; GluTr dimer; 1.
DR Pfam; PF05201; GluTr_N; 1.
DR Pfam; PF01488; Shikimate_DH; 1.
DR TIGRFAMs; TIGR01035; hema; 1.
DR PROSITE; PS00747; GLUTR; 1.
KW Chlorophyll biosynthesis; Complete proteome; NADP; Oxidoreductase;
KW Porphyrin biosynthesis.
FT ACT_SITE 50 50 Nucleophile (By similarity).
FT ACT_SITE 99 99 Proton acceptor (By similarity).
SQ SEQUENCE 430 AA; 48136 MW; 5491B16BF167B368 CRC64;

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Query Match 70.0%; Score 35; DB 1; Length 430;
Best Local Similarity 75.0%; Pred. No. 5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QSNEDPPT 9
   |||:||||
Db 422 QSNPEPPT 429

RESULT 43
ID O62338 CAEEL PRELIMINARY; PRT; 432 AA.
AC O62338;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein R06C1.6.
GN ORFNames=R06C1.6;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z81106; CAB03223.3; -; Genomic DNA.
DR EMBL; AL033536; CAD45609.2; -; Genomic DNA.
DR EMBL; AL033536; CAB03223.3; JOINED; Genomic DNA.
DR EMBL; Z81106; CAD45609.2; JOINED; Genomic DNA.
DR PIR; T23961; T23961.
DR WormBase; R06C1.6; Caenorhabditis elegans.
DR WormBase; R06C1.6; R06C1.6.
DR WormPep; R06C1.6; CB37541.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 432 AA; 47902 MW; 54D79FB7800803C8 CRC64;

Query Match 70.0%; Score 35; DB 2; Length 432;
Best Local Similarity 66.7%; Pred. No. 5.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSNEDPPT 9
   ||:|||||
Db 118 QEDNEDQPT 126

RESULT 44
ID Q7YTG7 CAEEL PRELIMINARY; PRT; 470 AA.
AC Q7YTG7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein D2030.2b.
GN ORFNames=D2030.2, D2030.2B;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z73906; CAB45047.1; -; Genomic DNA.
DR HSSP; O25926; 1UM8.

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DR Ensembl; D2030.2; Caenorhabditis elegans.
DR WormBase; WBGene00008412; D2030.2.
DR WormPep; D2030.2b; CE35176.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006457; F:protein folding; IEA.
DR GO; GO:0015031; P:protein transport; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR SMART; SM00382; ClpX.
DR TIGRFAMs; TIGR00382; ClpX; 1.
KW ATP-binding; Complete proteome; Hypothetical protein;
KW Nucleotide-binding; Transport.
SQ SEQUENCE 470 AA; 51239 MW; 682775F2C9FC4C11 CRC64;
    Query Match 70.0%; Score 35; DB 2; Length 470;
    Best Local Similarity 66.7%; Pred. No. 5.6e+02;
    Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Oy 1 QQSNEDPPT 9
Db 107 QQSNQPPS 115
RESULT 45
ID Q8HF4_ECOL6 PRELIMINARY; PRT; 472 AA.
AC Q8HF4_
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Protein hipA.
GN Name=hipA; OrderedLocusNames=c1940;
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=O6.H1 / CFT073 / ATCC 70028 / UPEC;
RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Raeko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
DR EMBL; AE016760; AAN0398.1; -; Genomic DNA.
DR GO; GO:0008237; F:metalloproteinase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006025; Pept_Mn_BS.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Complete proteome; Hydrolase; Metal-binding; Metalloprotease;
KW Protease; Zinc.
SQ SEQUENCE 472 AA; 52843 MW; F5758EFC9BD0393A CRC64;
    Query Match 70.0%; Score 35; DB 2; Length 472;
    Best Local Similarity 55.6%; Pred. No. 5.6e+02;
    Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Oy 1 QQSNEDPPT 9
Db 453 EQNNHPPPT 461
RESULT 46
Q8BXR2_MOUSE PRELIMINARY; PRT; 542 AA.
ID Q8BXR2_MOUSE
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AC DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus adult retina cDNA, RIKEN full-length enriched library,
DE clone:A930013F09 product:similar to OVARC1001010 PROTEIN.
GN Name=A933434L15Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Retina;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Retina;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Retina;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Retina;
RX MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Retina;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
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RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Schenck M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RA Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multipillar sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RC EMBL; AK020021; BAB31969.1; -; mRNA.
DR Ensembl; ENSMUSG0000028018; Mus musculus.
DR MGI; MGI:1914803; 4933434L15R1K.
DR GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransf. . .; IEA.
DR InterPro; IPR000051; SAM_bd.
FT NON TER 1
SQ SEQUENCE 564 AA; 62711 MW; 8EAF7A27E35B53DA CRC64;

Query Match 70.0%; Score 35; DB 2; Length 542;
Best Local Similarity 66.7%; Pred. No. 6.8e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSNEPPT 9
DB 164 QESSEHPT 172

RESULT 47
QIDT Q9CTV2_MOUSE PRELIMINARY; PRT; 564 AA.
AC Q9CTV2;
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mus musculus adult male thymus cDNA, RIKEN full-length enriched
DE library, clone:5830430H09 product:similar to OVARC1001010 PROTEIN
DE (Fragment).
GN Name=4933434L15R1K;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

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ID Q6LEX9 CAEBR PRELIMINARY; PRT; 572 AA.
 AC Q6LEX9
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein CBG11883 (Fragment).
 GN Name=CBG11883;
 OS Caenorhabditis briggsae.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=62328;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RG The C.briggsae Sequencing Consortium;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAC0100058; CAB66568.1; -; Genomic_DNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0016887; F:ATPase activity; IEA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0051082; F:unfolded protein binding; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR GO; GO:0015031; P:protein transport; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR004487; ClpX.
 DR SMART; SM00382; AAA; 1.
 DR TIGRFAMS; TIGR00382; clpX; 1.
 KW ATP-binding; Hypothetical protein; Nucleotide-binding.
 FT NON_TER 1
 SQ SEQUENCE 572 AA; 62028 MW; 01C238A71D7BF63F CRC64;

Query Match 70.0%; Score 35; DB 2; Length 572;
 Best Local Similarity 66.7%; Pred. No. 7e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOSNEDPPT 9
 Db 207 QOSNNQPS 215

RESULT 49
 EIL1_ARATH
 ID EIL1_ARATH STANDARD; PRT; 584 AA.
 AC Q9SLH0; O23114;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE ETHYLENE-INSENSITIVE3-like 1 protein.
 GN Name=EIL1; OrderedLocusNames=At2g27050; ORFNames=T20P8.10;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE, AND FUNCTION.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=97358539; PubMed=9215635; DOI=10.1016/S0092-8674(00)80300-1;
 RA Chao Q., Rothenberg M., Solano R., Roman G., Terzaghi W., Ecker J.R.;
 RT "Activation of the ethylene gas response pathway in Arabidopsis by the
 RT nuclear protein ETHYLENE-INSENSITIVE3 and related proteins.";
 RL Cell 89:1133-1144 [1997].
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083487; PubMed=10617197; DOI=10.1038/45471;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
 RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,

RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
 RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
 RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
 RA Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 402:761-768 (1999).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=cv. Columbia;
 RX MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;
 RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
 RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
 RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
 RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
 RA Chan M.T., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
 RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
 RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.P.,
 RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
 RA Khan S., Koeseema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
 RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
 RA Satou M., Tamse R., Vaysberg M., Wallander E.K., Wong C., Yamamura Y.,
 RA Yuan S., Shinzaki K., Davis R.W., Theologis A., Ecker J.R.;
 RT "Empirical analysis of transcriptional activity in the Arabidopsis
 RT genome.";
 RL Science 302:842-846 (2003).
 RN [4]
 RP CHARACTERIZATION, AND FUNCTION.
 RC MEDLINE=99069218; PubMed=9851977;
 RA Solano R., Stepanova A.N., Chao Q., Ecker J.R.;
 RT "Nuclear events in ethylene signaling: a transcriptional cascade
 RT mediated by ETHYLENE-INSENSITIVE3 and ETHYLENE-RESPONSE-FACTOR1.";
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 RP CHARACTERIZATION, AND MUTANTS EIL1-1 AND EIL1-2.
 RX MEDLINE=22506420; PubMed=12606727; DOI=10.1073/pnas.0438070100;
 RA Alonso J.M., Stepanova A.N., Solano R., Wisman E., Ferrari S.,
 RA Ausubel F.M., Ecker J.R.;
 RT "Five components of the ethylene-response pathway identified in a
 RT screen for weak ethylene-insensitive mutants in Arabidopsis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:2992-2997 (2003).
 CC -!- FUNCTION: Probable transcription factor acting as a positive
 CC regulator in the ethylene response pathway. Could bind the primary
 CC ethylene response element present in the ETHYLENE-RESPONSE-FACTOR1
 CC promoter.
 CC -!- SUBUNIT: Acts as homodimer to bind the primary ethylene response
 CC element (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -!- MISCELLANEOUS: Loss-of-function mutations (EIL1-1 and EIL1-2) in
 CC the gene show a weak ethylene-insensitive phenotype.
 CC -!- SIMILARITY: Belongs to the EIN3 family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; AF044213; AAC49746.1; -; mRNA.
 CC EMBL; AC005623; AAC77863.1; -; Genomic_DNA.
 CC EMBL; AY065191; AAL38367.1; -; mRNA.
 CC EMBL; BT003344; AAC29962.1; -; mRNA.
 CC PIR; B84668; B84668.
 CC SMR; Q9SLH0; 180-303.
 CC TRANSFAC; T02650; -.
 CC GeneFarm; 2366; -.
 CC GO; GO:0003700; P:transcription factor activity; TAS.
 CC GO; GO:0009873; P:ethylene mediated signaling pathway; TAS.
 CC InterPro; IPR006957; EIN3.
 CC Pfam; PF04873; EIN3; 1.
 KW Activator; Coiled coil; DNA-binding; Nuclear protein; Transcription;
 KW Transcription regulation.
 FT COILED 41 74 Potential.

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FT COMBIAS 570 578 Poly-Gln.
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SQ SEQUENCE 584 AA; 66495 MW; 471E1715D1483B11 CRC64;

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Db 491 QSNQTPPT 498

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DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein D2030.2a.
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OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
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RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2.
RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RT The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z73906; CAA98115.1; -; Genomic_DNA.
DR PIR; T20353; T20353.
DR HSP; O25926; IUM8.
DR Ensembl; D2030.2; Caenorhabditis elegans.
DR WormBase; WBGene0008412; D2030.2.
DR WormPep; D2030.2a; CR09079.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0051082; P:unfolded protein binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0015031; P:protein transport; IEA.
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DR SMART; SM00382; AAA; 1.
DR TIGRFAMs; TIGR00382; clpX; 1.
KW ATP-binding; Complete proteome; Hypothetical protein;
KW Nucleotide-binding; Transport.
SQ SEQUENCE 586 AA; 63606 MW; DFF205957A53A805 CRC64;

Query Match
Best Local Similarity 70.0%; Score 35; DB 2; Length 586;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSNEDPPT 9
Db 223 QOSNNQPPS 231

Search completed: February 23, 2006, 09:50:51
Job time : 118.538 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 09:29:34 ; Search time 60.3077 Seconds
(without alignments)
50.999 Million cell updates/sec

Title: US-10-723-872-22

Perfect score: 34

Sequence: 1 TSGMGVS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

- A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 34 | 100.0 | 7 | 2 | AAY23775 CDR of th |
| 3 | 34 | 100.0 | 7 | 2 | AAY18111 Heavy cha |
| 4 | 34 | 100.0 | 7 | 5 | AAR18530 Murine Ma |
| 5 | 34 | 100.0 | 7 | 6 | ABP58279 Murine mo |
| 6 | 34 | 100.0 | 7 | 9 | ADZ08828 Mammalian |
| 7 | 34 | 100.0 | 121 | 2 | AAY23780 Heavy cha |
| 8 | 34 | 100.0 | 121 | 2 | AAY18122 Heavy cha |
| 9 | 34 | 100.0 | 121 | 5 | AAR18528 Murine Ma |
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| 12 | 34 | 100.0 | 121 | 9 | AEA37667 Mouse CD4 |
| 13 | 34 | 100.0 | 122 | 8 | ADQ09631 Variable |
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| 15 | 34 | 100.0 | 123 | 6 | ABP58285 Humanised |
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| 17 | 34 | 100.0 | 140 | 2 | AAY23768 Heavy cha |
| 18 | 34 | 100.0 | 140 | 2 | AAY18121 Heavy cha |
| 19 | 34 | 100.0 | 141 | 2 | AAR70192 Humanized |
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| 21 | 34 | 100.0 | 141 | 2 | AAY23770 Heavy cha |
| 22 | 34 | 100.0 | 141 | 2 | AAY23769 Heavy cha |
| 23 | 34 | 100.0 | 141 | 2 | AAY18125 Chimeric |
| 24 | 34 | 100.0 | 141 | 2 | AAY18117 Heavy cha |

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| 26 | 34 | 100.0 | 142 | 8 | ADR88420 Murine 10 |
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| 37 | 31 | 91.2 | 142 | 7 | AAY42972 Chimeric |
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| 40 | 30 | 88.2 | 12 | 7 | ADD94204 Mouse HUI |
| 41 | 30 | 88.2 | 12 | 7 | ADD94153 Mouse HUI |
| 42 | 30 | 88.2 | 12 | 7 | ADD94205 Mouse HUI |
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| 44 | 30 | 88.2 | 111 | 2 | AAR66304 Human imm |
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| 49 | 30 | 88.2 | 120 | 6 | ABO10813 Mouse mon |
| 50 | 30 | 88.2 | 120 | 8 | ADQ09629 Variable |
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| 55 | 30 | 88.2 | 123 | 7 | ADD94127 Mouse HUI |
| 56 | 30 | 88.2 | 124 | 7 | ADB97818 HEV relat |
| 57 | 30 | 88.2 | 139 | 2 | AAR88107 Murine an |
| 58 | 30 | 88.2 | 228 | 8 | ADN41872 Amino aci |
| 59 | 30 | 88.2 | 253 | 4 | AU35322 Enterococ |
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| 65 | 30 | 88.2 | 292 | 9 | ABE49926 A. aeolic |
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| 104 | 29 | 85.3 | 352 | 5 | AAO17818 | AAO17818 Human cel | 177 | 28 | 82.4 | 349 | 3 | AAW44754 | Bovine co |
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| 107 | 29 | 85.3 | 410 | 6 | ADA14306 | ADA14306 Human Skp | 180 | 28 | 82.4 | 349 | 4 | AAW90791 | Human she |
| 108 | 29 | 85.3 | 410 | 8 | ABM80609 | ABM80609 Tumour-as | 181 | 28 | 82.4 | 349 | 4 | AAW60664 | Human con |
| 109 | 29 | 85.3 | 410 | 8 | ADS88278 | ADS88278 Human pro | 182 | 28 | 82.4 | 349 | 4 | AAW48831 | Human con |
| 110 | 29 | 85.3 | 424 | 4 | AAW52236 | AAW52236 Mouse Skp | 183 | 28 | 82.4 | 349 | 4 | AAW05923 | Human con |
| 111 | 29 | 85.3 | 424 | 5 | AAO17814 | AAO17814 Human cel | 184 | 28 | 82.4 | 349 | 5 | AAW68624 | Human pan |
| 112 | 29 | 85.3 | 424 | 8 | ABW80610 | ABW80610 Tumour-as | 185 | 28 | 82.4 | 349 | 6 | ABW92069 | Human cer |
| 113 | 29 | 85.3 | 435 | 2 | AAW11230 | AAW11230 S-phase k | 186 | 28 | 82.4 | 349 | 6 | ABW43135 | Human con |
| 114 | 29 | 85.3 | 435 | 4 | AAW48310 | AAW48310 Human Skp | 187 | 28 | 82.4 | 349 | 6 | ABW43137 | Porcine c |
| 115 | 29 | 85.3 | 435 | 4 | AAW52237 | AAW52237 Human Skp | 188 | 28 | 82.4 | 349 | 6 | ABW43136 | Bovine co |
| 116 | 29 | 85.3 | 442 | 5 | AAO17815 | AAO17815 Human cel | 189 | 28 | 82.4 | 349 | 6 | ADW43043 | Human con |
| 117 | 29 | 85.3 | 575 | 6 | ABU20567 | ABU20567 Protein e | 190 | 28 | 82.4 | 349 | 6 | ADW52763 | Human con |
| 118 | 29 | 85.3 | 645 | 8 | ADN27287 | ADN27287 Bacterial | 191 | 28 | 82.4 | 349 | 6 | ADW25761 | Human con |
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| 122 | 29 | 85.3 | 826 | 7 | ABO63824 | ABO63824 Klebsiell | 195 | 28 | 82.4 | 349 | 8 | ADH10248 | Human CTG |
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| 124 | 29 | 85.3 | 1103 | 2 | AAW13447 | AAW13447 Mouse aor | 197 | 28 | 82.4 | 349 | 8 | ADI27156 | Cow LRP b |
| 125 | 29 | 85.3 | 1128 | 2 | AAW49994 | AAW49994 Mouse car | 198 | 28 | 82.4 | 349 | 8 | ADL82863 | Human PRO |
| 126 | 29 | 85.3 | 1274 | 2 | AAW36817 | AAW36817 Mouse E2A | 199 | 28 | 82.4 | 349 | 8 | ADN04376 | Antipsori |
| 127 | 29 | 85.3 | 1278 | 2 | AAW34714 | AAW34714 Bacillus | 200 | 28 | 82.4 | 349 | 8 | ADQ26762 | Form proc |
| 128 | 29 | 85.3 | 1391 | 8 | ADN24279 | ADN24279 Bacterial | 201 | 28 | 82.4 | 349 | 8 | ADQ93890 | Human con |
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| 130 | 28 | 82.4 | 22 | 2 | AAW31612 | AAW31612 Fragment | 203 | 28 | 82.4 | 349 | 9 | ADW86252 | Human con |
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| 132 | 28 | 82.4 | 49 | 9 | ADG62172 | ADG62172 SRV SP20 | 205 | 28 | 82.4 | 349 | 9 | ADW72447 | Human con |
| 133 | 28 | 82.4 | 69 | 7 | ABO64308 | ABO64308 Klebsiell | 206 | 28 | 82.4 | 349 | 9 | ADW72445 | Human con |
| 134 | 28 | 82.4 | 71 | 6 | ABG72648 | ABG72648 Human con | 207 | 28 | 82.4 | 349 | 9 | ADW72448 | Human con |
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| 139 | 28 | 82.4 | 161 | 4 | AAW87616 | AAW87616 Bovine ma | 212 | 28 | 82.4 | 354 | 3 | AAW81438 | Human gro |
| 140 | 28 | 82.4 | 172 | 3 | AAW92941 | AAW92941 Human con | 213 | 28 | 82.4 | 354 | 5 | AAU99740 | Human con |
| 141 | 28 | 82.4 | 252 | 6 | ABW71071 | ABW71071 Staphyloc | 214 | 28 | 82.4 | 354 | 5 | ABG32500 | Human WIS |
| 142 | 28 | 82.4 | 282 | 8 | ADO61925 | ADO61925 Transcrip | 215 | 28 | 82.4 | 354 | 6 | ABG72639 | Human con |
| 143 | 28 | 82.4 | 339 | 2 | AAW17656 | AAW17656 Human put | 216 | 28 | 82.4 | 354 | 6 | ADW17597 | Amino aci |
| 144 | 28 | 82.4 | 339 | 2 | AAW17654 | AAW17654 Human put | 217 | 28 | 82.4 | 372 | 5 | ABG32501 | Human WIS |
| 145 | 28 | 82.4 | 339 | 6 | ADW17593 | ADW17593 Amino aci | 218 | 28 | 82.4 | 372 | 5 | ABG32501 | Human WIS |
| 146 | 28 | 82.4 | 339 | 6 | ADW17596 | ADW17596 Amino aci | 219 | 28 | 82.4 | 372 | 8 | ADP55718 | Amino aci |
| 147 | 28 | 82.4 | 347 | 2 | AAW12694 | AAW12694 Connectiv | 220 | 28 | 82.4 | 372 | 8 | ADP55718 | Human PRO |
| 148 | 28 | 82.4 | 347 | 2 | AAW24379 | AAW24379 Rat conne | 221 | 28 | 82.4 | 376 | 6 | ABW52664 | Protein s |
| 149 | 28 | 82.4 | 347 | 3 | AAW93340 | AAW93340 Amino aci | 222 | 28 | 82.4 | 376 | 7 | ADK61764 | Disease t |
| 150 | 28 | 82.4 | 347 | 6 | ABR43138 | ABR43138 Rat CTGf | 223 | 28 | 82.4 | 386 | 6 | ADA36321 | Actinotoba |
| 151 | 28 | 82.4 | 347 | 8 | ADH10252 | ADH10252 Rat CTGf | 224 | 28 | 82.4 | 386 | 6 | ADW07826 | Alloioococ |
| 152 | 28 | 82.4 | 347 | 8 | ADI27155 | ADI27155 Rat LRP b | 225 | 28 | 82.4 | 395 | 6 | ABU25125 | Protein e |
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| 154 | 28 | 82.4 | 348 | 2 | AAW35731 | AAW35731 Murine Fi | 227 | 28 | 82.4 | 471 | 4 | AAW78423 | Human pro |
| 155 | 28 | 82.4 | 348 | 3 | AAW44756 | AAW44756 Mouse con | 228 | 28 | 82.4 | 504 | 4 | AAW76759 | Corynebac |
| 156 | 28 | 82.4 | 348 | 4 | AAE05922 | AAE05922 Mouse fib | 229 | 28 | 82.4 | 504 | 4 | AAW93247 | C glutami |
| 157 | 28 | 82.4 | 348 | 5 | ABW09204 | ABW09204 Human ctg | 230 | 28 | 82.4 | 504 | 7 | ADL65515 | C. glutam |
| 158 | 28 | 82.4 | 348 | 5 | ABW09205 | ABW09205 Fisp-12 C | 231 | 28 | 82.4 | 507 | 3 | AAW10374 | Arabidops |
| 159 | 28 | 82.4 | 348 | 6 | ABR43139 | ABR43139 Mouse con | 232 | 28 | 82.4 | 507 | 3 | AAW43894 | Arabidops |
| 160 | 28 | 82.4 | 348 | 6 | ADW25766 | ADW25766 Mouse con | 233 | 28 | 82.4 | 530 | 2 | AAW57091 | Small rou |
| 161 | 28 | 82.4 | 348 | 6 | ADW25762 | ADW25762 Mouse con | 234 | 28 | 82.4 | 530 | 4 | AAW49701 | Small rou |
| 162 | 28 | 82.4 | 348 | 8 | ADH10250 | ADH10250 Mouse CTG | 235 | 28 | 82.4 | 530 | 5 | ADZ22152 | Norwalk v |
| 163 | 28 | 82.4 | 348 | 8 | ADI27153 | ADI27153 Mouse LRP | 236 | 28 | 82.4 | 582 | 5 | ABG32499 | Human WIS |
| 164 | 28 | 82.4 | 348 | 8 | ADQ26763 | ADQ26763 Form proc | 237 | 28 | 82.4 | 600 | 5 | ABG32498 | Human WIS |
| 165 | 28 | 82.4 | 348 | 8 | ADW49899 | ADW49899 Murine Cr | 238 | 28 | 82.4 | 611 | 6 | ADW07828 | Alloioococ |
| 166 | 28 | 82.4 | 348 | 9 | ADY72450 | ADY72450 Murine co | 239 | 28 | 82.4 | 654 | 8 | ADQ96510 | T cell ac |
| 167 | 28 | 82.4 | 348 | 9 | ADY72446 | ADY72446 Murine co | 240 | 28 | 82.4 | 706 | 5 | AAW79407 | Human pro |
| 168 | 28 | 82.4 | 348 | 9 | AEA00216 | AEA00216 Fisp12 pr | 241 | 28 | 82.4 | 706 | 5 | ABW92784 | Herbicida |
| 169 | 28 | 82.4 | 349 | 2 | AAW79964 | AAW79964 Connectiv | 242 | 28 | 82.4 | 723 | 8 | ADW21909 | Bacterial |
| 170 | 28 | 82.4 | 349 | 2 | AAW11302 | AAW11302 Connectiv | 243 | 28 | 82.4 | 765 | 4 | ABW70099 | Drosophil |

| | | | | | | | | | | | | | | | |
|-----|----|------|------|---|-----------|-----------|-----------|-----|----|------|-----|---|----------|----------|-----------|
| 244 | 28 | 82.4 | 827 | 6 | AD807830 | Adb07830 | Alloioioc | 317 | 27 | 79.4 | 451 | 8 | ADN26954 | Adn26954 | Bacterial |
| 245 | 28 | 82.4 | 830 | 6 | AD807832 | Adb07832 | Alloioioc | 318 | 27 | 79.4 | 463 | 8 | ADR31316 | Adr31316 | Aspergill |
| 246 | 28 | 82.4 | 1194 | 4 | ABBS59646 | Abbs59646 | Drosophil | 319 | 27 | 79.4 | 477 | 4 | AAB70765 | Aab70765 | Human bet |
| 247 | 28 | 82.4 | 1497 | 5 | ABP43711 | Abp43711 | Bullous p | 320 | 27 | 79.4 | 477 | 4 | ABO62389 | AbO62389 | Klebsiell |
| 248 | 28 | 82.4 | 1497 | 6 | ADA83846 | Ada83846 | Human COL | 321 | 27 | 79.4 | 553 | 4 | AUJ34282 | AuJ34282 | Staphyloc |
| 249 | 27 | 79.4 | 15 | 2 | AAR20275 | Aar20275 | Beta-2 in | 322 | 27 | 79.4 | 554 | 2 | AAR26271 | Aar26271 | Alpha-ace |
| 250 | 27 | 79.4 | 15 | 2 | AAR02063 | Aar02063 | Human bet | 323 | 27 | 79.4 | 554 | 2 | AAR26271 | Aar26271 | Alpha-ace |
| 251 | 27 | 79.4 | 29 | 7 | ADD71541 | Add71541 | Human uri | 324 | 27 | 79.4 | 554 | 5 | ABP39557 | Abp39557 | S. epider |
| 252 | 27 | 79.4 | 79 | 4 | AU46600 | Au46600 | Propionib | 325 | 27 | 79.4 | 554 | 5 | ABP39557 | Abp39557 | Staphyloc |
| 253 | 27 | 79.4 | 79 | 6 | ABM43119 | Abm43119 | Propionib | 326 | 27 | 79.4 | 554 | 5 | ABM4503 | Abm4503 | Lactococc |
| 254 | 27 | 79.4 | 85 | 4 | AAM96629 | Aam96629 | Human rep | 327 | 27 | 79.4 | 554 | 6 | ABU16377 | Abu16377 | Protein e |
| 255 | 27 | 79.4 | 85 | 4 | AAM96629 | Aam96629 | Human rep | 328 | 27 | 79.4 | 554 | 6 | ABU16377 | Abu16377 | Protein e |
| 256 | 27 | 79.4 | 85 | 4 | AAM96629 | Aam96629 | Human rep | 329 | 27 | 79.4 | 554 | 6 | ABU16377 | Abu16377 | Protein e |
| 257 | 27 | 79.4 | 85 | 4 | AAM96629 | Aam96629 | Human rep | 330 | 27 | 79.4 | 554 | 6 | ABU16377 | Abu16377 | Protein e |
| 258 | 27 | 79.4 | 95 | 4 | AAM92152 | Aam92152 | Human dig | 331 | 27 | 79.4 | 554 | 8 | AD805516 | Ad805516 | Staphyloc |
| 259 | 27 | 79.4 | 95 | 4 | AAM92152 | Aam92152 | Human dig | 332 | 27 | 79.4 | 554 | 8 | AD805516 | Ad805516 | Staphyloc |
| 260 | 27 | 79.4 | 95 | 5 | ABP40876 | Abp40876 | Human liv | 333 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 261 | 27 | 79.4 | 95 | 5 | ADJ14994 | Adj14994 | Human liv | 334 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 262 | 27 | 79.4 | 116 | 4 | AGC82646 | Agc82646 | S. epider | 335 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 263 | 27 | 79.4 | 124 | 8 | ADP09713 | Adp09713 | Glycosylt | 336 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 264 | 27 | 79.4 | 127 | 3 | AGG00027 | Agg00027 | Human sec | 337 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 265 | 27 | 79.4 | 128 | 4 | AAM15819 | Aam15819 | Peptide # | 338 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 266 | 27 | 79.4 | 128 | 4 | ABB34812 | Abb34812 | Peptide # | 339 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 267 | 27 | 79.4 | 128 | 4 | AAM28329 | Aam28329 | Peptide # | 340 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 268 | 27 | 79.4 | 128 | 4 | ABE29638 | AbE29638 | Peptide # | 341 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 269 | 27 | 79.4 | 128 | 4 | ABE20231 | AbE20231 | Protein # | 342 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 270 | 27 | 79.4 | 128 | 4 | AAM68001 | Aam68001 | Human bon | 343 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 271 | 27 | 79.4 | 128 | 4 | AAM55617 | Aam55617 | Human bra | 344 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 272 | 27 | 79.4 | 128 | 4 | ABG49644 | Abg49644 | Human liv | 345 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 273 | 27 | 79.4 | 128 | 4 | AAM03557 | Aam03557 | Peptide # | 346 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 274 | 27 | 79.4 | 128 | 5 | ABG37534 | Abg37534 | Human pep | 347 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 275 | 27 | 79.4 | 133 | 7 | ABM11310 | Abm11310 | Human ant | 348 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 276 | 27 | 79.4 | 141 | 2 | ADY07486 | Aay07486 | Anti-HIV | 349 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 277 | 27 | 79.4 | 145 | 8 | ADY75047 | Ady75047 | Plant ful | 350 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 278 | 27 | 79.4 | 170 | 8 | ADY75674 | Ady75674 | Plant ful | 351 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 279 | 27 | 79.4 | 170 | 8 | ADY75674 | Ady75674 | Plant ful | 352 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 280 | 27 | 79.4 | 178 | 8 | ADX89247 | Adx89247 | Plant ful | 353 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 281 | 27 | 79.4 | 179 | 8 | ADX89449 | Adx89449 | Plant ful | 354 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 282 | 27 | 79.4 | 200 | 8 | ADY23598 | Ady23598 | Plant ful | 355 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 283 | 27 | 79.4 | 235 | 2 | AAY34419 | Aay34419 | Porphorym | 356 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 284 | 27 | 79.4 | 243 | 4 | AAY37146 | Aay37146 | Staphyloc | 357 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 285 | 27 | 79.4 | 248 | 8 | ADS25781 | AdS25781 | Bacterial | 358 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 286 | 27 | 79.4 | 248 | 8 | ADS22481 | AdS22481 | Bacterial | 359 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 287 | 27 | 79.4 | 248 | 8 | ADS25361 | AdS25361 | Bacterial | 360 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 288 | 27 | 79.4 | 248 | 8 | ADS25961 | AdS25961 | Bacterial | 361 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 289 | 27 | 79.4 | 251 | 4 | AAM93928 | Aam93928 | Human pol | 362 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 290 | 27 | 79.4 | 251 | 8 | ADL32064 | AdL32064 | Human pro | 363 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 291 | 27 | 79.4 | 254 | 6 | ABU24674 | Abu24674 | Protein e | 364 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 292 | 27 | 79.4 | 255 | 8 | ADL05734 | AdL05734 | M. catar | 365 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 293 | 27 | 79.4 | 255 | 8 | ADS42386 | AdS42386 | Bacterial | 366 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 294 | 27 | 79.4 | 261 | 6 | ABP57624 | Abp57624 | S. muraya | 367 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 295 | 27 | 79.4 | 283 | 6 | ABU21546 | Abu21546 | Protein e | 368 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 296 | 27 | 79.4 | 294 | 9 | ADY251570 | AdY251570 | High-func | 369 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 297 | 27 | 79.4 | 319 | 8 | ADX94186 | Adx94186 | Plant ful | 370 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 298 | 27 | 79.4 | 328 | 7 | ADM25952 | Adm25952 | Hyperther | 371 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 299 | 27 | 79.4 | 385 | 2 | AAR45751 | Aar45751 | Erwinia a | 372 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 300 | 27 | 79.4 | 385 | 6 | AAM06598 | Aam06598 | Hypersens | 373 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 301 | 27 | 79.4 | 389 | 6 | AAM039461 | Aam039461 | Protein e | 374 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 302 | 27 | 79.4 | 403 | 2 | AAM61114 | Aam61114 | Hypersens | 375 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 303 | 27 | 79.4 | 403 | 2 | AAM62455 | Aam62455 | Erwinia a | 376 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 304 | 27 | 79.4 | 403 | 2 | AAM75863 | Aam75863 | Erwinia a | 377 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 305 | 27 | 79.4 | 403 | 3 | AAM87639 | Aam87639 | A hyperse | 378 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 306 | 27 | 79.4 | 403 | 3 | AAY71093 | Aay71093 | Erwinia a | 379 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 307 | 27 | 79.4 | 403 | 3 | AAY84854 | Aay84854 | A hyperse | 380 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 308 | 27 | 79.4 | 403 | 4 | AAS06710 | Aas06710 | Erwinia a | 381 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 309 | 27 | 79.4 | 403 | 5 | AO22547 | Ao22547 | Hypersens | 382 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 310 | 27 | 79.4 | 403 | 5 | AAE18295 | Aae18295 | Erwinia a | 383 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 311 | 27 | 79.4 | 403 | 5 | AAE16447 | Aae16447 | E. amylov | 384 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 312 | 27 | 79.4 | 403 | 5 | ADQ82182 | AdQ82182 | Erwinia a | 385 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 313 | 27 | 79.4 | 403 | 5 | ADQ82182 | AdQ82182 | Erwinia a | 386 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 314 | 27 | 79.4 | 403 | 8 | ADW76499 | Adw76499 | Protein e | 387 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 315 | 27 | 79.4 | 426 | 7 | ABO81279 | AbO81279 | Pseudomon | 388 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |
| 316 | 27 | 79.4 | 450 | 7 | ABO83538 | AbO83538 | Pseudomon | 389 | 27 | 79.4 | 559 | 6 | ABU44205 | Abu44205 | Bacterial |

| | | | | | | | | | | | | | |
|-----|----|------|----|---|----------|--------------------|-----|----|------|-----|---|-----------|---------------------|
| 390 | 26 | 76.5 | 15 | 8 | ADN65053 | Adn65053 HLA bindi | 463 | 26 | 76.5 | 82 | 4 | AAO02649 | Aao02649 Human pol |
| 391 | 26 | 76.5 | 15 | 9 | ADV22657 | Adv22657 HIV-1 Tat | 464 | 26 | 76.5 | 83 | 4 | AAM87360 | Aam87360 Human imm |
| 392 | 26 | 76.5 | 15 | 9 | ADV22658 | Adv22658 HIV-1 Tat | 465 | 26 | 76.5 | 86 | 2 | AAR09303 | Aar09303 Sequence |
| 393 | 26 | 76.5 | 16 | 8 | ADJ81753 | Adj81753 HIV vacci | 466 | 26 | 76.5 | 86 | 3 | AAG00043 | Aag00043 Human sec |
| 394 | 26 | 76.5 | 18 | 2 | AAV05141 | Aav05141 HIV Tat p | 467 | 26 | 76.5 | 86 | 4 | AAB46679 | Aab46679 HIV-1 Tat |
| 395 | 26 | 76.5 | 18 | 4 | AAV05141 | Aav05141 HIV Tat p | 468 | 26 | 76.5 | 86 | 4 | AAB46680 | Aab46680 HIV-1 Tat |
| 396 | 26 | 76.5 | 18 | 7 | ABO32488 | Ab032488 HIV-1 mul | 469 | 26 | 76.5 | 86 | 4 | AAB46685 | Aab46685 HIV-1 Tat |
| 397 | 26 | 76.5 | 18 | 7 | ADG71001 | Adg71001 HIV-1 Tat | 470 | 26 | 76.5 | 86 | 4 | AAB46682 | Aab46682 HIV-1 Tat |
| 398 | 26 | 76.5 | 18 | 7 | ADL94494 | Adl94494 HIV-1 Tat | 471 | 26 | 76.5 | 86 | 4 | AAB46681 | Aab46681 HIV-1 Tat |
| 399 | 26 | 76.5 | 20 | 4 | AAB46602 | Aab46602 HIV-1 Tat | 472 | 26 | 76.5 | 86 | 8 | ADS16231 | Ads16231 HIV-1 Tat |
| 400 | 26 | 76.5 | 20 | 8 | ADQ31334 | Adq31334 HIV-1 tat | 473 | 26 | 76.5 | 86 | 8 | ADS16232 | Ads16232 HIV-1 Tat |
| 401 | 26 | 76.5 | 20 | 8 | ADQ31332 | Adq31332 HIV-1 tat | 474 | 26 | 76.5 | 86 | 8 | ADS16233 | Ads16233 HIV-1 Tat |
| 402 | 26 | 76.5 | 21 | 5 | AAU89216 | Aau89216 Insulin/i | 475 | 26 | 76.5 | 87 | 8 | ADS16235 | Ads16235 HIV-1 Tat |
| 403 | 26 | 76.5 | 21 | 6 | ADA04039 | Ada04039 Insulin i | 476 | 26 | 76.5 | 91 | 5 | AAU87866 | Aau87866 Human PDZ |
| 404 | 26 | 76.5 | 21 | 8 | ADH95252 | Adh95252 Insulin r | 477 | 26 | 76.5 | 93 | 4 | AAU67982 | Aau67982 Propionib |
| 405 | 26 | 76.5 | 21 | 8 | ADL67943 | Adl67943 IGF-1R/IR | 478 | 26 | 76.5 | 93 | 6 | ABM64501 | Abm64501 Propionib |
| 406 | 26 | 76.5 | 21 | 8 | ADM37788 | Adm37788 Anti-IR f | 479 | 26 | 76.5 | 95 | 4 | AAO10614 | Aao10614 Human pol |
| 407 | 26 | 76.5 | 23 | 5 | AEE21950 | Aee21950 Human imm | 480 | 26 | 76.5 | 96 | 2 | AAW00723 | Aaw00723 Murine fi |
| 408 | 26 | 76.5 | 24 | 4 | AAW17673 | Aaw17673 Peptide # | 481 | 26 | 76.5 | 96 | 2 | AAW11890 | Aaw11890 Murine fi |
| 409 | 26 | 76.5 | 24 | 4 | ABB36692 | Abb36692 Peptide # | 482 | 26 | 76.5 | 96 | 5 | ABG78180 | Abg78180 Human Fv |
| 410 | 26 | 76.5 | 24 | 4 | AAW03189 | Aaw03189 Peptide # | 483 | 26 | 76.5 | 96 | 5 | ABG91871 | Abg91871 Human ant |
| 411 | 26 | 76.5 | 24 | 4 | ABB31481 | Abb31481 Peptide # | 484 | 26 | 76.5 | 99 | 3 | AAB69317 | Aab69317 HIV-1 non |
| 412 | 26 | 76.5 | 24 | 4 | ABB22029 | Abb22029 Protein # | 485 | 26 | 76.5 | 99 | 3 | AAB69312 | Aab69312 HIV-1 non |
| 413 | 26 | 76.5 | 24 | 4 | AAW69850 | Aaw69850 Human bon | 486 | 26 | 76.5 | 100 | 5 | ABG78181 | Abg78181 Human Fv |
| 414 | 26 | 76.5 | 24 | 4 | AAW57455 | Aaw57455 Human bra | 487 | 26 | 76.5 | 100 | 5 | ABG91872 | Abg91872 Human ant |
| 415 | 26 | 76.5 | 24 | 4 | ABG51543 | Abg51543 Human liv | 488 | 26 | 76.5 | 100 | 6 | ABO27079 | Ab027079 Human ger |
| 416 | 26 | 76.5 | 24 | 4 | AAW05336 | Aaw05336 Peptide # | 489 | 26 | 76.5 | 100 | 6 | ABO27081 | Ab027081 Human ger |
| 417 | 26 | 76.5 | 24 | 5 | ABG39478 | Abg39478 Human pep | 490 | 26 | 76.5 | 100 | 7 | ADF09906 | Adf09906 Antibody |
| 418 | 26 | 76.5 | 26 | 6 | ABR63239 | AbR63239 HIV-1 tat | 491 | 26 | 76.5 | 100 | 7 | ADF10116 | Adf10116 Antibody |
| 419 | 26 | 76.5 | 26 | 6 | ABR63238 | AbR63238 HIV-1 tat | 492 | 26 | 76.5 | 100 | 7 | ADF10014 | Adf10014 VEGF anti |
| 420 | 26 | 76.5 | 27 | 5 | AAE21938 | Aae21938 Human imm | 493 | 26 | 76.5 | 100 | 7 | ADJ80294 | Adj80294 VH gene 1 |
| 421 | 26 | 76.5 | 34 | 4 | AAO11320 | Aao11320 Human pol | 494 | 26 | 76.5 | 100 | 7 | ADJ80292 | Adj80292 VH gene 1 |
| 422 | 26 | 76.5 | 36 | 2 | AAO50599 | Aao50599 HIV Tat p | 495 | 26 | 76.5 | 100 | 9 | ADX40359 | Adx40359 HIV Tat p |
| 423 | 26 | 76.5 | 36 | 4 | AAW87931 | Aaw87931 Epitope I | 496 | 26 | 76.5 | 100 | 9 | ADX40404 | Adx40404 HIV Tat p |
| 424 | 26 | 76.5 | 36 | 7 | ABO32438 | Ab032438 HIV-1 mul | 497 | 26 | 76.5 | 100 | 9 | ADX40269 | Adx40269 HIV Tat p |
| 425 | 26 | 76.5 | 36 | 7 | ADE70951 | AdE70951 HIV-1 Tat | 498 | 26 | 76.5 | 100 | 9 | ADY75299 | Ady75299 Protein e |
| 426 | 26 | 76.5 | 36 | 7 | ADL94444 | Adl94444 HIV-1 Tat | 499 | 26 | 76.5 | 100 | 9 | ADY75297 | Ady75297 Protein e |
| 427 | 26 | 76.5 | 38 | 8 | ABO54457 | Ab054457 Human gen | 500 | 26 | 76.5 | 100 | 9 | AEC20846 | Aec20846 Human var |
| 428 | 26 | 76.5 | 57 | 2 | AAW95435 | Aaw95435 Apomyoglo | 501 | 26 | 76.5 | 101 | 3 | AAB69319 | Aab69319 HIV-1 non |
| 429 | 26 | 76.5 | 59 | 9 | AEC20857 | Aec20857 Human var | 502 | 26 | 76.5 | 101 | 3 | AAB69322 | Aab69322 HIV-1 non |
| 430 | 26 | 76.5 | 63 | 6 | AAU63218 | Aau63218 Propionib | 503 | 26 | 76.5 | 101 | 3 | AAB69320 | Aab69320 HIV-1 non |
| 431 | 26 | 76.5 | 63 | 6 | ABM59737 | Abm59737 Propionib | 504 | 26 | 76.5 | 101 | 3 | ABAB14224 | Abab14224 HIV Tat S |
| 432 | 26 | 76.5 | 64 | 4 | AAW20245 | Aaw20245 Peptide # | 505 | 26 | 76.5 | 101 | 6 | AAE37588 | Aae37588 HIV-1 sub |
| 433 | 26 | 76.5 | 64 | 4 | ABB40591 | Abb40591 Peptide # | 506 | 26 | 76.5 | 101 | 6 | AAE37594 | Aae37594 HIV-1 sub |
| 434 | 26 | 76.5 | 64 | 4 | AAW34351 | Aaw34351 Peptide # | 507 | 26 | 76.5 | 101 | 6 | AAE37587 | Aae37587 HIV-1 sub |
| 435 | 26 | 76.5 | 64 | 4 | ABB24881 | Abb24881 Protein # | 508 | 26 | 76.5 | 101 | 8 | ADOS2528 | Ado2528 HIV-1 rec |
| 436 | 26 | 76.5 | 64 | 4 | ABW74239 | Abw74239 Human bon | 509 | 26 | 76.5 | 101 | 8 | ADP20079 | Adp20079 Human imm |
| 437 | 26 | 76.5 | 64 | 4 | AAU56307 | Aau56307 Propionib | 510 | 26 | 76.5 | 101 | 8 | ADS16242 | Ads16242 HIV-1 Tat |
| 438 | 26 | 76.5 | 64 | 4 | AAU48126 | Aau48126 Propionib | 511 | 26 | 76.5 | 101 | 8 | ADS16243 | Ads16243 HIV-1 Tat |
| 439 | 26 | 76.5 | 64 | 4 | AAW61449 | Aaw61449 Human bra | 512 | 26 | 76.5 | 101 | 8 | ADS16244 | Ads16244 HIV-1 Tat |
| 440 | 26 | 76.5 | 64 | 4 | ABG56041 | Abg56041 Human liv | 513 | 26 | 76.5 | 101 | 8 | ADS16227 | Ads16227 HIV-1 Tat |
| 441 | 26 | 76.5 | 64 | 5 | AAO17223 | Aao17223 Human sec | 514 | 26 | 76.5 | 101 | 8 | ADS16230 | Ads16230 HIV-1 Tat |
| 442 | 26 | 76.5 | 64 | 5 | ABG44192 | Abg44192 Human pep | 515 | 26 | 76.5 | 101 | 9 | ADX40293 | Adx40293 HIV Tat p |
| 443 | 26 | 76.5 | 64 | 5 | ABG64787 | Abg64787 Human alb | 516 | 26 | 76.5 | 101 | 9 | ADX40349 | Adx40349 HIV Tat p |
| 444 | 26 | 76.5 | 64 | 6 | ABW52826 | Abw52826 Propionib | 517 | 26 | 76.5 | 101 | 9 | ADX40357 | Adx40357 HIV Tat p |
| 445 | 26 | 76.5 | 64 | 6 | ABW44645 | Abw44645 Propionib | 518 | 26 | 76.5 | 101 | 9 | ADX40267 | Adx40267 HIV Tat p |
| 446 | 26 | 76.5 | 64 | 8 | ADL78054 | Adl78054 Albumin f | 519 | 26 | 76.5 | 101 | 9 | ADX40287 | Adx40287 HIV Tat p |
| 447 | 26 | 76.5 | 65 | 4 | AAU55029 | Aau55029 Propionib | 520 | 26 | 76.5 | 101 | 9 | ADX40281 | Adx40281 HIV Tat p |
| 448 | 26 | 76.5 | 65 | 6 | ABW51548 | Abw51548 Propionib | 521 | 26 | 76.5 | 101 | 9 | ADX40291 | Adx40291 HIV Tat p |
| 449 | 26 | 76.5 | 69 | 2 | AAV48374 | Aav48374 Human pro | 522 | 26 | 76.5 | 101 | 9 | ADX40364 | Adx40364 HIV Tat p |
| 450 | 26 | 76.5 | 70 | 4 | AAU67965 | Aau67965 Propionib | 523 | 26 | 76.5 | 101 | 9 | ADX40400 | Adx40400 HIV Tat p |
| 451 | 26 | 76.5 | 70 | 6 | ABW64484 | Abw64484 Propionib | 524 | 26 | 76.5 | 101 | 9 | ADX40424 | Adx40424 HIV Tat p |
| 452 | 26 | 76.5 | 72 | 1 | AAW81864 | Aaw81864 Sequence | 525 | 26 | 76.5 | 101 | 9 | ADX40354 | Adx40354 HIV Tat p |
| 453 | 26 | 76.5 | 72 | 2 | AAW72996 | Aaw72996 HIV isola | 526 | 26 | 76.5 | 101 | 9 | ADX40402 | Adx40402 HIV Tat p |
| 454 | 26 | 76.5 | 72 | 2 | AAW05096 | Aaw05096 HIV Tat p | 527 | 26 | 76.5 | 101 | 9 | ADX40263 | Adx40263 HIV Tat p |
| 455 | 26 | 76.5 | 72 | 4 | AAW87878 | Aaw87878 Epitope p | 528 | 26 | 76.5 | 101 | 9 | ADX40277 | Adx40277 HIV Tat p |
| 456 | 26 | 76.5 | 72 | 5 | AAU11069 | Aau11069 HIV-1 Tat | 529 | 26 | 76.5 | 101 | 9 | ADX40405 | Adx40405 HIV Tat p |
| 457 | 26 | 76.5 | 72 | 7 | ABO32385 | Ab032385 Human imm | 530 | 26 | 76.5 | 101 | 9 | ADX40290 | Adx40290 HIV Tat p |
| 458 | 26 | 76.5 | 72 | 7 | ADE70897 | AdE70897 HIV-1 Tat | 531 | 26 | 76.5 | 101 | 9 | ADX40350 | Adx40350 HIV Tat p |
| 459 | 26 | 76.5 | 72 | 7 | ADL94390 | Adl94390 HIV-1 Tat | 532 | 26 | 76.5 | 101 | 9 | ADX40362 | Adx40362 HIV Tat p |
| 460 | 26 | 76.5 | 74 | 4 | AAW82713 | Aaw82713 Human imm | 533 | 26 | 76.5 | 101 | 9 | ADX40346 | Adx40346 HIV Tat p |
| 461 | 26 | 76.5 | 74 | 4 | AAU65129 | Aau65129 Propionib | 534 | 26 | 76.5 | 101 | 9 | ADX40327 | Adx40327 HIV Tat p |
| 462 | 26 | 76.5 | 74 | 6 | ABW61648 | Abw61648 Propionib | 535 | 26 | 76.5 | 101 | 9 | ADX40356 | Adx40356 HIV Tat p |

| | | | | | | | | | | | |
|-----|----|------|-----|---|-----------|---------------------|-----|-----|---|----------|---------------------|
| 536 | 26 | 76.5 | 101 | 9 | ADX40270 | Adx40270 HIV Tat p | 609 | 120 | 5 | ABB57583 | Abb57583 HLA-DR-ep |
| 537 | 26 | 76.5 | 101 | 9 | ADX40303 | Adx40303 HIV Tat p | 610 | 120 | 5 | ABB57577 | Abb57577 HLA-DR-ep |
| 538 | 26 | 76.5 | 101 | 9 | ADX40261 | Adx40261 HIV Tat p | 611 | 120 | 5 | ABB57585 | Abb57585 HLA-DR-ep |
| 539 | 26 | 76.5 | 101 | 9 | ADX40273 | Adx40273 HIV Tat p | 612 | 120 | 5 | ABB57565 | Abb57565 HLA-DR-ep |
| 540 | 26 | 76.5 | 101 | 9 | ADX40288 | Adx40288 HIV Tat p | 613 | 120 | 5 | ABB57567 | Abb57567 HLA-DR-ep |
| 541 | 26 | 76.5 | 101 | 9 | ADX40297 | Adx40297 HIV Tat p | 614 | 120 | 5 | ABB57581 | Abb57581 HLA-DR-ep |
| 542 | 26 | 76.5 | 101 | 9 | ADX40308 | Adx40308 HIV Tat p | 615 | 120 | 5 | ABB57587 | Abb57587 HLA-DR-ep |
| 543 | 26 | 76.5 | 101 | 9 | ADX40343 | Adx40343 HIV Tat p | 616 | 120 | 5 | ABB57569 | Abb57569 HLA-DR-ep |
| 544 | 26 | 76.5 | 101 | 9 | ADX40363 | Adx40363 HIV Tat p | 617 | 120 | 5 | ABB57551 | Abb57551 HLA-DR-ep |
| 545 | 26 | 76.5 | 101 | 9 | ADX40271 | Adx40271 HIV Tat p | 618 | 120 | 5 | ABB57579 | Abb57579 HLA-DR-ep |
| 546 | 26 | 76.5 | 101 | 9 | ADX40275 | Adx40275 HIV Tat p | 619 | 120 | 5 | ABB57589 | Abb57589 HLA-DR-ep |
| 547 | 26 | 76.5 | 101 | 9 | ADX40279 | Adx40279 HIV Tat p | 620 | 120 | 5 | ABJ18674 | Abj18674 Antibody |
| 548 | 26 | 76.5 | 101 | 9 | ADX40292 | Adx40292 HIV Tat p | 621 | 120 | 8 | ADU17898 | Adu17898 Humanised |
| 549 | 26 | 76.5 | 101 | 9 | ADX40345 | Adx40345 HIV Tat p | 622 | 120 | 8 | Aaw75552 | Aaw75552 Human Ab |
| 550 | 26 | 76.5 | 101 | 9 | ADX40358 | Adx40358 HIV Tat p | 623 | 121 | 6 | ABR63240 | AbR63240 HIV-1 shu |
| 551 | 26 | 76.5 | 101 | 9 | ADX40406 | Adx40406 HIV Tat p | 624 | 122 | 5 | ABB57563 | Abb57563 HLA-DR-ep |
| 552 | 26 | 76.5 | 101 | 9 | ADX40408 | Adx40408 HIV Tat p | 625 | 122 | 6 | AAE37591 | Aae37591 Tat conse |
| 553 | 26 | 76.5 | 101 | 9 | ADX40559 | Adx40559 HIV Tat p | 626 | 122 | 6 | ADV14358 | Adv14358 Hybriidoma |
| 554 | 26 | 76.5 | 101 | 9 | ADX40276 | Adx40276 HIV Tat p | 627 | 122 | 9 | ADY70835 | Ady70835 MS-GPC-8 |
| 555 | 26 | 76.5 | 101 | 9 | ADX40401 | Adx40401 HIV Tat p | 628 | 122 | 9 | ADY70837 | Ady70837 MS-GPC-10 |
| 556 | 26 | 76.5 | 101 | 9 | ADX40278 | Adx40278 HIV Tat p | 629 | 122 | 9 | ADY70831 | Ady70831 MS-GPC-1 |
| 557 | 26 | 76.5 | 101 | 9 | ADX40284 | Adx40284 HIV Tat p | 630 | 123 | 3 | ABA42043 | Aba42043 Human ORF |
| 558 | 26 | 76.5 | 101 | 9 | ADX40300 | Adx40300 HIV Tat p | 631 | 123 | 7 | ADD94131 | Add94131 Human VHI |
| 559 | 26 | 76.5 | 101 | 9 | ADX40325 | Adx40325 HIV Tat p | 632 | 126 | 5 | ABB57557 | Abb57557 HLA-DR-ep |
| 560 | 26 | 76.5 | 101 | 9 | ADX40326 | Adx40326 HIV Tat p | 633 | 126 | 5 | ADA90119 | Ada90119 Anti-Abet |
| 561 | 26 | 76.5 | 101 | 9 | ADX40403 | Adx40403 HIV Tat p | 634 | 128 | 6 | AAO31084 | Aao31084 Human ant |
| 562 | 26 | 76.5 | 101 | 9 | ADX40328 | Adx40328 HIV Tat p | 635 | 129 | 6 | AAU49156 | Aau49156 Propionib |
| 563 | 26 | 76.5 | 101 | 9 | ADX40360 | Adx40360 HIV Tat p | 636 | 129 | 6 | AAE35208 | Aae35208 Human IGE |
| 564 | 26 | 76.5 | 101 | 9 | AEB10595 | Aeb10595 Clade B t | 637 | 129 | 6 | ABM45675 | Abm45675 Propionib |
| 565 | 26 | 76.5 | 101 | 9 | AEB10644 | Aeb10644 Clade C t | 638 | 130 | 6 | ADA89117 | Ada89117 MS-Pro-12 |
| 566 | 26 | 76.5 | 101 | 9 | AEB10643 | Aeb10643 Clade C t | 639 | 130 | 7 | ADG74368 | Adg74368 MSPRO hea |
| 567 | 26 | 76.5 | 101 | 9 | AEB10594 | Aeb10594 Clade B t | 640 | 130 | 9 | ADM38823 | Adm38823 T-cell me |
| 568 | 26 | 76.5 | 101 | 9 | AEBA8170 | Aeba8170 Codon-opt | 641 | 133 | 4 | ADY70950 | Ady70950 Human mon |
| 569 | 26 | 76.5 | 102 | 3 | AEBA14225 | Aeba14225 HIV Tat C | 642 | 135 | 4 | AAU50347 | Aau50347 Propionib |
| 570 | 26 | 76.5 | 102 | 4 | AAU63446 | Aau63446 Propionib | 643 | 135 | 6 | ABM46866 | Abm46866 Propionib |
| 571 | 26 | 76.5 | 102 | 6 | ABM59965 | Abm59965 Propionib | 644 | 142 | 2 | ABO75180 | AbO75180 Pseudomon |
| 572 | 26 | 76.5 | 102 | 7 | ADC13228 | Adc13228 Protein o | 645 | 143 | 2 | AAr54092 | Aar54092 Sequence |
| 573 | 26 | 76.5 | 102 | 7 | ADJ32175 | Adj32175 Human int | 646 | 143 | 4 | AAg74815 | Aag74815 Human col |
| 574 | 26 | 76.5 | 102 | 8 | ADR46403 | Adr46403 HIV Tat p | 647 | 146 | 3 | AAg24917 | Aag24917 Arabidops |
| 575 | 26 | 76.5 | 102 | 9 | ADV23772 | Adv23772 HIV-1 ful | 648 | 146 | 3 | AAg29384 | Aag29384 Arabidops |
| 576 | 26 | 76.5 | 102 | 9 | ADW52520 | Adw52520 Human PDZ | 649 | 157 | 8 | ADL27471 | Adl27471 Amino aci |
| 577 | 26 | 76.5 | 102 | 9 | ADX40351 | Adx40351 HIV Tat p | 650 | 158 | 6 | ABU41238 | Abu41238 Protein e |
| 578 | 26 | 76.5 | 102 | 9 | ADX40331 | Adx40331 HIV Tat p | 651 | 166 | 7 | ADP06113 | Adp06113 Bacterial |
| 579 | 26 | 76.5 | 102 | 9 | ADX40392 | Adx40392 HIV Tat p | 652 | 171 | 7 | ABO72567 | AbO72567 Pseudomon |
| 580 | 26 | 76.5 | 102 | 9 | ADX40391 | Adx40391 HIV Tat p | 653 | 174 | 4 | ABB69946 | Abb69946 Drosophil |
| 581 | 26 | 76.5 | 103 | 3 | ABB43990 | Abb43990 Human can | 654 | 174 | 5 | AAU83090 | Aau83090 Noverl sec |
| 582 | 26 | 76.5 | 103 | 7 | ADD12404 | Add12404 PDZ ligan | 655 | 174 | 7 | ADC00012 | Adc00012 Enteroha |
| 583 | 26 | 76.5 | 103 | 8 | ADJ53426 | Adj53426 Human PDZ | 656 | 175 | 3 | AAg24916 | Aag24916 Arabidops |
| 584 | 26 | 76.5 | 103 | 8 | ADM33517 | Adm33517 Human PDZ | 657 | 179 | 3 | AAU63386 | Aau63386 Propionib |
| 585 | 26 | 76.5 | 103 | 8 | ADO20948 | Ado20948 PDZ domai | 658 | 179 | 6 | ABM59905 | Abm59905 Propionib |
| 586 | 26 | 76.5 | 103 | 8 | ADR82889 | Adr82889 PDZ domai | 659 | 184 | 4 | AAU61608 | Aau61608 Propionib |
| 587 | 26 | 76.5 | 103 | 8 | ADU15882 | Adu15882 KIAA0147 | 660 | 184 | 6 | ABM58127 | Abm58127 Propionib |
| 588 | 26 | 76.5 | 103 | 8 | ADU67306 | Adu67306 Human KIA | 661 | 191 | 9 | ADW17523 | Adw17523 Pinus rad |
| 589 | 26 | 76.5 | 103 | 9 | ADX40274 | Adx40274 HIV Tat p | 662 | 200 | 4 | AAU67891 | Aau67891 Propionib |
| 590 | 26 | 76.5 | 103 | 9 | AEBO7845 | Aebo7845 PDZ domai | 663 | 200 | 6 | ABM64410 | Abm64410 Propionib |
| 591 | 26 | 76.5 | 103 | 9 | AEA98859 | Aea98859 Human PDZ | 664 | 201 | 8 | ADX66908 | Adx66908 plant ful |
| 592 | 26 | 76.5 | 106 | 3 | AGL13773 | Agl13773 Arabidops | 665 | 202 | 2 | AAW11130 | Aaw11130 Anti-coag |
| 593 | 26 | 76.5 | 114 | 9 | AEBO7849 | Aebo7849 PDZ domai | 666 | 202 | 2 | AAW76691 | Aaw76691 R. prolix |
| 594 | 26 | 76.5 | 114 | 9 | AEA98863 | Aea98863 Human PDZ | 667 | 205 | 7 | ABO68682 | AbO68682 Pseudomon |
| 595 | 26 | 76.5 | 117 | 5 | ABR01692 | AbR01692 Human bre | 668 | 206 | 6 | ABU21029 | Abu21029 Protein e |
| 596 | 26 | 76.5 | 117 | 8 | ADF71914 | Adf71914 Hu3G8VH-2 | 669 | 220 | 4 | AAU16929 | Aau16929 Human nov |
| 597 | 26 | 76.5 | 118 | 2 | ADR625807 | Adr625807 Anti-CD30 | 670 | 230 | 5 | ABU52100 | Abu52100 Helicobac |
| 598 | 26 | 76.5 | 119 | 2 | AAR66299 | Aar66299 Human imm | 671 | 231 | 5 | ABU50921 | Abu50921 Helicobac |
| 599 | 26 | 76.5 | 120 | 5 | AAU83815 | Aau83815 MS-GPC-8 | 672 | 231 | 5 | ABU52067 | Abu52067 Helicobac |
| 600 | 26 | 76.5 | 120 | 5 | AAU83805 | Aau83805 MS-GPC-8 | 673 | 231 | 5 | ABU51779 | Abu51779 Helicobac |
| 601 | 26 | 76.5 | 120 | 5 | AAU83809 | Aau83809 MS-GPC-8 | 674 | 237 | 5 | ABU51029 | Abu51029 Helicobac |
| 602 | 26 | 76.5 | 120 | 5 | AAU83821 | Aau83821 MS-GPC-8 | 675 | 238 | 5 | ABU51303 | Abu51303 Helicobac |
| 603 | 26 | 76.5 | 120 | 5 | AAU83817 | Aau83817 MS-GPC-8 | 676 | 238 | 6 | ADA91405 | Ada91405 Anti-Abet |
| 604 | 26 | 76.5 | 120 | 5 | AAU83819 | Aau83819 MS-GPC-8 | 677 | 239 | 3 | AAE52590 | Aae52590 Helicobac |
| 605 | 26 | 76.5 | 120 | 5 | AAU83807 | Aau83807 MS-GPC-10 | 678 | 241 | 4 | AAE82740 | Aae82740 S. epider |
| 606 | 26 | 76.5 | 120 | 5 | AAU83811 | Aau83811 MS-GPC-8 | 679 | 243 | 6 | ABU48325 | Abu48325 Protein e |
| 607 | 26 | 76.5 | 120 | 5 | AAU83813 | Aau83813 MS-GPC-8 | 680 | 243 | 6 | ABU44978 | Abu44978 Protein e |
| 608 | 26 | 76.5 | 120 | 5 | AAU83801 | Aau83801 MS-GPC-1 | 681 | 245 | 8 | ADN26816 | Adn26816 Bacterial |

| | | | | | | | | | | | | | | |
|-----|----|------|-----|---|----------|------------|-----|----|------|------|----------|----------|-----------|-----------|
| 828 | 26 | 76.5 | 535 | 2 | Aaw04261 | Beta-amyl | 901 | 26 | 76.5 | 933 | 3 | AAB41685 | Aab41685 | Human ORF |
| 829 | 26 | 76.5 | 535 | 2 | AAW15746 | Mutated b | 902 | 26 | 76.5 | 1035 | 8 | ABM80057 | ABM80057 | Tumour-as |
| 830 | 26 | 76.5 | 535 | 8 | ADJ49120 | Oil-assoc | 903 | 26 | 76.5 | 1044 | 8 | ADR66107 | ADR66107 | Human pro |
| 831 | 26 | 76.5 | 535 | 8 | ADJ50119 | Oil-assoc | 904 | 26 | 76.5 | 1044 | 2 | ADR66449 | ADR66449 | Human pro |
| 832 | 26 | 76.5 | 535 | 8 | ADJ49037 | Oil-assoc | 905 | 26 | 76.5 | 1074 | 2 | ADR24102 | ADR24102 | Marek's d |
| 833 | 26 | 76.5 | 535 | 8 | ADJ50182 | Oil-assoc | 906 | 26 | 76.5 | 1103 | 8 | ADN20575 | ADN20575 | Bacterial |
| 834 | 26 | 76.5 | 541 | 2 | AAW13542 | Malolacti | 907 | 26 | 76.5 | 1185 | 6 | ABU18969 | ABU18969 | Protein e |
| 835 | 26 | 76.5 | 542 | 3 | AAW92902 | Human cer | 908 | 26 | 76.5 | 1223 | 7 | ADC30931 | ADC30931 | Human nov |
| 836 | 26 | 76.5 | 542 | 4 | AAW47274 | HOAT3 . 8/ | 909 | 26 | 76.5 | 1226 | 6 | ADC31436 | ADC31436 | Human nov |
| 837 | 26 | 76.5 | 542 | 7 | ADW82899 | Human sul | 910 | 26 | 76.5 | 1229 | 6 | AAE37597 | AAE37597 | HIV-1 Grt |
| 838 | 26 | 76.5 | 550 | 6 | ABU14986 | Protein e | 911 | 26 | 76.5 | 1372 | 4 | ABW59170 | ABW59170 | Drosophil |
| 839 | 26 | 76.5 | 553 | 6 | ABU49656 | Protein e | 912 | 26 | 76.5 | 1535 | 5 | AAU87934 | AAU87934 | Human pro |
| 840 | 26 | 76.5 | 553 | 6 | ABU47100 | Protein e | 913 | 26 | 76.5 | 1544 | 7 | AAE37934 | AAE37934 | Human CGD |
| 841 | 26 | 76.5 | 559 | 6 | ABU32254 | Protein e | 914 | 26 | 76.5 | 1550 | 6 | ABW71410 | ABW71410 | Staphyloc |
| 842 | 26 | 76.5 | 560 | 5 | ABP26763 | Streptoco | 915 | 26 | 76.5 | 1551 | 6 | ABO07162 | ABO07162 | Human p53 |
| 843 | 26 | 76.5 | 560 | 8 | ADW89303 | Streptoco | 916 | 26 | 76.5 | 1555 | 8 | ADQ96156 | ADQ96156 | T cell ac |
| 844 | 26 | 76.5 | 560 | 8 | ADW82725 | Streptoco | 917 | 26 | 76.5 | 1564 | 8 | ADQ43397 | ADQ43397 | Amino aci |
| 845 | 26 | 76.5 | 560 | 8 | ADW80556 | Streptoco | 918 | 26 | 76.5 | 1590 | 7 | ADD93657 | ADD93657 | Streptoco |
| 846 | 26 | 76.5 | 560 | 8 | ADW22341 | Plant ful | 919 | 26 | 76.5 | 1590 | 9 | ADX37280 | ADX37280 | Streptoco |
| 847 | 26 | 76.5 | 561 | 2 | AAW44196 | Human ost | 920 | 26 | 76.5 | 1592 | 2 | AAR32925 | AAR32925 | Glucosylt |
| 848 | 26 | 76.5 | 561 | 6 | ABU47760 | Protein e | 921 | 26 | 76.5 | 1609 | 7 | AAE37935 | AAE37935 | Human CGD |
| 849 | 26 | 76.5 | 562 | 7 | ABO63888 | Klebsiell | 922 | 26 | 76.5 | 1617 | 6 | ABW99403 | ABW99403 | Amino aci |
| 850 | 26 | 76.5 | 565 | 8 | ADO55107 | Protein # | 923 | 26 | 76.5 | 1630 | 8 | ADO34026 | ADO34026 | Human MBC |
| 851 | 26 | 76.5 | 568 | 9 | ADW69087 | SLC22A8 . | 924 | 26 | 76.5 | 1630 | 9 | ABW87779 | ABW87779 | Human scr |
| 852 | 26 | 76.5 | 577 | 4 | AAW04786 | Arabidops | 925 | 26 | 76.5 | 1739 | 4 | AAW42197 | AAW42197 | Human pol |
| 853 | 26 | 76.5 | 577 | 5 | ABW92416 | Herbicida | 926 | 26 | 76.5 | 1745 | 7 | ADF76869 | ADF76869 | Novel hum |
| 854 | 26 | 76.5 | 583 | 4 | AAU50840 | Propionib | 927 | 26 | 76.5 | 1745 | 8 | ADO71781 | ADO71781 | BFLP0169 |
| 855 | 26 | 76.5 | 583 | 6 | ABW47359 | Propionib | 928 | 26 | 76.5 | 1752 | 8 | ADO71766 | ADO71766 | BFLP0169 |
| 856 | 26 | 76.5 | 614 | 4 | AAW78899 | C. glutam | 929 | 26 | 76.5 | 1753 | 8 | ADO71777 | ADO71777 | BFLP0169 |
| 857 | 26 | 76.5 | 631 | 4 | ABW63273 | Drosophil | 930 | 26 | 76.5 | 1753 | 8 | ADO71767 | ADO71767 | BFLP0169 |
| 858 | 26 | 76.5 | 631 | 4 | AAU38950 | Drosophil | 931 | 26 | 76.5 | 1753 | 8 | ADO71775 | ADO71775 | BFLP0169 |
| 859 | 26 | 76.5 | 631 | 7 | ADC35832 | Drosophil | 932 | 26 | 76.5 | 1753 | 8 | ADO71768 | ADO71768 | BFLP0169 |
| 860 | 26 | 76.5 | 637 | 5 | ABE15862 | Corynebac | 933 | 26 | 76.5 | 1753 | 8 | ADO71771 | ADO71771 | BFLP0169 |
| 861 | 26 | 76.5 | 642 | 7 | ABW63521 | C. glutami | 934 | 26 | 76.5 | 1753 | 8 | ADO71780 | ADO71780 | BFLP0169 |
| 862 | 26 | 76.5 | 642 | 7 | ADD13234 | C. glutam | 935 | 26 | 76.5 | 1753 | 8 | ADO71772 | ADO71772 | BFLP0169 |
| 863 | 26 | 76.5 | 644 | 4 | AAW91576 | C. glutami | 936 | 26 | 76.5 | 1753 | 8 | ADO71764 | ADO71764 | BFLP0169 |
| 864 | 26 | 76.5 | 649 | 5 | ABW91538 | Herbicida | 937 | 26 | 76.5 | 1753 | 8 | ADO71765 | ADO71765 | BFLP0169 |
| 865 | 26 | 76.5 | 655 | 4 | ABG16601 | Novel hum | 938 | 26 | 76.5 | 1753 | 8 | ADO71773 | ADO71773 | BFLP0169 |
| 866 | 26 | 76.5 | 659 | 6 | ADA34734 | Acinetoba | 939 | 26 | 76.5 | 1753 | 8 | ADO71778 | ADO71778 | BFLP0169 |
| 867 | 26 | 76.5 | 660 | 6 | ABG00276 | Novel hum | 940 | 26 | 76.5 | 1753 | 8 | ADO71769 | ADO71769 | BFLP0169 |
| 868 | 26 | 76.5 | 669 | 6 | ABU42958 | Protein e | 941 | 26 | 76.5 | 1753 | 8 | ADO71770 | ADO71770 | BFLP0169 |
| 869 | 26 | 76.5 | 674 | 6 | ADA36807 | Acinetoba | 942 | 26 | 76.5 | 1753 | 8 | ADO71774 | ADO71774 | BFLP0169 |
| 870 | 26 | 76.5 | 676 | 9 | ADW09462 | Human pro | 943 | 26 | 76.5 | 1753 | 8 | ADO71779 | ADO71779 | BFLP0169 |
| 871 | 26 | 76.5 | 689 | 9 | ADW17625 | Pinus rad | 944 | 26 | 76.5 | 1753 | 8 | ADO71763 | ADO71763 | Human BFL |
| 872 | 26 | 76.5 | 691 | 8 | ADW10604 | Human the | 945 | 26 | 76.5 | 1753 | 8 | ADO71776 | ADO71776 | BFLP0169 |
| 873 | 26 | 76.5 | 705 | 4 | ABW68520 | Human GTP | 946 | 26 | 76.5 | 1767 | 8 | ADO71782 | ADO71782 | BFLP0169 |
| 874 | 26 | 76.5 | 715 | 6 | ABW71896 | Staphyloc | 947 | 26 | 76.5 | 1767 | 8 | ABW81078 | ABW81078 | Tumour-as |
| 875 | 26 | 76.5 | 719 | 8 | ADW07868 | Amino aci | 948 | 26 | 76.5 | 1889 | 4 | ABG09906 | ABG09906 | Novel hum |
| 876 | 26 | 76.5 | 731 | 5 | AAO15810 | Human but | 949 | 26 | 76.5 | 1893 | 4 | ABW59829 | ABW59829 | Drosophil |
| 877 | 26 | 76.5 | 731 | 8 | ADQ76307 | Human but | 950 | 26 | 76.5 | 1893 | 5 | AAU84593 | AAU84593 | HIV Casse |
| 878 | 26 | 76.5 | 733 | 4 | ABG28143 | Novel hum | 951 | 26 | 76.5 | 1896 | 5 | AAU84590 | AAU84590 | HIV Casse |
| 879 | 26 | 76.5 | 747 | 7 | ABO66339 | Klebsiell | 952 | 26 | 76.5 | 1906 | 4 | ABW57944 | ABW57944 | Drosophil |
| 880 | 26 | 76.5 | 752 | 2 | AAW82646 | Ehrlichia | 953 | 26 | 76.5 | 1916 | 4 | ABW62423 | ABW62423 | Drosophil |
| 881 | 26 | 76.5 | 752 | 3 | AAW78540 | Ehrlichia | 954 | 26 | 76.5 | 1916 | 4 | ABW66089 | ABW66089 | Drosophil |
| 882 | 26 | 76.5 | 752 | 5 | ABG93434 | Ehrlichia | 955 | 26 | 76.5 | 1954 | 4 | ABW59197 | ABW59197 | Drosophil |
| 883 | 26 | 76.5 | 752 | 5 | ABG33419 | Ehrlichia | 956 | 26 | 76.5 | 1990 | 9 | ABW92052 | ABW92052 | M. xanthu |
| 884 | 26 | 76.5 | 752 | 5 | AAU73231 | Human gra | 957 | 26 | 76.5 | 2022 | 6 | ABW63232 | ABW63232 | Glucanusc |
| 885 | 26 | 76.5 | 752 | 5 | AAU73216 | Human gra | 958 | 26 | 76.5 | 2022 | 6 | ABW64198 | ABW64198 | Drosophil |
| 886 | 26 | 76.5 | 754 | 7 | ABW86978 | Rice abio | 959 | 26 | 76.5 | 2408 | 8 | ADW10576 | ADW10576 | Human the |
| 887 | 26 | 76.5 | 766 | 8 | ADW27309 | Bacterial | 960 | 26 | 76.5 | 2680 | 7 | ABO61456 | ABO61456 | Klebsiell |
| 888 | 26 | 76.5 | 795 | 4 | AAU34003 | Staphyloc | 961 | 26 | 76.5 | 2765 | 5 | ADI16952 | ADI16952 | Rat NOVX |
| 889 | 26 | 76.5 | 827 | 6 | ADW20859 | Protein e | 962 | 26 | 76.5 | 2872 | 6 | ABU32213 | ABU32213 | Protein e |
| 890 | 26 | 76.5 | 846 | 9 | ABW96111 | M. xanthu | 963 | 26 | 76.5 | 2951 | 6 | ABW67717 | ABW67717 | Phototrab |
| 891 | 26 | 76.5 | 860 | 6 | ABU43912 | Protein e | 964 | 26 | 76.5 | 3286 | 6 | ABU21773 | ABU21773 | Protein e |
| 892 | 26 | 76.5 | 863 | 4 | AAW62458 | S. epider | 965 | 26 | 76.5 | 3930 | 6 | ABU18893 | ABU18893 | Protein e |
| 893 | 26 | 76.5 | 864 | 7 | ADW64664 | Disease t | 966 | 26 | 76.5 | 5002 | 4 | ABW63723 | ABW63723 | Drosophil |
| 894 | 26 | 76.5 | 873 | 8 | ADW23417 | Bacterial | 967 | 26 | 76.5 | 5291 | 7 | ADC01014 | ADC01014 | Microbiae |
| 895 | 26 | 76.5 | 876 | 5 | ABP39098 | Staphyloc | 968 | 26 | 76.5 | 5291 | 9 | ABW91571 | ABW91571 | Microbiae |
| 896 | 26 | 76.5 | 876 | 6 | ADW07310 | Staphyloc | 969 | 26 | 76.5 | 5746 | 5 | AAU84596 | AAU84596 | HIV compl |
| 897 | 26 | 76.5 | 901 | 6 | ABU15843 | Protein e | 970 | 25 | 73.5 | 9 | ADW66140 | ADW66140 | Human 273 | |
| 898 | 26 | 76.5 | 904 | 4 | AAU36814 | Staphyloc | 971 | 25 | 73.5 | 9 | ADW66395 | ADW66395 | Human 273 | |
| 899 | 26 | 76.5 | 904 | 6 | ABW71629 | Staphyloc | 972 | 25 | 73.5 | 9 | ADW66656 | ADW66656 | Human 273 | |
| 900 | 26 | 76.5 | 925 | 8 | ADP25031 | PRO polyp | 973 | 25 | 73.5 | 9 | ADW66912 | ADW66912 | Human 273 | |

974 25 73.5 9 8 ADN67181 Human 273
 975 25 73.5 9 8 ADN68831 Human 273
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ALIGNMENTS

RESULT 1
 ID AAR70198 standard; protein; 7 AA.
 XX AC AAR70198;
 XX DT 25-MAR-2003 (revised)
 XX DT 20-SEP-1995 (first entry)
 XX DE MAb 3B9 heavy chain CDR.
 XX KW Chimeric antibody; humanized antibody; antibody engineering;
 XX KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy; CDR;
 XX KW complementarity determining region.
 XX OS Mus sp.
 XX PN WO9507301-A1.
 XX PD 16-MAR-1995.
 XX PF 07-SEP-1994; 94WO-US010308.
 XX PR 07-SEP-1993; 93US-00117366.
 XX PR 14-OCT-1993; 93US-00136783.
 XX PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX PI Holmes S, Gross MS, Sylvester DR;
 XX DR WPI; 1995-123387/16.
 XX CC Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from
 XX CC high affinity mAbs - useful in treatment of IL-4-mediated and IgE-
 XX CC mediated allergic conditions.
 XX PS Disclosure; Page 56; 97pp; English.
 XX CC Spleen cells from mice immunized with human IL-4 were used to prepare
 XX CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only clone

CC 3B9 was positive. cDNA clones of the 3B9 light and heavy chains were
 CC cloned into pGEM7f+ and transformed into E. coli DH5-alpha. A heavy chain
 CC cDNA clone was sequenced (AAQ83491) that encoded the protein given in
 CC AAR70190. 3 CDRs (AAR70198-200) were identified. (Updated on 25-MAR-2003
 CC to correct PN field.)
 XX Sequence 7 AA;
 SQ Query Match 100.0%; Score 34; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TSGMGVS 7
 |||||
 Db 1 TSGMGVS 7

RESULT 2
 AAY23775
 ID AAY23775 standard; peptide; 7 AA.
 XX AC AAY23775;
 XX DT 13-SEP-1999 (first entry)
 XX DE CDR of the heavy chain variable region of antibody 3B9.
 XX KW Heavy chain variable region; interleukin-4; IL-4; antibody 3B9;
 XX KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
 XX KW Immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 XX KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 XX KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy;
 XX KW complementarity determining region.
 XX OS Mus sp.
 XX PN US928904-A.
 XX PD 27-JUL-1999.
 XX PF 07-JUN-1995; 95US-00483632.
 XX PR 07-SEP-1993; 93US-00117366.
 XX PR 14-OCT-1993; 93US-00136783.
 XX PR 07-SEP-1994; 94WO-US010308.
 XX PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX PI Holmes SD, Sylvester DR, Gross MS;
 XX DR WPI; 1999-429500/36.
 XX DR N-PSDB; AAX85892.
 XX PF New DNA molecules encoding recombinant antibodies useful for treating IL4
 XX PT -mediated conditions.
 XX PS Example 3; Col 45; 50pp; English.
 XX CC The present sequence represents a complementarity determining region
 XX CC (CDR) of the heavy chain variable region of murine interleukin-4 (IL-4)
 XX CC antibody 3B9. The specification describes chimeric and humanised IL-4
 XX CC monoclonal antibodies. The antibodies of the invention are used in
 XX CC therapeutic and pharmaceutical compositions for treating IL-4 mediated
 XX CC and Immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis,
 XX CC conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock,
 XX CC rheumatoid arthritis, host-versus-graft disease and renal disease. They
 XX CC are also useful in the diagnosis of an allergy or condition associated
 XX CC with excess IL-4 production through the measurement e.g. by ELISA of
 XX CC circulating endogenous IL-4 levels in humans
 XX SQ Sequence 7 AA;

```

Query Match      100.0%; Score 34; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
DB 1 TSGMGVS 7

RESULT 3
AA018530
ID AAY18111 standard; peptide; 7 AA.
XX
AC AAY18111;
XX
DT 11-AUG-1999 (first entry)
XX
DE Heavy chain CDR for hIL-4 specific antibody.
XX
KW Antibody; interleukin-4; IL4; immunoglobulin E; IGE mediated disease;
KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
KW autoimmune disease; graft versus host disease;
KW complementarity determining region; CDR.
XX
OS Synthetic.
XX
PN US5914110-A.
XX
PD 22-JUN-1999.
XX
PF 07-JUN-1995; 95US-00483636.
XX
PR 07-SEP-1993; 93US-00117366.
XX
PR 14-OCT-1993; 93US-00136783.
XX
PR 07-SEP-1994; 94WO-US010308.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI Sylvester DR, Holmes SD, Gross MS;
XX
WPI; 1999-370482/31.
DR N-PSDB; AAX79510.
XX
PT Recombinant IL4 antibodies useful for treatment of allergic rhinitis,
PT atopic asthma and anaphylactic shock.
XX
PS Claim 7; Col 45; 50pp; English.
XX
This sequence represents a heavy chain complementarity determining region
(CDR) from an antibody of the invention. The antibody is a chimeric or
humanised interleukin-4 (IL4) monoclonal antibody for the treatment of
immunoglobulin E (IGE) mediated diseases. The antibodies are useful for
the treatment of allergic disorders such as allergic rhinitis,
conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.
The antibodies are also useful for regulating B and T cell proliferation
and as such are useful in the treatment of autoimmune diseases and graft
versus host disease
XX
SQ Sequence 7 AA;
Query Match      100.0%; Score 34; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
DB 1 TSGMGVS 7

RESULT 4
AA018530
ID AAY18111 standard; peptide; 7 AA.
XX
AC AAY18111;
XX
DT 11-AUG-1999 (first entry)
XX
DE Heavy chain CDR for hIL-4 specific antibody.
XX
KW Antibody; interleukin-4; IL4; immunoglobulin E; IGE mediated disease;
KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
KW autoimmune disease; graft versus host disease;
KW complementarity determining region; CDR.
XX
OS Synthetic.
XX
PN US5914110-A.
XX
PD 22-JUN-1999.
XX
PF 07-JUN-1995; 95US-00483636.
XX
PR 07-SEP-1993; 93US-00117366.
XX
PR 14-OCT-1993; 93US-00136783.
XX
PR 07-SEP-1994; 94WO-US010308.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI Sylvester DR, Holmes SD, Gross MS;
XX
WPI; 1999-370482/31.
DR N-PSDB; AAX79510.
XX
PT Recombinant IL4 antibodies useful for treatment of allergic rhinitis,
PT atopic asthma and anaphylactic shock.
XX
PS Claim 7; Col 45; 50pp; English.
XX
This sequence represents a heavy chain complementarity determining region
(CDR) from an antibody of the invention. The antibody is a chimeric or
humanised interleukin-4 (IL4) monoclonal antibody for the treatment of
immunoglobulin E (IGE) mediated diseases. The antibodies are useful for
the treatment of allergic disorders such as allergic rhinitis,
conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.
The antibodies are also useful for regulating B and T cell proliferation
and as such are useful in the treatment of autoimmune diseases and graft
versus host disease
XX
SQ Sequence 7 AA;
Query Match      100.0%; Score 34; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
DB 1 TSGMGVS 7

RESULT 5
ABP58279
ID ABP58279 standard; peptide; 7 AA.
XX
AC ABP58279;
XX
DT 31-MAR-2003 (first entry)
XX
DE Murine monoclonal antibody 10D5 heavy chain CDR1.
XX
KW Monoclonal antibody; 10D5; complementarity determining region; CDR;
KW mouse; humanised antibody; antibody; Alzheimer's disease;
KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
XX
OS Mus sp.
XX
PN WO200288307-A2.
XX
PD 07-NOV-2002.

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ID AAO18530 standard; peptide; 7 AA.
XX
AC AAO18530;
XX
DT 11-OCT-2002 (first entry)
XX
DE Murine Mab 1F7 heavy chain CDR1 region.
XX
KW Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR;
KW complementarity determining region; framework-determining region; PR;
KW heavy chain; light chain; HIV infection.
XX
OS Mus sp.
XX
PN WO200255668-A2.
XX
PD 18-JUL-2002.
XX
PF 11-JAN-2002; 2002WO-US000927.
XX
PR 11-JAN-2001; 2001US-00759112.
XX
PA (IMMP-) IMMOPHERON INC.
XX
PI Muller S, Kohler H;
XX
WPI; 2002-590668/63.
DR N-PSDB; AAL48654.
XX
New polynucleotide encoding a complementarity- or framework-determining
region of an anti-idiotypic antibody that binds to human or primate anti-
human immunodeficiency virus (HIV) antibodies, for use in vaccines
against HIV.
XX
PS Claim 4; Page 20; 27pp; English.
XX
The present invention relates to coding sequences of the murine 1F7 anti-
idiotypic antibody complementarity-determining region (CDR) or framework-
determining region (FR). The antibody binds to human or primate anti-
human immunodeficiency virus (HIV) antibodies and can be used in the
treatment of HIV infection. The present sequence is a region of the 1F7
heavy chain
XX
SQ Sequence 7 AA;
Query Match      100.0%; Score 34; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
DB 1 TSGMGVS 7

RESULT 5
ABP58279
ID ABP58279 standard; peptide; 7 AA.
XX
AC ABP58279;
XX
DT 31-MAR-2003 (first entry)
XX
DE Murine monoclonal antibody 10D5 heavy chain CDR1.
XX
KW Monoclonal antibody; 10D5; complementarity determining region; CDR;
KW mouse; humanised antibody; antibody; Alzheimer's disease;
KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
XX
OS Mus sp.
XX
PN WO200288307-A2.
XX
PD 07-NOV-2002.

```

XX 26-APR-2002; 2002WO-US011854.
 XX 30-APR-2001; 2001US-0287653P.
 XX (ELIL) LILLY & CO ELI.
 XX Hinton PR, Vasquez M;
 XX WPI; 2003-183836/18.
 XX New humanized 10D5 antibody, useful for the manufacture of a medicament
 XX for treating Down's syndrome, clinical or pre-clinical Alzheimer's
 XX disease or cerebral amyloid angiopathy.
 XX Claim 2; Page 29; 52pp; English.
 XX The present sequence is that of complementarity determining region (CDR)
 XX 1 of the heavy chain of murine monoclonal antibody 10D5. Novel humanised
 XX antibodies of the invention have CDRs from 10D5 and human framework
 XX sequences. These humanised antibodies have binding affinities (affinity
 XX and epitope location) approximately the same as those of the mouse 10D5
 XX antibody. The invention includes antibodies, single chain antibodies, and
 XX their fragments, as well as nucleotide sequences, vectors, transformed
 XX host cells, and methods of using the humanised antibody to treat,
 XX prevent, alleviate, reverse or otherwise ameliorate symptoms and/or
 XX pathology associated with Down's syndrome, (pre-)clinical Alzheimer's
 XX disease or (pre-)clinical cerebral amyloid angiopathy, and to inhibit
 XX formation or reduce Abeta plaque in the brain
 XX Sequence 7 AA;
 XX Query Match 100.0%; Score 34; DB 6; Length 7;
 XX Best Local Similarity 100.0%; Pred. No. 2e+06;
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TSGMGVS 7
 Db 1 TSGMGVS 7
 RESULT 6
 ID AD208828 standard; peptide; 7 AA.
 XX AC AD208828;
 XX 16-JUN-2005 (first entry)
 XX Mammalian amyloid antibody, heavy chain CDR SEQ ID No:53.
 XX amyloid; antibody engineering; antibody production;
 XX amyloid-associated disorder; Alzheimers disease; cancer; allergy;
 XX autoimmune disease; Parkinsons disease;
 XX acquired immune deficiency syndrome; multiple sclerosis; migraine;
 XX dementia; infection; neurotropic; neuroprotective; cytostatic;
 XX antiallergic; immunosuppressive; antiparkinsonian; antimigraine;
 XX antimicrobial; anti-HIV; heavy chain; complementarity determining region.
 XX OS Mammalia.
 XX WO2005028511-A2.
 XX 31-MAR-2005.
 XX 26-MAR-2004; 2004WO-US009522.
 XX 28-MAR-2003; 2003US-0458469P.
 XX 28-MAR-2003; 2003US-0458474P.
 XX 28-MAR-2003; 2003US-0458509P.
 XX 28-MAR-2003; 2003US-0458510P.
 XX (CENZ) CENTOCOR INC.
 PA (MERC/) MERCKEN M.
 PA (BENS/) BENSON J M.
 XX Mercken M, Benson JM;
 XX WPI; 2005-242565/25.
 XX New isolated mammalian anti-amyloid antibodies useful for treating
 XX amyloid-associated disorders, such as Alzheimer's disease, cancer,
 XX allergies, autoimmune disease, Parkinson's disease, multiple sclerosis,
 XX migraine and dementia.
 XX Claim 6; SEQ ID NO 53; 306pp; English.
 XX The invention relates to at least one isolated mammalian amyloid antibody
 XX comprising at least one variable region comprising at least one heavy
 XX chain and at least one light chain, of a fully defined sequence of SEQ ID
 XX NOS: 48, 49, 59, 60, 69, 70, 79 and 80, respectively. Also described are:
 XX (i) at least one isolated mammalian amyloid antibody that binds to the
 XX same region of an amyloid polypeptide as an antibody comprising at least
 XX one heavy chain or light chain complementarity determining region (CDR)
 XX having the amino acid sequence of at least one of SEQ ID NO: 73-78, (ii)
 XX at least one isolated mammalian amyloid antibody, comprising at least one
 XX human CDR, where the antibody specifically binds at least one epitope
 XX selected from amino acids 2-7, 3-8, 33-42, or 34-40 of a fully defined
 XX sequence of 42 amino acids (SEQ ID NO: 50), (iii) an isolated nucleic
 XX acid encoding at least one of any of the isolated mammalian amyloid
 XX antibodies mentioned and having at least one human CDR of a fully defined
 XX sequence of SEQ ID NO: 51, 52, 61, 62, 71, 72, 81 and 82, (iv) an
 XX isolated nucleic acid vector comprising an isolated nucleic acid encoding
 XX an amyloid antibody, (v) a prokaryotic or eukaryotic host cell comprising
 XX an isolated nucleic acid encoding an amyloid antibody, (vi) a method of
 XX producing at least one amyloid antibody, (vii) a composition comprising
 XX at least one of any of the isolated mammalian amyloid antibodies
 XX mentioned, and at least one pharmaceutical carrier or diluent, (viii) an
 XX anti-idiotypic antibody or fragment that specifically binds at least one
 XX of the amyloid antibodies mentioned, (ix) a method of diagnosing or
 XX treating an amyloid related condition in a cell, tissue, organ or animal,
 XX comprising contacting or administering a composition comprising at least
 XX one of the antibodies mentioned, with, or to, the cell, tissue, organ or
 XX animal, (x) a medical device comprising at least one amyloid antibody
 XX mentioned, where the device is suitable for contacting or administering
 XX at least one amyloid antibody, (xi) an article of manufacture for human
 XX pharmaceutical or diagnostic use, comprising packaging material and a
 XX container comprising a solution or a lyophilized form of at least one of
 XX the amyloid antibodies mentioned, and (xii) a method of producing at
 XX least one of the isolated mammalian amyloid antibodies, comprising
 XX providing a host cell or transgenic animal or transgenic plant or plant
 XX cell capable of expressing the antibody in recoverable amounts. The
 XX methods and compositions of the present invention are useful for
 XX producing therapeutic compositions and devices for treating amyloid-
 XX associated disorders, such as Alzheimer's disease, cancer, allergies,
 XX autoimmune disease, Parkinson's disease, AIDS, multiple sclerosis,
 XX migraine, dementia and infections. This sequence represents a heavy chain
 XX CDR useful in the antibody of the invention.
 XX Sequence 7 AA;
 Qy 1 TSGMGVS 7
 Db 1 TSGMGVS 7
 RESULT 7
 AAY23780
 ID AAY23780 standard; protein; 121 AA.
 XX AC AAY23780;
 XX

DT 13-SEP-1999 (first entry)
 XX Heavy chain variable region of Ig NEW.
 DE
 XX
 XX Light chain variable region; interleukin-4; IL-4; antibody 3B9;
 KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
 KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy;
 KW Ig NEW.
 XX
 XX Synthetic.
 OS
 XX US5928904-A.
 PN
 XX 27-JUL-1999.
 PD
 XX
 XX 07-JUN-1995; 95US-00483632.
 PF
 XX 07-SEP-1993; 93US-00117366.
 PR
 XX 14-OCT-1993; 93US-00136783.
 PR
 XX 07-SEP-1994; 94WO-US010308.
 XX
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 XX Holmes SD, Sylvester DR, Gross MS;
 PI
 XX WPI; 1999-429500/36.
 XX N-PSDB; AAX85929.
 DR
 XX
 XX New DNA molecules encoding recombinant antibodies useful for treating IL4
 PT -mediated conditions.
 PT
 XX Disclosure; Col 65-66; 50pp; English.
 PS
 XX
 XX The specification describes chimeric and humanised IL-4 monoclonal
 CC antibodies. The antibodies of the invention are used in therapeutic and
 CC pharmaceutical compositions for treating IL-4 mediated and immunoglobulin
 CC E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis,
 CC atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid
 CC arthritis, host-versus-graft disease and renal disease. They are also
 CC useful in the diagnosis of an allergy or condition associated with excess
 CC IL-4 production through the measurement e.g. by ELISA of circulating
 CC endogenous IL-4 levels in humans. The present sequence represents the
 CC heavy chain variable region of Ig NEW, and is used in the course of the
 CC invention
 XX
 XX Sequence 121 AA;
 SQ
 Query Match 100.0%; Score 34; DB 2; Length 121;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TSGMGVS 7
 DB 31 TSGMGVS 37
 |||||
 RESULT 8
 AAY18122
 ID AAY18122 standard; protein; 121 AA.
 XX
 XX AAY18122;
 AC
 XX
 XX 11-AUG-1999 (first entry)
 DT
 XX
 XX Heavy chain sequence for humanised 3B9 antibody.
 DE
 XX Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;
 KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
 KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
 KW autoimmune disease; graft versus host disease.
 XX
 XX
 XX Synthetic.
 OS
 XX US5914110-A.
 PN
 XX 22-JUN-1999.
 PD
 XX
 XX 07-JUN-1995; 95US-00483636.
 PF
 XX 07-SEP-1993; 93US-00117366.
 PR
 XX 14-OCT-1993; 93US-00136783.
 PR
 XX 07-SEP-1994; 94WO-US010308.
 XX
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 XX Sylvester DR, Holmes SD, Gross MS;
 PI
 XX WPI; 1999-370482/31.
 XX N-PSDB; AAX79527.
 DR
 XX
 XX Recombinant IL4 antibodies useful for treatment of allergic rhinitis,
 PT atopic asthma and anaphylactic shock.
 PT
 XX Example 3; Col 65-66; 50pp; English.
 PS
 XX
 XX This sequence represents the heavy chain of the humanised 3B9 antibody of
 CC the invention. The antibody is a chimeric or humanised interleukin-4
 CC (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE)
 CC mediated diseases. The antibodies are useful for the treatment of
 CC allergic disorders such as allergic rhinitis, conjunctivitis, atopic
 CC dermatitis, atopic asthma and anaphylactic shock. The antibodies are also
 CC useful for regulating B and T cell proliferation and as such are useful
 CC in the treatment of autoimmune diseases and graft versus host disease
 XX
 XX Sequence 121 AA;
 SQ
 Query Match 100.0%; Score 34; DB 2; Length 121;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TSGMGVS 7
 DB 31 TSGMGVS 37
 |||||
 RESULT 9
 AAO18528
 ID AAO18528 standard; protein; 121 AA.
 XX
 XX AAO18528;
 AC
 XX
 XX 11-OCT-2002 (first entry)
 DT
 XX
 XX Murine Mab 1F7 heavy chain.
 DE
 XX
 XX Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR;
 KW complementarity determining region; framework-determining region; FR;
 KW heavy chain; light chain; HIV infection.
 XX
 XX Mus sp.
 OS
 XX WO200255668-A2.
 PN
 XX
 XX 18-JUL-2002.
 PD
 XX
 XX 11-JAN-2002; 2002WO-US000927.
 PF
 XX
 XX 11-JAN-2001; 2001US-00759112.
 PR
 XX (IMMP-) IMPHERON INC.
 PA
 XX Muller S, Kohler H;
 PI

XX WPI; 2002-590668/63.
DR N-PSDB; AAL48652.
XX
PT New polynucleotide encoding a complementarity- or framework-determining
PT region of an anti-idiotypic antibody that binds to human or primate anti-
PT human immunodeficiency virus (HIV) antibodies, for use in vaccines
PT against HIV.
XX
PS Disclosure; Page 18-19; 27pp; English.
XX
CC The present invention relates to coding sequences of the murine 1F7 anti-
CC idiotypic antibody complementarity-determining region (CDR) or framework-
CC determining region (FR). The antibody binds to human or primate anti-
CC human immunodeficiency virus (HIV) antibodies and can be used in the
CC treatment of HIV infection. The present sequence is the 1F7 heavy chain
CC
SQ Sequence 121 AA;
XX
Query Match 100.0%; Score 34; DB 5; Length 121;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TSGMGVS 7
Db ||||| 31 TSGMGVS 37
XX
RESULT 10
ID ABG67188 standard; protein; 121 AA.
XX
AC ABG67188;
XX
DT 24-SEP-2002 (first entry)
XX
DE Human IgG1 antibody heavy chain variable region 15H4VH.
XX
KW Hepatitis C virus vaccine; HCV; hypervariable region 1; HVR1;
KW envelope protein E2; antibody; helper T-lymphocyte; IgG1;
KW cytotoxic T-lymphocyte; HCV infection; virucide; heavy chain.
XX
OS Homo sapiens.
XX
FN WO200245743-A2.
XX
PD 13-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-GB005421.
XX
PR 09-DEC-2000; 2000GB-00030102.
PR 18-DEC-2000; 2000GB-00030789.
XX
PA (ALLA/) ALLAIN J.
XX
PI Allain J, Li C, Piccolella E;
XX
DR WPI; 2002-508540/54.
XX
PT Hepatitis C virus (HCV) vaccines able to raise antibodies, helper T
PT lymphocytes and/or cytotoxic T lymphocytes able to bind to the
PT hypervariable 1 region of the infecting HCV strain.
XX
PS Example 4; Fig 2; 52pp; English.
XX
CC The present invention relates to a hepatitis C virus (HCV) vaccine
CC comprising different groups of peptides each group being capable of
CC raising, in an infected individual, an antibody able to bind to the
CC hypervariable 1 (HVR1) region of the envelope protein E2 of the infecting
CC HCV strain. The different groups of peptides are administered
CC sequentially to raise antibodies, helper T-lymphocytes, and cytotoxic T-
CC lymphocytes which are cross-reactive to the HVR1 region of the infecting
CC HCV. The vaccines are useful for preventing and treating chronic HCV

CC infections. ABG67186-ABG67189 represent variable regions of human IgG1
CC antibody heavy chain
XX
SQ Sequence 121 AA;
XX
Query Match 100.0%; Score 34; DB 5; Length 121;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TSGMGVS 7
Db ||||| 31 TSGMGVS 37
XX
RESULT 11
ID ADG25814 standard; protein; 121 AA.
XX
AC ADG25814;
XX
DT 11-MAR-2004 (first entry)
XX
DE Anti-CD30 monoclonal antibody VH variable region T105 SEQ ID NO:14.
XX
KW antibody; CD30; anti-CD30 antibody; cytostatic; gene therapy; cancer.
XX
OS Synthetic.
XX
FN WO2003104432-A2.
XX
PD 18-DEC-2003.
XX
PF 09-JUN-2003; 2003WO-US018373.
XX
PR 07-JUN-2002; 2002US-0387293P.
PR 16-SEP-2002; 2002US-0411032P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Pastan IH, Nagata S, Onda M, Numata Y, Santora K, Beers R;
PI Kreitman R, Sinha A;
XX
DR WPI; 2004-062352/06.
XX
PT New antibody that binds specifically to a stalk of CD30 of a cell, or to
PT an epitope destroyed upon cleavage of soluble CD30 (sCD30) from intact
PT CD30, useful for inhibiting the growth of a CD30+ cancer cell.
XX
PS Claim 38; SEQ ID NO 14; 102pp; English.
XX
CC The present invention describes an isolated antibody that binds
CC specifically to a stalk of CD30 of a cell, or to an epitope destroyed
CC upon cleavage of soluble CD30 (sCD30) from intact CD30. Also described:
CC (1) a composition comprising the antibody conjugated or fused to a
CC therapeutic part; (2) a nucleic acid encoding an antibody that binds
CC specifically to a stalk of CD30 of a cell, or to an epitope destroyed
CC upon cleavage of sCD30 from intact CD30; (3) an expression vector
CC comprising the nucleic acid operably linked to a promoter; (4) inhibiting
CC growth of a CD30+ cancer cell; (5) detecting the presence of a CD30+ cell
CC in a biological sample; (6) a host cell expressing the isolated nucleic
CC acid encoding the antibody having variable heavy and variable light
CC chains; and (7) a kit for detecting the presence of a CD30+ cancer cell
CC in a biological sample comprising a container and an anti-CD30 antibody.
CC An anti-CD30 antibody has cytostatic activity, and can be used in gene
CC therapy. The anti-CD30 antibody that binds specifically to a stalk of
CC CD30 of a cell, or to an epitope destroyed upon cleavage of sCD30 from
CC intact CD30 is useful for the manufacture of a medicament for inhibiting
CC the growth of a CD30+ cancer cell. The present sequence is used in the
CC exemplification of the present invention.
XX
SQ Sequence 121 AA;
XX
Query Match 100.0%; Score 34; DB 8; Length 121;

Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
DB 31 TSGMGVS 37
|||||

RESULT 12
AEA37667
ID AEA37667 standard; protein; 121 AA.
XX
AC AEA37667;
XX
DT 28-JUL-2005 (first entry)
XX
DE Mouse CD44 antibody V segment.
XX
KW antibody engineering; CD44; leukemia; hematological disease; neoplasm;
KW cytostatic.
XX
OS Mus musculus.
XX
PN CN1552735-A.
XX
PD 08-DEC-2004.
XX
PF 18-DEC-2003; 2003CN-01107583.
XX
PR 18-DEC-2003; 2003CN-01107583.
XX
PA (HEMA-) HEMATOLOGY INST CHINESE MEDICINE ACAD.
XX
PI Han Z, Song G;
XX
DR WPI: 2005-173920/19.
DR N-PSDB; AEA37666.
XX
PT Engineering antibody against CD44 for inducing leukemia cell
PT differentiation and necrosis.
XX
PS Claim 2; SEQ ID NO 2; 19pp; Chinese.
XX
CC The invention relates to an engineered CD44 antibody for inducing the
CC differentiation and wither of leukemia cells, the gene in the heavy chain
CC and light chain variable region of monoclonal antibody H144a of CD44, the
CC polypeptide coded by said gene, the carrier containing said gene, and the
CC application of said gene and polypeptide in preparing medicines for
CC diagnosing and treating leukemia and disclosed. The present sequence
CC represents the amino acid sequence of the mouse CD44 antibody V segment.
XX
SQ Sequence 121 AA;

Query Match 100.0%; Score 34; DB 9; Length 121;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
DB 31 TSGMGVS 37
|||||

RESULT 13
ADQ09631
ID ADQ09631 standard; protein; 122 AA.
XX
AC ADQ09631;
XX
DT 07-OCT-2004 (first entry)
XX
DE Variable heavy chain protein of murine anti-human GPR64-18 antibody ID17.
XX
KW murine; mouse; antibody; GPR64; cytotoxic; ovarian cancer;

Query Match 100.0%; Score 34; DB 8; Length 122;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
DB 31 TSGMGVS 37
|||||

RESULT 14
ABP58283
ID ABP58283 standard; protein; 123 AA.
XX
AC ABP58283;
XX
DT 23-OCT-2003 (revised)
DT 31-MAR-2003 (first entry)
XX
DE Humanised 10D5 antibody heavy chain variable region.
XX
KW Monoclonal antibody; 10D5; complementarity determining region; CDR;
KW mouse; human; humanised antibody; antibody; Alzheimer's disease;
KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Misc-difference 1

uterine cancer; Ewing's sarcoma; cell death; cytostatic; gene therapy;
immunotherapy; cellular proliferation.

OS Mus sp.
XX WO2004058171-A2.
XX
XX 15-JUL-2004.
XX
XX 19-DEC-2003; 2003WO-US040820.
XX
XX 20-DEC-2002; 2002US-0435618P.
XX
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Law D, Wang Q, Dubridge R, Bhaskar V;
XX
XX WPI: 2004-525780/50.
XX N-PSDB; ADQ09621.
XX
XX New antibody that inhibits binding of a GPR64 polypeptide to an antibody
XX comprising GPR64-18, GPR64-81, GPR64-93 or GPR64-101, useful in preparing
XX a composition for diagnosing or treating ovarian cancer.
XX
XX Example 2; SEQ ID NO 17; 75pp; English.
XX
XX This invention relates to novel antibodies that bind to the G protein
XX coupled receptor protein identified as GPR64, namely GPR64-1, GPR64-16,
XX GPR64-18, GPR64-20 and GPR64-48. Specifically, it refers to the use of
XX these anti-GPR64 antibodies as selective cytotoxic agents against GPR64
XX expressing tumour cells such as those associated with ovarian cancer,
XX uterine cancer and Ewing's sarcoma. The present invention describes
XX GPR64 through competitive binding analyses, such that the antibodies can
XX be assessed for GPR64 dependent cell death in vitro. Accordingly, they
XX can be used to develop cytostatic compositions for gene therapy or
XX immunotherapy that inhibit cellular proliferation of an ovarian cancerous
XX cell and furthermore can diagnose and inhibit growth of tumour cells.
XX This polypeptide is encoded by a heavy chain variable region DNA sequence
XX of a murine anti-human GPR64 antibody of the invention.
XX
XX Sequence 122 AA;

```
FT Misc-difference 2 /label= Gln, Glu
FT /label= Val, Ala
FT Region 31. .35
FT /note= "CDR1"
FT Region 52. .67
FT /note= "CDR2"
FT Misc-difference 64
FT /label= Ser, Thr
FT Misc-difference 77
FT /label= Lys, Arg
FT Misc-difference 78
FT /label= Ser, Thr
FT Misc-difference 83
FT /label= Thr, Ser
FT Misc-difference 84
FT /label= Met, Ile, Leu
FT Misc-difference 86
FT /label= Asn, Ser, Thr
FT Misc-difference 87
FT /label= Met, Val, Leu
FT Region 100. .112
FT /note= "CDR3"
FT Misc-difference 118
FT /label= Leu, Ser
XX
XX WO200288307-A2.
XX
XX 07-NOV-2002.
XX
XX 26-APR-2002; 2002WO-US011854.
XX
XX 30-APR-2001; 2001US-0287653P.
XX
XX (ELIL ) LILLY & CO ELI.
XX
XX Hinton PR, Vasquez M;
XX
XX WPI; 2003-183836/18.
XX
XX New humanized 10D5 antibody, useful for the manufacture of a medicament
XX for treating Down's syndrome, clinical or pre-clinical Alzheimer's
XX disease or cerebral amyloid angiopathy.
XX
XX Claim 3; Page 8; 52pp; English.
XX
XX The present sequence is that of a preferred heavy chain variable region
XX of a humanised antibody of the present invention. In this sequence, the
XX complementarity determining regions (CDRs) originate from murine
XX monoclonal antibody 10D5 and the framework region originates from human
XX germline VH segment DP-28 and J segment JH4. Novel humanised antibodies
XX of the invention have CDRs from 10D5 and human framework sequences. These
XX humanised antibodies have binding affinities (affinity and epitope
XX location) approximately the same as those of the mouse 10D5 antibody. The
XX invention includes antibodies, single chain antibodies, and their
XX fragments, as well as nucleotide sequences, vectors, transformed host
XX cells, and methods of using the humanised antibody to treat, prevent,
XX alleviate, reverse or otherwise ameliorate symptoms and/or pathology
XX associated with Down's syndrome, (pre-)clinical Alzheimer's disease or
XX (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or
XX reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
XX OS field)
XX
XX Sequence 123 AA;
XX
XX Query Match 100.0%; Score 34; DB 6; Length 123;
XX Best Local Similarity 100.0%; Pred. No. 37;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 TSGMGVS 7
XX |
XX 31 TSGMGVS 37
XX |
XX
XX Query Match 100.0%; Score 34; DB 6; Length 123;
XX Best Local Similarity 100.0%; Pred. No. 37;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 TSGMGVS 7
XX |
XX 31 TSGMGVS 37
XX |
XX
XX RESULT 15
XX ABP58285
XX ID ABP58285 standard; protein; 123 AA.
XX
XX AC ABP58285;
XX
XX DT 23-OCT-2003 (revised)
XX DT 31-MAR-2003 (first entry)
XX
XX DB Humanised 10D5 antibody heavy chain variable region.
XX
XX KW Monoclonal antibody; 10D5; complementarity determining region; CDR;
XX mouse; human; humanised antibody; antibody; Alzheimer's disease;
XX Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
XX
XX OS Mus sp.
XX OS Homo sapiens.
XX OS Chimeric.
XX
XX FH Key Location/Qualifiers
XX FT Region 31. .35
XX FT /note= "CDR1"
XX FT Region 52. .67
XX FT /note= "CDR2"
XX FT Region 100. .112
XX FT /note= "CDR3"
XX
XX WO200288307-A2.
XX
XX 07-NOV-2002.
XX
XX 26-APR-2002; 2002WO-US011854.
XX
XX 30-APR-2001; 2001US-0287653P.
XX
XX (ELIL ) LILLY & CO ELI.
XX
XX Hinton PR, Vasquez M;
XX
XX WPI; 2003-183836/18.
XX
XX New humanized 10D5 antibody, useful for the manufacture of a medicament
XX for treating Down's syndrome, clinical or pre-clinical Alzheimer's
XX disease or cerebral amyloid angiopathy.
XX
XX Claim 4; Page 9; 52pp; English.
XX
XX The present sequence is that of a particularly preferred heavy chain
XX variable region of a humanised antibody of the present invention. In this
XX sequence, the complementarity determining regions originate from murine
XX monoclonal antibody 10D5 and the framework region originates from human
XX germline VH segment DP-28 and J segment JH4. Novel humanised antibodies
XX of the invention have CDRs from 10D5 and human framework sequences. These
XX humanised antibodies have binding affinities (affinity and epitope
XX location) approximately the same as those of the mouse 10D5 antibody. The
XX invention includes antibodies, single chain antibodies, and their
XX fragments, as well as nucleotide sequences, vectors, transformed host
XX cells, and methods of using the humanised antibody to treat, prevent,
XX alleviate, reverse or otherwise ameliorate symptoms and/or pathology
XX associated with Down's syndrome, (pre-)clinical Alzheimer's disease or
XX (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or
XX reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
XX OS field)
XX
XX Sequence 123 AA;
XX
XX Query Match 100.0%; Score 34; DB 6; Length 123;
XX Best Local Similarity 100.0%; Pred. No. 37;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 TSGMGVS 7
XX |
XX 31 TSGMGVS 37
XX |
XX
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```

Db          31 TSGMGVS 37

RESULT 16
AAR70190
ID AAR70190 standard; protein; 140 AA.
XX
XX
AC AAR70190;
XX
XX 25-MAR-2003 (revised)
DT 20-SEP-1995 (first entry)
XX
XX Mouse Mab 3B9 heavy chain.
DE
XX Chimeric antibody; humanized antibody; antibody engineering;
KW monoclonal antibody; Mab; interleukin-4; IL-4; allergy.
KW
XX Mus sp.
OS
XX
XX Key Location/Qualifiers
FH Key 1..19
FT Peptide /label= Sig_peptide
FT Region 50..56
FT /label= CDR
FT /note= "complementarity determining region"
FT Region 71..86
FT /label= CDR
FT /note= "complementarity determining region"
FT Region 119..129
FT /label= CDR
FT /note= "complementarity determining region"
XX
XX WO9507301-A1.
XX
XX 16-MAR-1995.
XX
XX 07-SEP-1994; 94WO-US010308.
XX
XX 07-SEP-1993; 93US-00117366.
PR 14-OCT-1993; 93US-00136783.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Holmes S, Gross MS, Sylvestre DR;
XX
XX WPI: 1995-123387/16.
DR N-PSDB; AAQ83491.
XX
XX Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from
PT high affinity mAbs - useful in treatment of IL-4-mediated and Ige-
PT mediated allergic conditions.
XX
XX Disclosure; Fig 2; 97pp; English.
XX
XX Spleen cells from mice immunized with human IL-4 were used to prepare
CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only clone
CC 3B9 was positive. cDNA clones of the 3B9 light and heavy chains were
CC cloned into pSEM7f+ and transformed into E. coli DH5-alpha. The clones
CC were sequenced (AAQ83490-91), and used for antibody engineering. (Updated
CC on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 140 AA;
SQ
Query Match 100.0%; Score 34; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
|||
Db 50 TSGMGVS 56

RESULT 17
AAV23768
ID AAV23768 standard; protein; 140 AA.
XX
XX
AC AAV23768;
XX
XX 13-SEP-1999 (first entry)
DT
XX Heavy chain variable region of murine IL-4 antibody 3B9.
XX
XX Heavy chain variable region; interleukin-4; IL-4; antibody 3B9;
KW Chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
KW Immunoglobulin E-mediated allergic reaction; allergic rhinitis;
KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.
KW
XX Mus sp.
OS
XX
XX US5928904-A.
PN
XX 27-JUL-1999.
XX
XX 07-JUN-1995; 95US-00483632.
XX
XX 07-SEP-1993; 93US-00117366.
PR 14-OCT-1993; 93US-00136783.
XX
XX 07-SEP-1994; 94WO-US010308.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Holmes SD, Sylvestre DR, Gross MS;
XX
XX WPI: 1999-429500/36.
DR N-PSDB; AAX85885.
XX
XX New DNA molecules encoding recombinant antibodies useful for treating IL4
PT -mediated conditions.
XX
XX Example 3; Fig 2; 50pp; English.
XX
XX The present sequence represents the heavy chain variable region of murine
CC interleukin-4 (IL-4) antibody 3B9. The sequences are used in the
CC production chimeric and humanised IL-4 monoclonal antibodies. The
CC antibodies of the invention are used in therapeutic and pharmaceutical
CC compositions for treating IL-4 mediated and immunoglobulin E-mediated
CC allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic
CC dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host
CC -versus-graft disease and renal disease. They are also useful in the
CC diagnosis of an allergy or condition associated with excess IL-4
CC production through the measurement e.g. by ELISA of circulating
CC endogenous IL-4 levels in humans
XX
XX Sequence 140 AA;
SQ
Query Match 100.0%; Score 34; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
|||
Db 50 TSGMGVS 56

RESULT 18
AAV18121
ID AAV18121 standard; protein; 140 AA.
XX
XX
AC AAV18121;
XX
XX 11-AUG-1999 (first entry)
DT
XX Heavy chain sequence for murine 3B9 antibody.
XX

```

XX Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;
 KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
 KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
 KW autoimmune disease; graft versus host disease.
 XX Mus sp.
 XX US5914110-A.
 XX 22-JUN-1999.
 XX 07-JUN-1995; 95US-00483636.
 XX 07-SEP-1993; 93US-00117366.
 PR 14-OCT-1993; 93US-00136783.
 PR 07-SEP-1994; 94WO-US010308.
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX Sylvester DR, Holmes SD, Gross MS;
 XX WPI; 1999-370482/31.
 DR N-PSDB; AAX79520.
 DR Recombinant IL4 antibodies useful for treatment of allergic rhinitis,
 XX atopic asthma and anaphylactic shock.
 XX Claim 24; Fig 2; 50pp; English.
 XX This sequence represents the heavy chain of the murine 3B9 antibody of
 CC the invention. The antibody is a chimeric or humanised interleukin-4
 CC (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE)
 CC mediated diseases. The antibodies are useful for the treatment of
 CC allergic disorders such as allergic rhinitis, conjunctivitis, atopic
 CC dermatitis, atopic asthma and anaphylactic shock. The antibodies are also
 CC useful for regulating B and T cell proliferation and as such are useful
 CC in the treatment of autoimmune diseases and graft versus host disease
 XX Sequence 140 AA;
 Query Match 100.0%; Score 34; DB 2; Length 140;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TSGMGVS 7
 DB 50 TSGMGVS 56
 RESULT 19
 AAR70192
 ID AAR70192 standard; protein; 141 AA.
 XX AAR70192;
 XX 25-MAR-2003 (revised)
 DT 20-SEP-1995 (first entry)
 XX Humanized antibody 3B9 heavy chain.
 XX Humanized antibody; antibody engineering; monoclonal antibody; MAb;
 KW interleukin-4; IL-4; allergy.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH Peptide 1..19
 FT /label= Sig_peptide
 FT Region 51..57
 FT /label= CDR
 FT /note= "complementarity determining region"

FT Region 72..87
 FT /label= CDR
 FT /note= "complementarity determining region"
 FT Region 120..130
 FT /label= CDR
 FT /note= "complementarity determining region"
 XX WO9507301-A1.
 XX 16-MAR-1995.
 XX 07-SEP-1994; 94WO-US010308.
 XX 07-SEP-1993; 93US-00117366.
 PR 14-OCT-1993; 93US-00136783.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX Holmes S, Gross MS, Sylvester DR;
 XX WPI; 1995-123387/16.
 DR N-PSDB; AAQ83493.
 DR Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from
 XX high affinity mAbs - useful in treatment of IL-4-mediated and IgE-
 XX mediated allergic conditions.
 XX Disclosure; Fig 4; 97pp; English.
 XX A humanized antibody heavy chain variable region and signal sequence is
 CC given in AAR70192. The signal sequence is also provided in AAR70193. The
 CC CDR sequences of the construct are identical to the native CDRs of mouse
 CC anti-human IL-4 MAB 3B9 (AAR70198-200). (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX Sequence 141 AA;
 Query Match 100.0%; Score 34; DB 2; Length 141;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TSGMGVS 7
 DB 51 TSGMGVS 57
 RESULT 20
 AAR70191
 ID AAR70191 standard; protein; 141 AA.
 XX AAR70191;
 XX 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 20-SEP-1995 (first entry)
 XX Chimeric antibody 3B9 heavy chain.
 XX Chimeric antibody; antibody engineering; monoclonal antibody; MAB;
 KW interleukin-4; IL-4; allergy.
 XX Homo sapiens.
 OS Mus sp.
 XX Key Location/Qualifiers
 FH Peptide 1..19
 FT /label= Sig_peptide
 FT Region 51..57
 FT /label= CDR
 FT /note= "complementarity determining region"
 FT Region 72..87
 FT /label= CDR

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FT Peptide /note= "complementarity determining region"
FT 120. .130 /label= CDR
FT FT /note= "complementarity determining region"
XX
XX WO9507301-A1.
XX PD 16-MAR-1995.
XX XX
XX 07-SEP-1994; 94WO-US010308.
XX PF
XX 07-SEP-1993; 93US-00117366.
XX PR 14-OCT-1993; 93US-00136783.
XX XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Holmes S, Gross MS, Sylvester DR;
XX WPI; 1995-123387/16.
XX DR N-PSDB; AAQ83492.
XX XX
XX Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from
XX PT high affinity mAbs - useful in treatment of IL-4-mediated and Ige-
XX PT mediated allergic conditions.
XX PS Disclosure; Fig 3; 97pp; English.
XX XX
XX A human/mouse chimeric antibody heavy chain variable region was
XX CC constructed (given in AAR70191) that contained the mouse anti-human IL-4
XX CC MAb 3B9 variable region including 3 CDRs (AAR70198-200) and a human
XX CC antibody signal peptide (AAR70193). The construct was used for humanized
XX CC antibody production. (Updated on 25-MAR-2003 to correct PN field.)
XX CC (Updated on 27-AUG-2003 to correct OS field.)
XX SQ Sequence 141 AA;
XX
XX Query Match 100.0%; Score 34; DB 2; Length 141;
XX Best Local Similarity 100.0%; Pred. No. 42;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TSGMGVS 7
XX DB 51 TSGMGVS 57
XX
XX RESULT 21
XX ID AAY23770 standard; protein; 141 AA.
XX AC AAY23770;
XX XX
XX DT 13-SEP-1999 (first entry)
XX DE Heavy chain variable region of humanised murine IL-4 antibody 3B9.
XX KW Heavy chain variable region; interleukin-4; IL-4; antibody 3B9;
XX KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
XX KW Immunoglobulin E-mediated allergic reaction; allergic rhinitis;
XX KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
XX KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.
XX OS Synthetic.
XX OS Mus sp.
XX OS Homo sapiens.
XX XX
XX PN US5928904-A.
XX PD 27-JUL-1999.
XX XX
XX PF 07-JUN-1995; 95US-00483632.
XX XX
XX PR 14-OCT-1993; 93US-00136783.
XX PD 07-SEP-1994; 94WO-US010308.
XX XX
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX PR 14-OCT-1993; 93US-00136783.
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX XX

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PR 14-OCT-1993; 93US-00136783.
PR 07-SEP-1994; 94WO-US010308.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Holmes SD, Sylvester DR, Gross MS;
XX WPI; 1999-429500/36.
XX DR N-PSDB; AAX85887.
XX XX
XX New DNA molecules encoding recombinant antibodies useful for treating IL4
XX PT -mediated conditions.
XX PS Example 3; Fig 4; 50pp; English.
XX XX
XX The present sequence represents the heavy chain variable region of a
XX CC humanised murine interleukin-4 (IL-4) antibody 3B9. The specification
XX CC describes chimeric and humanised IL-4 monoclonal antibodies. The
XX CC antibodies of the invention are used in therapeutic and pharmaceutical
XX CC compositions for treating IL-4 mediated and Immunoglobulin E-mediated
XX CC allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic
XX CC dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host
XX CC -versus-graft disease and renal disease. They are also useful in the
XX CC diagnosis of an allergy or condition associated with excess IL-4
XX CC production through the measurement e.g. by ELISA of circulating
XX CC endogenous IL-4 levels in humans
XX SQ Sequence 141 AA;
XX
XX Query Match 100.0%; Score 34; DB 2; Length 141;
XX Best Local Similarity 100.0%; Pred. No. 42;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TSGMGVS 7
XX DB 51 TSGMGVS 57
XX
XX RESULT 22
XX ID AAY23769 standard; protein; 141 AA.
XX AC AAY23769;
XX XX
XX DT 17-OCT-2003 (revised)
XX DT 13-SEP-1999 (first entry)
XX XX
XX DE Heavy chain variable region of murine/human chimeric antibody 3B9.
XX KW Heavy chain variable region; interleukin-4; IL-4; antibody 3B9;
XX KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
XX KW Immunoglobulin E-mediated allergic reaction; allergic rhinitis;
XX KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
XX KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.
XX OS Mus sp.
XX OS Homo sapiens.
XX OS Chimeric.
XX XX
XX PN US5928904-A.
XX PD 27-JUL-1999.
XX XX
XX PF 07-JUN-1995; 95US-00483632.
XX XX
XX PR 07-SEP-1993; 93US-00117366.
XX PR 14-OCT-1993; 93US-00136783.
XX PR 07-SEP-1994; 94WO-US010308.
XX XX
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX PR 14-OCT-1993; 93US-00136783.
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX XX

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PI Holmes SD, Sylvester DR, Gross MS;
XX WPI; 1999-429500/36.
DR N-PSDB; AAX85886.
XX
XX New DNA molecules encoding recombinant antibodies useful for treating IL4
PT -mediated conditions.
XX
XX Example 3; Fig 3; 50pp; English.
XX
XX The present sequence represents the heavy chain variable region of
CC murine/human interleukin-4 (IL-4) chimeric antibody 3B9. The
CC specification describes chimeric and humanised IL-4 monoclonal
CC antibodies. The antibodies of the invention are used in therapeutic and
CC pharmaceutical compositions for treating IL-4 mediated and immunoglobulin
CC E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis,
CC atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid
CC arthritis, host-versus-graft disease and renal disease. They are also
CC useful in the diagnosis of an allergy or condition associated with excess
CC IL-4 production through the measurement e.g. by ELISA of circulating
CC endogenous IL-4 levels in humans. (Updated on 17-OCT-2003 to standardise
CC OS field)
XX
XX SQ Sequence 141 AA;
XX
XX Query Match 100.0%; Score 34; DB 2; Length 141;
XX Best Local Similarity 100.0%; Pred. No. 42;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TSGMGVS 7
Db 51 TSGMGVS 57
XX
XX RESULT 23
XX AAY18125
XX ID AAY18125 standard; protein; 141 AA.
XX AC AAY18125;
XX XX
XX DT 11-AUG-1999 (first entry)
XX
XX DE Chimeric 3B9 monoclonal antibody heavy chain.
XX
XX KW Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;
XX allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
XX atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
XX autoimmune disease; graft versus host disease.
XX
XX OS Synthetic.
XX
XX PN US5914110-A.
XX
XX PD 22-JUN-1999.
XX
XX PF 07-JUN-1995; 95US-00483636.
XX
XX PR 07-SEP-1993; 93US-00117366.
XX
XX PR 14-OCT-1993; 93US-00136783.
XX
XX PR 07-SEP-1994; 94WO-US010308.
XX
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX PI Sylvester DR, Holmes SD, Gross MS;
XX
XX PN US5914110-A.
XX
XX PD 22-JUN-1999.
XX
XX PF 07-JUN-1995; 95US-00483636.
XX
XX PR 07-SEP-1993; 93US-00117366.
XX
XX PR 14-OCT-1993; 93US-00136783.
XX
XX PR 07-SEP-1994; 94WO-US010308.
XX
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX PI Sylvester DR, Holmes SD, Gross MS;
XX
XX PN WPI; 1999-370482/31.
XX
XX DR N-PSDB; AAX79542.
XX
XX PT Recombinant IL4 antibodies useful for treatment of allergic rhinitis,
XX atopic asthma and anaphylactic shock.
XX
XX PS Claim 15; Fig 3; 50pp; English.
XX
XX This sequence represents the heavy chain of the humanised 3B9 antibody of
CC the invention. The antibody is a chimeric or humanised interleukin-4
CC (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE)
CC mediated diseases. The antibodies are useful for the treatment of
CC allergic disorders such as allergic rhinitis, conjunctivitis, atopic
CC dermatitis, atopic asthma and anaphylactic shock. The antibodies are also
CC useful for regulating B and T cell proliferation and as such are useful
CC in the treatment of autoimmune diseases and graft versus host disease
XX
XX SQ Sequence 141 AA;
XX
XX Query Match 100.0%; Score 34; DB 2; Length 141;
XX Best Local Similarity 100.0%; Pred. No. 42;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TSGMGVS 7
Db 51 TSGMGVS 57
XX
XX RESULT 24
XX AAY18117
XX ID AAY18117 standard; protein; 141 AA.
XX AC AAY18117;
XX XX
XX DT 11-AUG-1999 (first entry)
XX
XX DE Heavy chain sequence for humanised 3B9 antibody.
XX
XX KW Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;
XX allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
XX atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
XX autoimmune disease; graft versus host disease.
XX
XX OS Synthetic.
XX
XX PN US5914110-A.
XX
XX PD 22-JUN-1999.
XX
XX PF 07-JUN-1995; 95US-00483636.
XX
XX PR 07-SEP-1993; 93US-00117366.
XX
XX PR 14-OCT-1993; 93US-00136783.
XX
XX PR 07-SEP-1994; 94WO-US010308.
XX
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX PI Sylvester DR, Holmes SD, Gross MS;
XX
XX PN WPI; 1999-370482/31.
XX
XX DR N-PSDB; AAX79516.
XX
XX PT Recombinant IL4 antibodies useful for treatment of allergic rhinitis,
XX atopic asthma and anaphylactic shock.
XX
XX PS Claim 15; Fig 4; 50pp; English.
XX
XX This sequence represents the heavy chain of the humanised 3B9 antibody of
CC the invention. The antibody is a chimeric or humanised interleukin-4
CC (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE)
CC mediated diseases. The antibodies are useful for the treatment of
CC allergic disorders such as allergic rhinitis, conjunctivitis, atopic
CC dermatitis, atopic asthma and anaphylactic shock. The antibodies are also
CC useful for regulating B and T cell proliferation and as such are useful
CC in the treatment of autoimmune diseases and graft versus host disease
XX
XX SQ Sequence 141 AA;
XX
XX Query Match 100.0%; Score 34; DB 2; Length 141;
XX Best Local Similarity 100.0%; Pred. No. 42;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TSGMGVS 7
Db 51 TSGMGVS 57
XX
XX RESULT 25
XX AAY18117
XX ID AAY18117 standard; protein; 141 AA.
XX AC AAY18117;
XX XX
XX DT 11-AUG-1999 (first entry)
XX
XX DE Heavy chain sequence for humanised 3B9 antibody.
XX
XX KW Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;
XX allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
XX atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
XX autoimmune disease; graft versus host disease.
XX
XX OS Synthetic.
XX
XX PN US5914110-A.
XX
XX PD 22-JUN-1999.
XX
XX PF 07-JUN-1995; 95US-00483636.
XX
XX PR 07-SEP-1993; 93US-00117366.
XX
XX PR 14-OCT-1993; 93US-00136783.
XX
XX PR 07-SEP-1994; 94WO-US010308.
XX
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX PI Sylvester DR, Holmes SD, Gross MS;
XX
XX PN WPI; 1999-370482/31.
XX
XX DR N-PSDB; AAX79542.
XX
XX PT Recombinant IL4 antibodies useful for treatment of allergic rhinitis,
XX atopic asthma and anaphylactic shock.
XX
XX PS Example 5; Fig 3; 50pp; English.
XX

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Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
|||||
Db 51 TSGMGVS 57

RESULT 25
ABG76934
ID ABG76934 standard; protein; 142 AA.
XX
XX
AC ABG76934;
XX
XX 05-NOV-2002 (first entry)
XX
XX Mouse 10D5 VH protein.
XX
XX Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;
KW variable region complementarity determining region; 3D6; 10D5;
KW variable framework region; amyloidogenic disease; Alzheimer's disease;
KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;
KW notropic; neuroprotective; inhibitor of beta amyloid accumulation;
KW Abeta.
XX
XX Mus musculus.
OS
XX
XX WO200246237-A2.
XX
XX 13-JUN-2002.
XX
XX 06-DEC-2001; 2001WO-US046587.
XX
XX 06-DEC-2000; 2000US-0251892P.
XX
XX (NEUR-) NEURALAB LTD.
PA (AMHP) WYETH.
XX
XX Basi G, Saldanha J, Yednock T;
XX
XX WPI; 2002-519658/55.
DR N-PSDB; ABS59429.
XX
XX Novel light/heavy chain of humanized immunoglobulin for treating
PT amyloidogenic disease, has 3D6/10D5 variable region complementarity
PT determining regions and variable framework region from human acceptor
PT immunoglobulin.
XX
XX Claim 142; Fig 10; 171pp; English.

XX The present invention relates to new humanized immunoglobulin (Ig) light
CC chain (LC) or heavy chain (HC) comprising variable region complementarity
CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,
CC and variable framework region from human acceptor Ig LC or HC sequence.
CC The invention is useful for preventing or treating an amyloidogenic
CC disease or Alzheimer's disease in a patient. The invention is also useful
CC for in vivo imaging amyloid deposits in a patient. The present amino acid
CC sequence represents a mouse 3D6/10D5 variable light (VL) chain or
CC variable heavy (VH) chain protein of the invention
XX
XX Sequence 142 AA;
Query Match 100.0%; Score 34; DB 5; Length 142;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
|||||
Db 50 TSGMGVS 56

RESULT 26
ADR88420

ID ADR88420 standard; protein; 142 AA.
XX
XX ADR88420;
XX
XX 16-DEC-2004 (first entry)
XX
XX Murine 10D5 immunoglobulin heavy chain variable region SEQ ID NO:16.
XX
XX 3D6; heavy chain variable region; immunoglobulin;
KW complementarity determining region; CDR; 10D5; variable framework region;
KW neuroprotective; notropic; gene therapy; amyloidogenic disease;
KW Alzheimer's disease.
XX
XX Mus musculus.
OS
XX
XX Key Location/Qualifiers
FH Peptide 1..19
FT /label= signal peptide
FT Protein 20..142
FT /label= mature protein
PN WO2004080419-A2.
XX
XX 23-SEP-2004.
XX
XX 12-MAR-2004; 2004WO-US007503.
XX
XX 12-MAR-2003; 2003US-00388389.
XX
XX (NEUR-) NEURALAB LTD.
PA (AMHP) WYETH.
XX
XX Basi G, Saldanha JW, Yednock T;
XX
XX WPI; 2004-668880/65.
DR N-PSDB; ADR88419.
XX
XX New humanized antibodies that recognize beta amyloid peptides, useful for
PT preventing or treating amyloidogenic diseases, such as Alzheimer's
PT disease.
XX
XX Claim 85; SEQ ID NO 16; 176pp; English.

XX The invention relates to a novel humanised immunoglobulin light or heavy
CC chain. The humanised immunoglobulin light or heavy chain comprises:
CC variable region complementarity determining regions (CDR's) from the 3D6
CC immunoglobulin light chain variable region sequence of 132 amino acids
CC fully defined in the specification (ADR88406), or heavy chain variable
CC region sequence of 138 amino acids fully defined in the specification
CC (ADR88408); or from the 10D5 immunoglobulin light chain variable region
CC sequence of 131 amino acids given in the specification (ADR88418) or
CC heavy chain variable region sequence of 142 amino acids fully defined in
CC the specification (ADR88420); and a variable framework region from a
CC human acceptor immunoglobulin light or heavy chain sequence, provided
CC that at least one framework residue is substituted with the corresponding
CC amino acid residue from the mouse 3D6 or 10D5 light or heavy chain
CC variable region sequence, where the framework residue is a residue that
CC non-covalently binds antigen directly, a residue adjacent to a CDR, a CDR
CC -interacting residue or a residue participating in the VL-VH interface.
CC An antibody of the invention has neuroprotective and notropic activity,
CC and may have a use in gene therapy. The composition and methods are
CC useful for preventing or treating an amyloidogenic disease, such as
CC Alzheimer's disease. The variable region sequence is useful in producing
CC a three-dimensional image of a 3D6 or 10D5 immunoglobulin, immunoglobulin
CC chain, or its domain. The present sequence represents the murine 10D5
XX immunoglobulin heavy chain variable region.
XX
XX Sequence 142 AA;
Query Match 100.0%; Score 34; DB 8; Length 142;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7
 Db 50 TSGMGVS 56

RESULT 27
 ADZ08834
 ID ADZ08834 standard; peptide; 142 AA.
 XX
 AC ADZ08834;
 XX
 DT 16-JUN-2005 (first entry)
 XX
 DE Mammalian amyloid antibody, heavy chain variable region SEQ ID No:59.
 KW amyloid; antibody engineering; antibody production;
 KW amyloid-associated disorder; Alzheimer's disease; cancer; allergy;
 KW autoimmune disease; Parkinson's disease;
 KW acquired immune deficiency syndrome; multiple sclerosis; migraine;
 KW dementia; infection; neurotropic; neuroprotective; cytostatic;
 KW anti-allergic; immunosuppressive; antiparkinsonian; antimigraine;
 KW antimicrobial; anti-HIV; heavy chain variable region.
 XX
 OS Mammalia.
 XX
 FN WO2005028511-A2.
 XX
 PD 31-MAR-2005.
 XX
 PF 26-MAR-2004; 2004WO-US009522.
 XX
 PR 28-MAR-2003; 2003US-0458469P.
 PR 28-MAR-2003; 2003US-0458474P.
 PR 28-MAR-2003; 2003US-0458509P.
 PR 28-MAR-2003; 2003US-0458510P.
 XX
 PA (CENZ) CENTOCOR INC.
 PA (MERC/) MERCKEN M.
 PA (BENS/) BENSON J M.
 XX
 PI Mercken M, Benson JM;
 XX
 DR WPI; 2005-242565/25.
 DR N-PSDB; ADZ08836.
 XX
 PT New isolated mammalian anti-amyloid antibodies useful for treating
 PT amyloid-associated disorders, such as Alzheimer's disease, cancer,
 PT allergies, autoimmune disease, Parkinson's disease, multiple sclerosis,
 PT migraine and dementia.
 XX
 PS Claim 5; SEQ ID NO 59; 306pp; English.

The invention relates to at least one isolated mammalian amyloid antibody comprising at least one variable region comprising at least one heavy chain and at least one light chain, of a fully defined sequence of SEQ ID NOS: 48, 49, 59, 60, 69, 70, 79 and 80, respectively. Also described are: (i) at least one isolated mammalian amyloid antibody that binds to the same region of an amyloid polypeptide as an antibody comprising at least one heavy chain or light chain complementarity determining region (CDR) having the amino acid sequence of at least one of SEQ ID NO: 73-78, (ii) at least one isolated mammalian amyloid antibody, comprising at least one human CDR, where the antibody specifically binds at least one epitope selected from amino acids 2-7, 3-8, 33-42, or 34-40 of a fully defined sequence of 42 amino acids (SEQ ID NO: 50), (iii) an isolated nucleic acid encoding at least one of any of the isolated mammalian amyloid antibodies mentioned and having at least one human CDR of a fully defined sequence of SEQ ID NO: 51, 52, 61, 62, 71, 72, 81 and 82, (iv) an isolated nucleic acid vector comprising an isolated nucleic acid encoding an amyloid antibody, (v) a prokaryotic or eukaryotic host cell comprising an isolated nucleic acid encoding an amyloid antibody, (vi) a method of producing at least one amyloid antibody, (vii) a composition comprising at least one of any of the isolated mammalian amyloid antibodies mentioned, and at least one pharmaceutical carrier or diluent, (viii) an

CC anti-idiotypic antibody or fragment that specifically binds at least one of the amyloid antibodies mentioned, (ix) a method of diagnosing or treating an amyloid related condition in a cell, tissue, organ or animal, comprising contacting or administering a composition comprising at least one of the antibodies mentioned, with, or to, the cell, tissue, organ or animal, (x) a medical device comprising at least one amyloid antibody mentioned, where the device is suitable for contacting or administering at least one amyloid antibody, (xi) an article of manufacture for human pharmaceutical or diagnostic use, comprising packaging material and a container comprising a solution or a lyophilized form of at least one of the amyloid antibodies mentioned, and (xii) a method of producing at least one of the isolated mammalian amyloid antibodies, comprising providing a host cell or transgenic animal or transgenic plant or plant cell capable of expressing the antibody in recoverable amounts. The methods and compositions of the present invention are useful for producing therapeutic compositions and devices for treating amyloid-associated disorders, such as Alzheimer's disease, cancer, allergies, autoimmune disease, Parkinson's disease, AIDS, multiple sclerosis, migraine, dementia and infections. This sequence represents a heavy chain variable region useful in the antibody of the invention.

XX
 SQ Sequence 142 AA;
 Query Match 100.0%; Score 34; DB 9; Length 142;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7
 Db 50 TSGMGVS 56

RESULT 28
 AAR58612
 ID AAR58612 standard; protein; 246 AA.
 XX
 AC AAR58612;
 XX
 DT 25-MAR-2003 (revised)
 DT 28-APR-1995 (first entry)
 XX
 DE IL-6 binding inhibitor.
 XX
 KW Human interleukin-6 binding inhibitor; IL-6; rheumatoid arthritis;
 KW septic shock; multiple myeloma; ss.
 XX
 OS Homo sapiens.
 XX
 FN EP617126-A2.
 XX
 PD 28-SEP-1994.
 XX
 PF 16-FEB-1994; 94EP-00102346.
 XX
 PR 17-FEB-1993; 93JP-00028173.
 XX
 PA (AJIN) AJINOMOTO KK.
 PI Shimamura T, Nakazawa H, Hamuro J;
 XX
 DR WPI; 1994-295777/37.
 DR N-PSDB; AAQ70612.
 XX
 PT Polypeptide inhibiting binding of human interleukin-6 (IL-6) to its
 PT receptor - useful for treating auto-immune disease induced or aggravated by IL-6.
 XX
 PS Claim 5; Page 18; 26pp; English.

AAQ70612 codes for human interleukin-6 binding inhibitor, the polypeptide described in AAR58612. This polypeptide inhibits the binding of human IL-6 to its receptor, and can therefore be useful in the treatment of a variety of autoimmune diseases; specifically in the treatment of

CC rheumatoid arthritis, septic shock due to bacterial infection and
CC multiple myeloma. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 246 AA;
Query Match 100.0%; Score 34; DB 2; Length 246;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TSGMGVS 7
Db 153 TSGMGVS 159
RESULT 29
ABP58287
ID ABP58287 standard; protein; 453 AA.
XX
AC ABP58287;
XX
DT 23-OCT-2003 (revised)
DT 31-MAR-2003 (first entry)
XX
DE Humanised 10D5 antibody heavy chain.
XX
KW Monoclonal antibody; 10D5; complementarity determining region; CDR;
KW mouse; human; humanised antibody; antibody; Alzheimer's disease;
KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region 1..123
FT /note= "light chain variable region"
FT Region 31..35
FT /note= "CDR1"
FT Region 52..67
FT /note= "CDR2"
FT Region 100..112
FT /note= "CDR3"
XX
PN WO200288307-A2.
XX
PD 07-NOV-2002.
XX
PF 26-APR-2002; 2002WO-US011854.
XX
PR 30-APR-2001; 2001US-0287653P.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Hinton PR, Vasquez M;
XX
DR WPI; 2003-183836/18.
XX
PT New humanized 10D5 antibody, useful for the manufacture of a medicament
PT for treating Down's syndrome, clinical or pre-clinical Alzheimer's
PT disease or cerebral amyloid angiopathy.
XX
PS Claim 5; Page 10-12; 52pp; English.
XX
CC The present sequence is the protein sequence of the heavy chain of a
CC humanised antibody of the present invention. In the variable portion, the
CC complementarity determining regions (CDRs) originate from murine
CC monoclonal antibody 10D5 and the framework region originates from human
CC germline VH segment Dp-28 and J segment JH4. Novel humanised antibodies
CC of the invention have CDRs from 10D5 and human framework sequences. These
CC humanised antibodies have binding affinities (affinity and epitope
CC location) approximately the same as those of the mouse 10D5 antibody. The
CC invention includes antibodies, single chain antibodies, and their
CC fragments, as well as nucleotide sequences, vectors, transformed host

CC cells, and methods of using the humanised antibody to treat, prevent,
CC alleviate, reverse or otherwise ameliorate symptoms and/or pathology
CC associated with Down's syndrome, (pre-)clinical Alzheimer's disease or
CC (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or
CC reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
CC OS field)
XX
SQ Sequence 453 AA;
Query Match 100.0%; Score 34; DB 6; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TSGMGVS 7
Db 31 TSGMGVS 37
RESULT 30
ABP58289
ID ABP58289 standard; protein; 472 AA.
XX
AC ABP58289;
XX
DT 23-OCT-2003 (revised)
DT 31-MAR-2003 (first entry)
XX
DE Humanised 10D5 antibody heavy chain.
XX
KW Monoclonal antibody; 10D5; complementarity determining region; CDR;
KW mouse; human; humanised antibody; antibody; Alzheimer's disease;
KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Signal_peptide
FT Peptide 20..472
FT /label= Mature_protein
FT /note= "the mature light chain is claimed in Claim 5"
FT Region 20..142
FT /note= "light chain variable region, claimed in Claim 4"
FT Region 50..56
FT /note= "CDR1"
FT Region 71..86
FT /note= "CDR2"
FT Region 119..131
FT /note= "CDR3"
XX
PN WO200288307-A2.
XX
PD 07-NOV-2002.
XX
PF 26-APR-2002; 2002WO-US011854.
XX
PR 30-APR-2001; 2001US-0287653P.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Hinton PR, Vasquez M;
XX
DR WPI; 2003-183836/18.
XX
PT New humanized 10D5 antibody, useful for the manufacture of a medicament
PT for treating Down's syndrome, clinical or pre-clinical Alzheimer's
PT disease or cerebral amyloid angiopathy.
XX
PS Disclosure; Page 13-15; 52pp; English.
XX

CC The present sequence is the protein sequence of the heavy chain of a
 CC humanised antibody of the present invention. In the variable portion, the
 CC complementarity determining regions (CDRs) originate from murine
 CC monoclonal antibody 10D5 and the framework region originates from human
 CC germline VH segment DP-28 and J segment JH4. Novel humanised antibodies
 CC of the invention have CDRs from 10D5 and human framework sequences. These
 CC humanised antibodies have binding affinities (affinity and epitope
 CC location) approximately the same as those of the mouse 10D5 antibody. The
 CC invention includes antibodies, single chain antibodies, and their
 CC fragments, as well as nucleotide sequences, vectors, transformed host
 CC cells, and methods of using the humanised antibody to treat, prevent,
 CC alleviate, reverse or otherwise ameliorate symptoms and/or pathology
 CC associated with Down's syndrome, (pre-)clinical Alzheimer's disease or
 CC (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or
 CC reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
 CC OS field)
 CC
 CC SQ Sequence 472 AA;

Query Match 100.0%; Score 34; DB 6; Length 472;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
 |||||
 DB 50 TSGMGVS 56

RESULT 31
 ADD94206
 ID ADD94206 standard; peptide; 12 AA.

XX AC ADD94206;

XX 29-JAN-2004 (first entry)

XX Mouse HUI77 antibody mutant heavy chain CDR amino acid sequence SeqID91.

XX grafted antibody; complementarity determining region; CDR; light CDR;
 KW heavy CDR; cryptic collagen epitope; solid tumour;
 KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;
 KW collagen agonist; collagen antagonist; cancer metastasis;
 KW anti-cryptic collagen; HUI77; variable region heavy chain; mouse; murine;
 KW mutant; mutein.

XX Synthetic.

OS Mus musculus.

XX WO2003046204-A2.

XX 05-JUN-2003.

XX 26-NOV-2002; 2002WO-US038147.

XX 26-NOV-2001; 2001US-00995529.

XX 06-DEC-2001; 2001US-00011250.

XX (CELL-) CELL MATRIX INC.

XX Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;

XX WPI; 2003-513649/48.

XX New cryptic collagen antibody with one or more complementarity
 PT determining regions, useful for diagnosing and treating disorders
 PT associated with angiogenesis, tumor growth and/or cancer metastasis.

XX Claim 24; SEQ ID NO 91; 232pp; English.

XX This invention relates to a novel grafted antibody or its functional
 CC fragment comprising one or more complementarity determining regions
 CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino
 CC acid (aa) substitution where the antibody has specific binding activity

CC for a cryptic collagen epitope. The growth of all solid tumours requires
 CC new blood vessel growth, angiogenesis, inhibition of which is an approach
 CC to limiting tumour growth. The invention may allow development of
 CC therapeutics with a cytostatic activity as a collagen agonist or
 CC antagonist. The invention is useful for diagnosing and treating disorders
 CC associated with angiogenesis, tumour growth and/or cancer metastasis. The
 CC present sequence is the amino acid sequence of a mutant mouse anti-
 CC cryptic collagen site antibody HUI77 variable region heavy chain CDR
 CC which may be used during the creation of an antibody of the invention.

XX SQ Sequence 12 AA;

Query Match 91.2%; Score 31; DB 7; Length 12;
 Best Local Similarity 85.7%; Pred. No. 15;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
 |||||
 DB 6 TSGMGVA 12

RESULT 32
 AAY25396
 ID AAY25396 standard; protein; 121 AA.

XX AC AAY25396;

XX 07-SEP-1999 (first entry)

XX WO9932630 Seq ID 35.

XX Paraquat; antibody; light chain; herbicide; resistant; crop plant;
 KW weed control; tolerant; diquat; photosynthesis inhibitor; photosystem I;
 KW free radical; lipid peroxidation; electron transport; photosystem II;
 KW vacuole; cell surface; cytotoxic; sensitive.

XX Unidentified.

XX WO9932630-A1.

XX 01-JUL-1999.

XX 15-DEC-1998; 98WO-GB003760.

XX 19-DEC-1997; 97GB-00026955.

XX (ZENEC) ZENEC LTD.

XX Holt DC, Jones PG;

XX WPI; 1999-405173/34.

XX Herbicide binding proteins and related polynucleotides.

XX Disclosure; Page 43-44; 60pp; English.

XX This invention describes a novel herbicide binding protein which can
 CC confer herbicide resistance activity. Crop plants, such as soybean,
 CC cotton, tobacco, sugarbeet, oilseed rape, canola, flax, sunflower,
 CC potato, tomato, alfalfa, lettuce, maize, wheat, sorghum, rye, bananas,
 CC barley, oat, turf grass, forage grass, sugar cane, pea, field bean, rice,
 CC pine, poplar, apple, grape, citrus or nut plants, transformed with a
 CC herbicide binding protein gene are resistant to the herbicide. Hence,
 CC weeds can be selectively controlled in a field of the transformed crops.
 CC The plants are substantially resistant or tolerant to herbicides, such as
 CC paraquat or diquat, that inhibit photosynthesis by accepting electrons
 CC from photosystem I thus generating free radicals which cause lipid
 CC peroxidation or by blocking electron transport in photosystem II. The
 CC herbicide binding proteins advantageously sequester the herbicide, e.g.
 CC at the cell surface or in the vacuoles of a treated plant. Sequestration
 CC at the cell surface prevents the entry of the herbicide into the cell so
 CC that the herbicide cannot reach its intracellular target and exert any
 CC significant cytotoxic effect. The herbicide binding protein inhibits the

CC mobility of the herbicide from the application site to the whole plant
 CC preventing the herbicide reaching particularly sensitive organs.
 CC Additionally, tolerant plants can be produced against herbicides that
 CC have more than one target site
 XX
 SQ Sequence 121 AA;

Query Match 91.2%; Score 31; DB 2; Length 121;
 Best Local Similarity 85.7%; Pred. No. 1.5e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
 |||||:
 Db 31 TSGMGVT 37

RESULT 33
 AAY42963
 ID AAY42963 standard; protein; 123 AA.
 XX
 AC AAY42963;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Mouse 12B4 antibody Vh mature peptide sequence.
 XX
 KW Immunoglobulin; Ig; neuroprotective; nootropic; gene therapy; vaccine;
 KW amyloidogenic disease; antibody.
 XX
 OS Mus sp.
 XX
 PN WO2003077858-A2.
 XX
 PD 25-SEP-2003.
 XX
 PF 12-MAR-2003; 2003WO-US007715.
 XX
 PR 12-MAR-2002; 2002US-0363751P.
 XX
 PA (NEUR-) NEURALAB LTD.
 PA (AMHP) WYETH.
 XX
 PI Basi G, Saldanha J;
 XX
 DR WPI; 2003-779077/73.
 XX
 PT New humanized immunoglobulin light or heavy chains comprising variable
 PT region complementary determining regions and variable framework regions,
 PT useful for preventing or treating e.g., Alzheimer's disease.
 XX
 PS Example 5; Fig 2A-B; 122pp; English.
 XX
 CC The invention relates to humanized immunoglobulin (Ig) light or heavy
 CC chains comprising variable region complementary determining regions
 CC (CDRs) from the 12B4 Ig variable region sequence and variable framework
 CC regions from a human acceptor Ig light chain or heavy chain sequence. The
 CC humanized Ig light or heavy chain or its nucleic acid molecule is useful
 CC for preventing or treating an amyloidogenic disease in humans, associated
 CC with amyloid deposits of Abeta in the brain, e.g., Alzheimer's disease,
 CC Down's syndrome or mild cognitive impairment, all characterized by
 CC cognitive impairment. The variable region sequence is useful in producing
 CC a three-dimensional image of a 12B4 Ig, 12B4 Ig chain or its domain. A
 CC humanized antibody is useful for reducing plaque or neuritic burden in a
 CC subject. The present sequence represents a mouse 12B4 antibody variable
 CC heavy chain mature peptide sequence
 XX
 SQ Sequence 123 AA;

Query Match 91.2%; Score 31; DB 7; Length 123;
 Best Local Similarity 85.7%; Pred. No. 1.5e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7

Db 31 TNGMGVS 37
 |||||:
 RESULT 34
 AAY42964
 ID AAY42964 standard; protein; 123 AA.
 XX
 AC AAY42964;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Humanised 12B4VHV1 mature peptide.
 XX
 KW Immunoglobulin; Ig; neuroprotective; nootropic; gene therapy; vaccine;
 KW amyloidogenic disease; antibody; 12B4v1.
 XX
 OS Synthetic.
 XX
 PN WO2003077858-A2.
 XX
 PD 25-SEP-2003.
 XX
 PF 12-MAR-2003; 2003WO-US007715.
 XX
 PR 12-MAR-2002; 2002US-0363751P.
 XX
 PA (NEUR-) NEURALAB LTD.
 PA (AMHP) WYETH.
 XX
 PI Basi G, Saldanha J;
 XX
 DR WPI; 2003-779077/73.
 XX
 PT New humanized immunoglobulin light or heavy chains comprising variable
 PT region complementary determining regions and variable framework regions,
 PT useful for preventing or treating e.g., Alzheimer's disease.
 XX
 PS Claim 49; Fig 2A-B; 122pp; English.
 XX
 CC The invention relates to humanized immunoglobulin (Ig) light or heavy
 CC chains comprising variable region complementary determining regions
 CC (CDRs) from the 12B4 Ig variable region sequence and variable framework
 CC regions from a human acceptor Ig light chain or heavy chain sequence. The
 CC humanized Ig light or heavy chain or its nucleic acid molecule is useful
 CC for preventing or treating an amyloidogenic disease in humans, associated
 CC with amyloid deposits of Abeta in the brain, e.g., Alzheimer's disease,
 CC Down's syndrome or mild cognitive impairment, all characterized by
 CC cognitive impairment. The variable region sequence is useful in producing
 CC a three-dimensional image of a 12B4 Ig, 12B4 Ig chain or its domain. A
 CC humanized antibody is useful for reducing plaque or neuritic burden in a
 CC subject. The present sequence represents the humanised 12B4VHV1 mature
 CC peptide sequence
 XX
 SQ Sequence 123 AA;

Query Match 91.2%; Score 31; DB 7; Length 123;
 Best Local Similarity 85.7%; Pred. No. 1.5e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
 |||||:
 Db 31 TNGMGVS 37

RESULT 35
 AAY42973
 ID AAY42973 standard; protein; 142 AA.
 XX
 AC AAY42973;
 XX
 DT 12-FEB-2004 (first entry)
 XX

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DE Humanised 12B4VHv1 sequence.
XX
KW Immunoglobulin; Ig; neuroprotective; nootropic; gene therapy; vaccine;
KW amyloidogenic disease; antibody; 12B4v1.
XX
OS Synthetic.
XX
FN WO2003077858-A2.
XX
PD 25-SEP-2003.
XX
PF 12-MAR-2003; 2003WO-US007715.
XX
PR 12-MAR-2002; 2002US-0363751P.
XX
PA (NEUR-) NEURALAB LTD.
PA (AMHP ) WYETH.
XX
PI Basi G, Saldanha J;
XX
DR WPI; 2003-779077/73.
DR N-PSDB; ACF58541.
XX
XX New humanized immunoglobulin light or heavy chains comprising variable
PT region complementary determining regions and variable framework regions,
PT useful for preventing or treating e.g., Alzheimer's disease.
XX
PS Example; Fig 4A-D; 122pp; English.
XX
CC The invention relates to humanized immunoglobulin (Ig) light or heavy
CC chains comprising variable region complementary determining regions
CC (CDRs) from the 12B4 Ig variable region sequence and variable framework
CC regions from a human acceptor Ig light chain or heavy chain sequence. The
CC humanized Ig light or heavy chain or its nucleic acid molecule is useful
CC for preventing or treating an amyloidogenic disease in humans, associated
CC with amyloid deposits of Abeta in the brain, e.g., Alzheimer's disease,
CC Down's syndrome or mild cognitive impairment, all characterized by
CC cognitive impairment. The variable region sequence is useful in producing
CC a three-dimensional image of a 12B4 Ig, 12B4 Ig chain or its domain. A
CC humanized antibody is useful for reducing plaque or neuritic burden in a
CC subject. The present sequence represents the humanised 12B4VHv1 sequence
XX
SQ Sequence 142 AA;

Query Match 91.2%; Score 31; DB 7; Length 142;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7
Db 50 TNGMGVS 56
|:|||||

RESULT 36
AAY42957
ID AAY42957 standard; protein; 142 AA.
XX
AC AAY42957;
XX
DT 12-FEB-2004 (first entry)
XX
DE Mouse 12B4 antibody VH region.
XX
KW Immunoglobulin; Ig; neuroprotective; nootropic; gene therapy; vaccine;
KW amyloidogenic disease; antibody.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT /note= "leader peptide"
FT Protein 21..142
FT /note= "mature protein"

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FT Region 51..56
FT /note= "CDR 1"
FT Region 71..86
FT /note= "CDR 2"
FT Region 119..131
FT /note= "CDR 3"
XX
FN WO2003077858-A2.
XX
PD 25-SEP-2003.
XX
PF 12-MAR-2003; 2003WO-US007715.
XX
PR 12-MAR-2002; 2002US-0363751P.
XX
PA (NEUR-) NEURALAB LTD.
PA (AMHP ) WYETH.
XX
PI Basi G, Saldanha J;
XX
DR WPI; 2003-779077/73.
DR N-PSDB; ACF58516.
XX
XX New humanized immunoglobulin light or heavy chains comprising variable
PT region complementary determining regions and variable framework regions,
PT useful for preventing or treating e.g., Alzheimer's disease.
XX
PS Claim 2; Page 63; 122pp; English.
XX
CC The invention relates to humanized immunoglobulin (Ig) light or heavy
CC chains comprising variable region complementary determining regions
CC (CDRs) from the 12B4 Ig variable region sequence and variable framework
CC regions from a human acceptor Ig light chain or heavy chain sequence. The
CC humanized Ig light or heavy chain or its nucleic acid molecule is useful
CC for preventing or treating an amyloidogenic disease in humans, associated
CC with amyloid deposits of Abeta in the brain, e.g., Alzheimer's disease,
CC Down's syndrome or mild cognitive impairment, all characterized by
CC cognitive impairment. The variable region sequence is useful in producing
CC a three-dimensional image of a 12B4 Ig, 12B4 Ig chain or its domain. A
CC humanized antibody is useful for reducing plaque or neuritic burden in a
CC subject. The present sequence represents a mouse 12B4 antibody variable
CC heavy chain sequence
XX
SQ Sequence 142 AA;

Query Match 91.2%; Score 31; DB 7; Length 142;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7
Db 50 TNGMGVS 56
|:|||||

RESULT 37
AAY42972
ID AAY42972 standard; protein; 142 AA.
XX
AC AAY42972;
XX
DT 12-FEB-2004 (first entry)
XX
DE Chimeric 12B4VH region sequence.
XX
KW Immunoglobulin; Ig; neuroprotective; nootropic; gene therapy; vaccine;
KW amyloidogenic disease; antibody; 12B4; chimeric.
XX
OS Chimeric - Mus sp.
XX
FN WO2003077858-A2.
PD 25-SEP-2003.
XX

```

PF 12-MAR-2003; 2003WO-US007715.
 XX
 PR 12-MAR-2002; 2002US-0363751P.
 XX
 PA (NEUR-) NEURALAB LTD.
 PA (AMHP) WYETH.
 XX
 PI Basi G, Saldanha J;
 XX
 DR WPI; 2003-779077/73.
 DR N-PSDB; ACF58540.
 XX
 XX New humanized immunoglobulin light or heavy chains comprising variable
 PT region complementary determining regions and variable framework regions,
 PT useful for preventing or treating e.g., Alzheimer's disease.
 XX
 PS Example; Fig 4A-D; 122pp; English.
 XX
 CC The invention relates to humanized immunoglobulin (Ig) light or heavy
 CC chains comprising variable region complementary determining regions
 CC (CDRs) from the 12B4 Ig variable region sequence and variable framework
 CC regions from a human acceptor Ig light chain or heavy chain sequence. The
 CC humanized Ig light or heavy chain or its nucleic acid molecule is useful
 CC for preventing or treating an amyloidogenic disease in humans, associated
 CC with amyloid deposits of Abeta in the brain, e.g., Alzheimer's disease,
 CC Down's syndrome or mild cognitive impairment, all characterized by
 CC cognitive impairment. The variable region sequence is useful in producing
 CC a three-dimensional image of a 12B4 Ig, 12B4 Ig chain or its domain. A
 CC humanized antibody is useful for reducing plaque or neuritic burden in a
 CC subject. The present sequence represents a chimeric 12B4VH region
 CC sequence
 XX
 SQ Sequence 142 AA;
 Query Match 91.2%; Score 31; DB 7; Length 142;
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TSGMGVS 7
 DB 50 TNGMGVS 56
 RESULT 38
 ADC00282
 ID ADC00282 standard; protein; 2793 AA.
 XX
 AC ADC00282;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Enterohaemorrhagic E. coli 0157:H7-specific protein SEQ ID NO: 327.
 XX
 KW enterohaemorrhagic; anti-bacterial.
 XX
 OS Escherichia coli; 0157:H7.
 XX
 PN JP2002355074-A.
 XX
 PD 10-DEC-2002.
 XX
 PF 24-JAN-2002; 2002JP-00015959.
 XX
 PR 24-JAN-2001; 2001JP-00112010.
 XX
 PA (UYTS-) UNIV TSUKUBA.
 XX
 DR WPI; 2003-451640/43.
 XX
 PT Enterohaemorrhagic Escherichia coli 0157:H7-specific nucleic acid molecule
 PT and a polypeptide and its use, a polypeptide, a vector and a host cell.
 XX
 PS Claim 3; SEQ ID NO 327; 2067pp; Japanese.

XX The invention relates to a novel enterohaemorrhagic Escherichia coli
 CC O157:H7-specific nucleic acid molecule. A polynucleotide of the invention
 CC has anti-bacterial activity. The polypeptide can be used in detection
 CC and/or treatment of O157:H7 infection. The nucleotide sequence of the
 CC genome of Enterohaemorrhagic E. coli O157:H7 was determined. The present
 CC sequence represents an E. coli 0157:H7-specific polypeptide of the
 XX invention.
 XX
 SQ Sequence 2793 AA;
 Query Match 91.2%; Score 31; DB 7; Length 2793;
 Best Local Similarity 85.7%; Pred. No. 3.4e+03;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TSGMGVS 7
 DB 391 TAGMGVS 397
 RESULT 39
 AAB21368
 ID AAB21368 standard; protein; 7 AA.
 XX
 AC AAB21368;
 XX
 DT 25-JAN-2001 (first entry)
 XX
 DE Mouse antibody 13G9 heavy chain variable region CDR I.
 XX
 KW Mouse; antibody 13G9; antiarthritic; immunosuppressive; neuroprotective;
 KW antiinflammatory; antipsoriatic; interleukin-18; IL-18;
 KW autoimmune disease; multiple sclerosis; rheumatoid arthritis;
 KW type I diabetes; insulin dependent diabetes; IDDM; psoriasis;
 KW inflammatory bowel disease; complementarity determining region; CDR.
 XX
 OS Mus musculus.
 XX
 PN WO200056771-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 17-MAR-2000; 2000WO-US007349.
 XX
 PR 19-MAR-1999; 99US-0125299P.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Ho YS, Holmes SD, Taylor AH, Abdel-Meguid SS;
 XX
 DR WPI; 2000-628249/60.
 DR N-PSDB; AAR99647.
 XX
 PT Novel anti-human interleukin (IL)-18 rodent neutralizing monoclonal
 PT antibody having high affinity and useful for treating IL-18 mediated
 PT disorders such as multiple sclerosis, rheumatoid arthritis and psoriasis.
 XX
 PS Disclosure; Fig 4; 64pp; English.
 XX
 CC The present sequence is complementarity determining region (CDR) I of the
 CC mouse antibody 13G9 heavy chain variable region. The antibody has high
 CC affinity for human interleukin-18 (IL-18) and is useful for treating and
 CC diagnosing IL-18-mediated disorders, e.g. autoimmune diseases such as
 CC multiple sclerosis, rheumatoid arthritis, type I or insulin dependent
 CC diabetes, inflammatory bowel disease and psoriasis. Specific changes can
 CC be introduced into the nucleotide sequences encoding the complementarity
 CC determining regions (CDRs) or framework regions of the variable light
 CC chain and heavy chain peptides. The resulting modified or fusion nucleic
 CC acid sequences can then be introduced into a plasmid for expression
 XX
 SQ Sequence 7 AA;

```

Query Match      88.2%; Score 30; DB 3; Length 7;
Best Local Similarity 71.4%; Pred. No. 2e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 TSGMGVS 7
      |||||:
Db      1 TSGMGIA 7

RESULT 40
ADD94204
ID ADD94204 standard; peptide; 12 AA.
XX
AC ADD94204;
XX
DT 29-JAN-2004 (first entry)
XX
DE Mouse HUI77 antibody mutant heavy chain CDR amino acid sequence SeqID89.
XX
KW grafted antibody; complementarity determining region; CDR; light CDR;
KW heavy CDR; cryptic collagen epitope; solid tumour;
KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;
KW collagen agonist; collagen antagonist; cancer metastasis;
KW anti-cryptic collagen; HUI77; variable region heavy chain; mouse; murine;
KW mutant; mutein.
XX
OS Synthetic.
OS Mus musculus.
XX
PN WO2003046204-A2.
XX
PD 05-JUN-2003.
XX
PF 26-NOV-2002; 2002WO-US038147.
XX
PR 26-NOV-2001; 2001US-00995529.
PR 06-DEC-2001; 2001US-00011250.
XX
PA (CELL-) CELL MATRIX INC.
XX
PI Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;
XX
PP WPI; 2003-513649/48.
XX
DR New cryptic collagen antibody with one or more complementarity
PT determining regions, useful for diagnosing and treating disorders
PT associated with angiogenesis, tumor growth and/or cancer metastasis.
XX
XX Claim 24; SEQ ID NO 89; 232pp; English.
XX
PS This invention relates to a novel grafted antibody or its functional
CC fragment comprising one or more complementarity determining regions
CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino
CC acid (aa) substitution where the antibody has specific binding activity
CC for a cryptic collagen epitope. The growth of all solid tumours requires
CC new blood vessel growth, angiogenesis, inhibition of which is an approach
CC to limiting tumour growth. The invention may allow development of
CC therapeutics with a cytostatic activity as a collagen agonist or
CC antagonist. The invention is useful for diagnosing and treating disorders
CC associated with angiogenesis, tumour growth and/or cancer metastasis. The
CC present sequence is the amino acid sequence of a mutant mouse anti-
CC cryptic collagen site antibody HUI77 variable region heavy chain CDR
CC which may be used during the creation of an antibody of the invention.
XX
SQ Sequence 12 AA;

Query Match      88.2%; Score 30; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TSGMGV 6
      |||||
Db      6 TSGMGV 11

RESULT 42
ADD94205
ID ADD94205 standard; peptide; 12 AA.
XX
AC ADD94205;

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RESULT 41
ADD94153
ID ADD94153 standard; peptide; 12 AA.
XX
AC ADD94153;
XX
DT 29-JAN-2004 (first entry)
XX
DE Mouse HUI77 light chain CDR1 partial amino acid sequence SeqID38.
XX
KW grafted antibody; complementarity determining region; CDR; light CDR;
KW heavy CDR; cryptic collagen epitope; solid tumour;
KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;
KW collagen agonist; collagen antagonist; cancer metastasis;
KW anti-cryptic collagen; antibody; HUI77; variable region heavy chain;
KW mouse; murine.
XX
OS Mus musculus.
XX
PN WO2003046204-A2.
XX
PD 05-JUN-2003.
XX
PF 26-NOV-2002; 2002WO-US038147.
XX
PR 26-NOV-2001; 2001US-00995529.
PR 06-DEC-2001; 2001US-00011250.
XX
PA (CELL-) CELL MATRIX INC.
XX
PI Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;
XX
PP WPI; 2003-513649/48.
XX
DR N-PSDB; ADD94152.
XX
PT New cryptic collagen antibody with one or more complementarity
PT determining regions, useful for diagnosing and treating disorders
PT associated with angiogenesis, tumor growth and/or cancer metastasis.
XX
XX Claim 25; SEQ ID NO 38; 232pp; English.
XX
PS This invention relates to a novel grafted antibody or its functional
CC fragment comprising one or more complementarity determining regions
CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino
CC acid (aa) substitution where the antibody has specific binding activity
CC for a cryptic collagen epitope. The growth of all solid tumours requires
CC new blood vessel growth, angiogenesis, inhibition of which is an approach
CC to limiting tumour growth. The invention may allow development of
CC therapeutics with a cytostatic activity as a collagen agonist or
CC antagonist. The invention is useful for diagnosing and treating disorders
CC associated with angiogenesis, tumour growth and/or cancer metastasis. The
CC present sequence is the partial amino acid sequence of a mouse anti-
CC cryptic collagen site antibody HUI77 variable region heavy chain CDR
CC which is related to the invention.
XX
SQ Sequence 12 AA;

Query Match      88.2%; Score 30; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TSGMGV 6
      |||||
Db      6 TSGMGV 11

RESULT 42
ADD94205
ID ADD94205 standard; peptide; 12 AA.
XX
AC ADD94205;

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| | | |
|-----------|--|---|
| XX | 29-JAN-2004 | (first entry) |
| DT | | |
| XX | | |
| DE | Mouse HUI177 antibody mutant heavy chain CDR amino acid sequence SeqID90. | |
| XX | | |
| DE | grafted antibody; complementarity determining region; CDR; light CDR; | |
| XX | heavy CDR; cryptic collagen epitope; solid tumour; | |
| KW | new blood vessel growth; angiogenesis; tumour growth; cytostatic; | |
| KW | collagen agonist; collagen antagonist; cancer metastasis; | |
| KW | anti-cryptic collagen; HUI177; variable region heavy chain; mouse; murine; | |
| KW | mutant; mutein. | |
| XX | | |
| OS | Synthetic. | |
| OS | Mus musculus. | |
| XX | | |
| PN | WO2003046204-A2. | |
| XX | | |
| PN | 05-JUN-2003. | |
| XX | | |
| XX | 26-NOV-2002; 2002WO-US038147. | |
| XX | | |
| XX | 26-NOV-2001; 2001US-00995529. | |
| XX | | |
| PR | 06-DEC-2001; 2001US-00011250. | |
| XX | | |
| XX | | |
| PA | (CELL-) CELL MATRIX INC. | |
| XX | | |
| PI | Watking JD, Huse WD, Tang Y, Broek D, Brooks PC; | |
| XX | | |
| XX | WPI; 2003-513649/48. | |
| DR | | |
| XX | | |
| XX | New cryptic collagen antibody with one or more complementarity | |
| PT | determining regions, useful for diagnosing and treating disorders | |
| PT | associated with angiogenesis, tumor growth and/or cancer metastasis. | |
| XX | | |
| PS | Claim 24; SEQ ID NO 90; 232pp; English. | |
| XX | | |
| CC | This invention relates to a novel grafted antibody or its functional | |
| CC | fragment comprising one or more complementarity determining regions | |
| CC | (CDRs) of a defined light CDR and a heavy CDR with at least one amino | |
| CC | acid (aa) substitution where the antibody has specific binding activity | |
| CC | for a cryptic collagen epitope. The growth of all solid tumours requires | |
| CC | new blood vessel growth, angiogenesis, inhibition of which is an approach | |
| CC | to limiting tumour growth. The invention may allow development of | |
| CC | therapeutics with a cytostatic activity as a collagen agonist or | |
| CC | antagonist. The invention is useful for diagnosing and treating disorders | |
| CC | associated with angiogenesis, tumour growth and/or cancer metastasis. The | |
| CC | present sequence is the amino acid sequence of a mutant mouse anti- | |
| CC | cryptic collagen site antibody HUI177 variable region heavy chain CDR | |
| CC | which may be used during the creation of an antibody of the invention. | |
| XX | | |
| SQ | Sequence 12 AA; | |
| | | |
| | Query Match | 88.2%; Score 30; DB 7; Length 12; |
| | Best Local Similarity | 100.0%; Pred.No. 25; |
| | Matches | 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0 |
| | | |
| Qy | 1 TSGMGV 6 | |
| | | |
| Db | 6 TSGMGV 11 | |
| | | |
| RESULT 43 | | |
| ADZ47747 | | |
| ID | ADZ47747 standard; protein; 100 AA. | |
| XX | | |
| AC | ADZ47747; | |
| XX | | |
| DT | 30-JUN-2005 (first entry) | |
| XX | | |
| XX | Human germline heavy chain variable region VK-1 O18/O8. | |
| XX | | |
| XX | Drug screening; antibody identification; cell signaling; inflammation; | |
| KW | antiinflammatory; antibody engineering; humanized antibody; | |

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XX AC AAR66304;
XX DT 25-MAR-2003 (revised)
XX DT 02-AUG-1995 (first entry)
XX DE Human immunoglobulin variable heavy chain #10.
XX KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
KW cosmid; placenta; vector; pJB81; E.coli; mammalian.
XX OS Homo sapiens.
XX PN WO9426895-A1.
XX PD 24-NOV-1994.
XX PF 10-MAY-1993; 93WO-JP000603.
XX PR 10-MAY-1993; 93WO-JP000603.
XX PA (NIBS) JAPAN TOBACCO INC.
XX PI Honjo T, Matsuda F;
XX DR WPI; 1995-006791/01.
XX DR N-PSDB; AAQ78948.
XX PT DNA fragment comprising human immunoglobulin Vh genes - for the
PT production of human immunoglobulin in mammalian hosts.
XX PS Claim 19; Page 43-44; 130pp; Japanese.
XX CC Protein sequences (AAR66295-51) are novel human immunoglobulin heavy
CC chain sequences encoded by novel isolated genes. The genes (AAQ78939-
CC 79002) were isolated and cloned from a series of cosmid constructs: Y202;
CC Y103; Y21; Y6; Y24; 3-31; M84; M118 and M131, by PCR amplification using
CC primers AAQ78917-38. The genes are subdivided into 5 families of Vh
CC genes. The fragments cover a region of 800 kb. The DNA fragments were
CC isolated from high molecular weight DNA from human placenta. The DNA was
CC partially digested with TagI restriction enzyme. The fragments were
CC separated by gel electrophoresis and 35-45 kb fractions were collected.
CC The fragments were ligated with ClaI-digested cosmid vector pJB81. The
CC ligation products were in vitro packed and infected into E.coli 490A. The
CC fragments were then subcloned by colony hybridisation. The Vh genes and
CC the DNA fragments encoding them are useful in producing human
CC immunoglobulin in mammalian hosts. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX SQ Sequence 111 AA;
XX Query Match 88.2%; Score 30; DB 2; Length 111;
XX Best Local Similarity 100.0%; Pred. No. 2.2e+02;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 1 TSGMGV 6
XX Db 49 TSGMGV 54
XX RESULT 45
XX ADF71905
XX ID ADF71905 standard; protein; 118 AA.
XX AC ADF71905;
XX DT 26-FEB-2004 (first entry)
XX DE Hu3G8VH-1 amino acid sequence SEQ ID NO:104.
XX KW anti-CD16A antibody; mouse; 3G8 antibody; humanised anti-CD16A antibody;
KW immune response; haemostatic; antirheumatic; antiarthritic;
KW dermatological; immunosuppressive; antiinflammatory; antianaemic;

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KW vasotropic; nephrotropic; neuroprotective; antipsoriatic; uropathic;
KW ophthalmological; antiasthmatic; inflammatory response;
KW autoimmune disease; idiopathic thrombocytopenic purpura;
KW rheumatoid arthritis; systemic lupus erythematosus;
KW autoimmune haemolytic anaemia; scleroderma;
KW autoantibody triggered urticaria; pemphigus; vasculitis syndrome;
KW systemic vasculitis; Goodpasture's syndrome; multiple sclerosis;
KW psoriatic arthritis; ankylosing spondylitis; Sjogren's syndrome;
KW Reiter's syndrome; Kawasaki's disease; polymyositis; dermatomyositis;
KW allergic asthma.
XX OS Synthetic.
XX OS Mus sp.
XX OS Homo sapiens.
XX PN WO2003101485-A1.
XX PD 11-DEC-2003.
XX PF 29-MAY-2003; 2003WO-US017111.
XX PR 30-MAY-2002; 2002US-0384689P.
XX PR 10-JAN-2003; 2003US-0439320P.
XX PA (MACR-) MACROGENICS INC.
XX PI Johnson LS, Huang L, Li H, Tuailon N;
XX DR WPI; 2004-042985/04.
XX PT Novel anti-CD16A antibody comprising complementarity determining regions
PT derived from mouse 3G8 antibody and humanized anti-CD16A antibody that
PT lacks effector function, useful for treating deleterious immune response.
XX PS Claim 12; SEQ ID NO 104; 103pp; English.
XX CC The present invention describes an anti-CD16A antibody (I) comprising a
CC VH domain comprising complementarity determining regions (CDRs) derived
CC from the mouse 3G8 antibody heavy chain and a VL domain comprising CDRs
CC derived from the mouse 3G8 antibody light chain or a humanised anti-CD16A
CC antibody (II) that lacks effector function and comprises all six CDRs of
CC mouse antibody 3G8. Also described is a method (M1) for reducing a
CC deleterious immune response in a mammal in need of such reduction, which
CC involves administering to the mammal a CD16A binding protein comprising
CC an Fc region derived from a human IgG heavy chain, where the Fc region
CC lacks effector function or is modified to reduce binding to an Fc
CC effector ligand. (I) and (II) have haemostatic, antirheumatic,
CC antiarthritic, dermatological, immunosuppressive, antiinflammatory,
CC antianaemic, vasotropic, nephrotropic, neuroprotective, antipsoriatic,
CC uropathic, ophthalmological and antiasthmatic activities. (I) or (II) is
CC useful for reducing a deleterious immune response in a mammal which
CC involves administering to the mammal (I) or (II). The deleterious immune
CC response is an inflammatory response caused by autoimmune disease such as
CC idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA),
CC systemic lupus erythematosus (SLE), autoimmune haemolytic anaemia (AHA),
CC scleroderma, autoantibody triggered urticaria, pemphigus, vasculitis
CC syndrome, systemic vasculitis, Goodpasture's syndrome, multiple sclerosis
CC (MS), psoriatic arthritis, ankylosing spondylitis, Sjogren's syndrome,
CC Reiter's syndrome, Kawasaki's disease, polymyositis and dermatomyositis
CC and also for treating diseases susceptible to treatment with intravenous
CC immunoglobulin (IVIG) therapy e.g., allergic asthma. The present sequence
CC is used in the exemplification of the present invention.
XX SQ Sequence 118 AA;
XX Query Match 88.2%; Score 30; DB 8; Length 118;
XX Best Local Similarity 100.0%; Pred. No. 2.4e+02;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 1 TSGMGV 6
XX Db 31 TSGMGV 36

```

RESULT 46
ADF71910
ID ADF71910 standard; protein; 118 AA.
XX
AC ADF71910;
XX
DT 26-FEB-2004 (first entry)
XX
DE Hu3G8VH-5 amino acid sequence SEQ ID NO:109.
XX
KW anti-CD16A antibody; mouse; 3G8 antibody; humanised anti-CD16A antibody;
KW immune response; haemostatic; antirheumatic; antiarthritic;
KW dermatological; immunosuppressive; antiinflammatory; antianaemic;
KW vasotropic; nephrotropic; neuroprotective; antipsoriatic; uropathic;
KW ophthalmological; antiaesthetic; inflammatory response;
KW autoimmune disease; idiopathic thrombocytopenic purpura;
KW rheumatoid arthritis; systemic lupus erythematosus;
KW autoimmune haemolytic anaemia; scleroderma;
KW autoantibody triggered urticaria; pemphigus; vasculitis syndrome;
KW systemic vasculitis; Goodpasture's syndrome; multiple sclerosis;
KW psoriatic arthritis; ankylosing spondylitis; Sjogren's syndrome;
KW Reiter's syndrome; Kowasaki's disease; polymyositis; dermatomyositis;
KW allergic asthma.
XX
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
PN WO2003101485-A1.
XX
PD 11-DEC-2003.
XX
XX 29-MAY-2003; 2003WO-US017111.
XX
PF 30-MAY-2002; 2002US-0384689P.
PR 10-JAN-2003; 2003US-0439320P.
XX
XX (MACR-) MACROGENICS INC.
XX
XX Johnson LS, Huang L, Li H, Tuallon N;
XX WPI; 2004-042985/04.
XX
PT Novel anti-CD16A antibody comprising complementarity determining regions
PT derived from mouse 3G8 antibody and humanized anti-CD16A antibody that
PT lacks effector function, useful for treating deleterious immune response.
XX
PS Claim 12; SEQ ID NO 109; 103pp; English.
XX
CC The present invention describes an anti-CD16A antibody (I) comprising a
CC VH domain comprising complementarity determining regions (CDRs) derived
CC from the mouse 3G8 antibody heavy chain and a VL domain comprising CDRs
CC derived from the mouse 3G8 antibody light chain or a humanised anti-CD16A
CC antibody (II) that lacks effector function and comprises all six CDRs of
CC mouse antibody 3G8. Also described is a method (M1) for reducing a
CC deleterious immune response in a mammal in need of such reduction, which
CC involves administering to the mammal a CD16A binding protein comprising
CC an Fc region derived from a human IgG heavy chain, where the Fc region
CC lacks effector function or is modified to reduce binding to an Fc
CC effector ligand. (I) and (II) have haemostatic, antirheumatic,
CC antiarthritic, dermatological, immunosuppressive, antiinflammatory,
CC antianaemic, vasotropic, nephrotropic, neuroprotective, antipsoriatic,
CC uropathic, ophthalmological and antiaesthetic activities. (I) or (II) is
CC useful for reducing a deleterious immune response in a mammal which
CC involves administering to the mammal (I) or (II). The deleterious immune
CC response is an inflammatory response caused by autoimmune disease such as
CC idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA),
CC systemic lupus erythematosus (SLE), autoimmune haemolytic anaemia (AHA),
CC scleroderma, autoantibody triggered urticaria, pemphigus, vasculitis
CC syndrome, systemic vasculitis, Goodpasture's syndrome, multiple sclerosis
CC (MS), psoriatic arthritis, ankylosing spondylitis, Sjogren's syndrome,
CC Reiter's syndrome, Kowasaki's disease, polymyositis and dermatomyositis

CC and also for treating diseases susceptible to treatment with intravenous
CC immunoglobulin (IVIg) therapy e.g., allergic asthma. The present sequence
CC is used in the exemplification of the present invention.
XX
SQ Sequence 118 AA;
Query Match 88.2%; Score 30; DB 8; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TSGMGV 6
DB 31 TSGMGV 36
RESULT 47
AAR88109
ID AAR88109 standard; peptide; 120 AA.
XX
AC AAR88109;
XX
DT 25-JUL-1996 (first entry)
XX
DE Murine anti-Protein C MAb HPC-4 VH gamma mature peptide.
XX
KW Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;
KW zymogen; cleavage; mouse; humanised antibody; variable region;
KW light chain; inhibition; anticoagulant; coagulation; tumour.
XX
OS Mus musculus.
XX
XX WO9534652-A1.
XX
PD 21-DEC-1995.
XX
XX 09-JUN-1995; 95WO-US007372.
XX
XX 10-JUN-1994; 94US-00259321.
XX
XX (OKLA-) OKLAHOMA MED RES FOUND.
XX
XX Rezaie A, Esmon CT;
XX
XX WPI; 1996-049681/05.
XX
XX N-PSDB; AAT09300.
XX
PT Calcium-binding monoclonal antibody immunoreactive with Protein C -
PT inhibits Protein C anticoagulant activation by thrombin-thrombomodulin,
PT e.g. for treating tumours.
XX
PS Claim 2; Page 29; 41pp; English.
XX
CC This is the amino acid sequence of the mature peptide from the murine
CC anti-protein C monoclonal antibody HPC-4 heavy chain variable region. HPC
CC -4 recognises the activation peptide region (AAR88106) of the heavy chain
CC of protein C, a vitamin K-dependent plasma protein zymogen. Protein C is
CC converted to activated protein C (APC) by cleavage between the Arg-Leu
CC amino acid contained within the activation peptide sequence. HPC-4
CC prevents protein C activation to APC by binding to this region. The DNA
CC sequences encoding the variable regions of the heavy and light chains of
CC the antibody (AAT09299-302) were used to construct humanised antibodies
CC using the PCR primers AAT09303-9. The humanised antibodies are useful as
CC inhibitors of coagulation and can be used for the treatment of tumours by
CC inhibiting the anticoagulant activity of APC by preventing conversion of
CC protein C to APC
XX
SQ Sequence 120 AA;
Query Match 88.2%; Score 30; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TSGMGV 6

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Db      31 TSGMGV 36
|||||
RESULT 48
ABO10820
ID ABO10820 standard; protein; 120 AA.
XX
AC ABO10820;
XX
DT 21-AUG-2003 (first entry)
XX
DE Human germline region variable region VH-2 2-70.
XX
KW Human; interleukin-1; IL-1 alpha; IL-1 beta; acute pancreatitis; ALS;
KW amyotrophic lateral sclerosis; Alzheimer's disease; cachexia; anorexia;
KW asthma; pulmonary disease; atherosclerosis; autoimmune vasculitis;
KW chronic fatigue syndrome; coronary condition; congestive heart failure;
KW cancer; diabetes; endometriosis; fever; glomerulonephritis; ARDS;
KW graft versus host disease; haemorrhagic shock; inflammatory condition;
KW inflammatory bowel disease; osteoarthritis; rheumatoid arthritis;
KW ischaemia; stroke; lung disease; adult respiratory distress syndrome;
KW multiple sclerosis; pain; Parkinson's disease; psoriasis; septic shock;
KW reperfusion injury; sleep disturbance; uveitis; infection; antibody;
KW MAB201; germline variable region.
XX
OS Homo sapiens.
XX
PN US2003026806-A1.
XX
PD 06-FEB-2003.
XX
PF 29-OCT-2001; 2001US-00011931.
XX
PR 27-OCT-2000; 2000US-0244118P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Witte A, Varnum BC, Qian X, Vezina C;
XX WPI; 2003-479525/45.
XX
DR Treating interleukin-1 mediated disease, by administering an IL-1
XX selective binding agent that binds to IL-1alpha or IL-1beta, such that
XX the complex binds to IL-1 receptor without activating the receptor.
XX
PS Example 2; Fig 6B; 39pp; English.
XX
CC The invention relates to treating interleukin-1 (IL-1)-mediated disease,
CC or blocking IL-1alpha and IL-1beta from binding to the IL-1 receptor,
CC involving administering an IL-1 selective binding agent (e.g. a humanised
CC mouse anti-IL-1 antibody) that is capable of binding to IL-1 alpha or IL-
CC 1beta, where the selective binding agent-IL-1 complex is capable of
CC binding to IL-1 receptor without activating the receptor. The activities
CC of mouse, chimaeric and humanised monoclonal antibody (MAB)201 in
CC blocking formation of IL-1beta/IL-1 receptor/IL-1Racp complex were
CC studied. The results showed that anti-IL-1beta antibody MAB201 is the
CC most effective inhibitor of IL-1beta signalling. The method is useful for
CC treating IL-1-mediated disease e.g. acute pancreatitis, amyotrophic
CC lateral sclerosis (ALS), Alzheimer's disease, cachexia, anorexia, asthma,
CC pulmonary diseases, atherosclerosis, autoimmune vasculitis, chronic
CC fatigue syndrome, Clostridium associated illness, coronary conditions
CC (e.g. congestive heart failure, coronary restenosis, myocardial
CC infarction, myocardial dysfunction and coronary artery bypass graft),
CC cancers, diabetes, endometriosis, fever, fibromyalgia, hyperalgesia,
CC glomerulonephritis, adult versus host disease; haemorrhagic shock,
CC inflammatory bowel disease, inflammatory conditions (e.g. osteoarthritis,
CC psoriatic arthritis and rheumatoid arthritis), inflammatory eye disease,
CC ischaemia including cerebral ischaemia, stroke, Kawasaki's disease,
CC learning impairment, lung diseases (adult respiratory distress syndrome
CC (ARDS)), multiple sclerosis, myopathies, neurotoxicity, osteoporosis,
CC pain, Parkinson's disease, periodontal disease, preterm labour,
CC psoriasis, reperfusion injury, septic shock, side effects from radiation

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CC therapy, temporal mandibular joint disease, sleep disturbance, uveitis
CC and inflammatory conditions resulting from strain, sprain, cartilage
CC damage, trauma, orthopaedic surgery and infection. The present sequence
CC is a human germline variable region used to determine which residues or
CC CDRs required to be changed in mouse anti-IL-1 monoclonal antibody MAB201
CC in order to humanise it or make it into a chimaeric molecule with human
CC CDR (complementarity determining region) sequences
XX
SQ Sequence 120 AA;
XX
Query Match      88.2%; Score 30; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 TSGMGV 6
Db 31 TSGMGV 36
|||||
RESULT 49
ABO10813
ID ABO10813 standard; protein; 120 AA.
XX
AC ABO10813;
XX
DT 21-AUG-2003 (first entry)
XX
DE Mouse monoclonal antibody heavy chain V region.
XX
KW Mouse; interleukin-1; IL-1 alpha; IL-1 beta; acute pancreatitis; ALS;
KW amyotrophic lateral sclerosis; Alzheimer's disease; cachexia; anorexia;
KW asthma; pulmonary disease; atherosclerosis; autoimmune vasculitis;
KW chronic fatigue syndrome; coronary condition; congestive heart failure;
KW cancer; diabetes; endometriosis; fever; glomerulonephritis; ARDS;
KW graft versus host disease; haemorrhagic shock; inflammatory condition;
KW inflammatory bowel disease; osteoarthritis; rheumatoid arthritis;
KW ischaemia; stroke; lung disease; adult respiratory distress syndrome;
KW multiple sclerosis; pain; Parkinson's disease; psoriasis; septic shock;
KW reperfusion injury; sleep disturbance; uveitis; infection; antibody;
KW MAB201.
XX
OS Mus sp.
XX
PN US2003026806-A1.
XX
PD 06-FEB-2003.
XX
PF 29-OCT-2001; 2001US-00011931.
XX
PR 27-OCT-2000; 2000US-0244118P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Witte A, Varnum BC, Qian X, Vezina C;
XX WPI; 2003-479525/45.
XX
DR Treating interleukin-1 mediated disease, by administering an IL-1
XX selective binding agent that binds to IL-1alpha or IL-1beta, such that
XX the complex binds to IL-1 receptor without activating the receptor.
XX
PS Example 2; Page 19; 39pp; English.
XX
CC The invention relates to treating interleukin-1 (IL-1)-mediated disease,
CC or blocking IL-1alpha and IL-1beta from binding to the IL-1 receptor,
CC involving administering an IL-1 selective binding agent (e.g. a humanised
CC mouse anti-IL-1 antibody) that is capable of binding to IL-1 alpha or IL-
CC 1beta, where the selective binding agent-IL-1 complex is capable of
CC binding to IL-1 receptor without activating the receptor. The activities
CC of mouse, chimaeric and humanised monoclonal antibody (MAB)201 in
CC blocking formation of IL-1beta/IL-1 receptor/IL-1Racp complex were
CC studied. The results showed that anti-IL-1beta antibody MAB201 is the
CC most effective inhibitor of IL-1beta signalling. The method is useful for

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CC treating IL-1-mediated disease e.g. acute pancreatitis, amyotrophic
 CC lateral sclerosis (ALS), Alzheimer's disease, cachexia, anorexia, asthma,
 CC pulmonary diseases, atherosclerosis, autoimmune vasculitis, chronic
 CC fatigue syndrome, Clostridium associated illness, coronary conditions
 CC (e.g. congestive heart failure, coronary restenosis, myocardial
 CC infarction, myocardial dysfunction and coronary artery bypass graft),
 CC cancers, diabetes, endometriosis, fever, fibromyalgia, hyperalgesia,
 CC glomerulonephritis, graft versus host disease; haemorrhagic shock,
 CC inflammatory bowel disease, inflammatory conditions (e.g. osteoarthritis,
 CC psoriatic arthritis and rheumatoid arthritis), inflammatory eye disease,
 CC ischaemia including cerebral ischaemia, stroke, Kawasaki's disease,
 CC learning impairment, lung diseases (adult respiratory distress syndrome
 CC (ARDS)), multiple sclerosis, myopathies, neurotoxicity, osteoporosis,
 CC pain, Parkinson's disease, periodontal disease, preterm labour,
 CC psoriasis, reperfusion injury, septic shock, side effects from radiation
 CC therapy, temporal mandibular joint disease, sleep disturbance, uveitis
 CC and inflammatory conditions resulting from strain, sprain, cartilage
 CC damage, trauma, orthopaedic surgery and infection. The present sequence
 CC is a heavy, light or kappa chain of the mouse anti-IL-1 monoclonal
 CC antibody MAB201 which was humanised or made into a chimaeric molecule
 CC with human CDR (complementarity determining region) sequences
 XX
 SQ Sequence 120 AA;

Query Match 88.2%; Score 30; DB 6; Length 120;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGV 6
 |||||
 DB 31 TSGMGV 36

RESULT 50
 ADQ09629
 ID ADQ09629 standard; protein; 120 AA.
 XX

AC ADQ09629;

DT 07-OCT-2004 (first entry)

DE Variable heavy chain protein of murine anti-human GPR64-16 antibody ID15.

KW murine; mouse; antibody; GPR64; cytotoxic; ovarian cancer;
 KW uterine cancer; Ewing's sarcoma; cell death; cytostatic; gene therapy;
 KW immunotherapy; cellular proliferation.

XX

OS Mus sp.

XX WO2004058171-A2.

XX 15-JUL-2004.

XX PF 19-DEC-2003; 2003WO-US040820.

XX PR 20-DEC-2002; 2002US-0435618P.

XX PA (PROT-) PROTEIN DESIGN LABS INC.

XX PI Law D, Wang Q, Dubridge R, Bhaskar V;

XX DR WPI; 2004-525780/50.

XX DR N-PSDB; ADQ09619.

XX PT New antibody that inhibits binding of a GPR64 polypeptide to an antibody
 PT comprising GPR64-18, GPR64-81, GPR64-93 or GPR64-101, useful in preparing
 PT a composition for diagnosing or treating ovarian cancer.

XX Example 2; SEQ ID NO 15; 75pp; English.

XX This invention relates to novel antibodies that bind to the G protein
 CC coupled receptor protein identified as GPR64, namely GPR64-1, GPR64-16,
 CC GPR64-18, GPR64-20 and GPR64-48. Specifically, it refers to the use of

CC these anti-GPR64 antibodies as selective cytotoxic agents against GPR64
 CC expressing tumour cells such as those associated with ovarian cancer,
 CC uterine cancer and Ewing's sarcoma. The present invention describes
 CC epitope mapping of those antibodies that show high affinity binding to
 CC GPR64 through competitive binding analyses, such that the antibodies can
 CC be assessed for GPR64 dependent cell death in vitro. Accordingly, they
 CC can be used to develop cytostatic compositions for gene therapy or
 CC immunotherapy that inhibit cellular proliferation of an ovarian cancerous
 CC cell and furthermore can diagnose and inhibit growth of tumour cells.
 CC This polypeptide is encoded by a heavy chain variable region DNA sequence
 CC of a murine anti-human GPR64 antibody of the invention.

XX Sequence 120 AA;

Query Match 88.2%; Score 30; DB 8; Length 120;
 Best Local Similarity 85.7%; Pred. No. 2.4e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7

DB 31 TSGVGVS 37

Search completed: February 23, 2006, 09:40:40
 Job time : 90.3077 secs

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OM protein - protein search, using sw model

Run on: February 23, 2006, 09:41:24 ; Search time 9.90769 Seconds
(without alignments)
67.979 Million cell updates/sec

Title: US-10-723-872-22
Perfect score: 34
Sequence: 1 TSGMGVS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 34 | 100.0 | 122 | 2 | S11740 |
| 2 | 34 | 100.0 | 143 | 2 | PT0174 |
| 3 | 31 | 91.2 | 1068 | 2 | S73091 |
| 4 | 31 | 91.2 | 1340 | 2 | A39808 |
| 5 | 31 | 91.2 | 2327 | 2 | T42630 |
| 6 | 31 | 91.2 | 2793 | 2 | B90784 |
| 7 | 31 | 91.2 | 2806 | 2 | D85644 |
| 8 | 30 | 88.2 | 113 | 2 | S26465 |
| 9 | 30 | 88.2 | 188 | 2 | H75057 |
| 10 | 30 | 88.2 | 537 | 2 | T04078 |
| 11 | 30 | 88.2 | 1079 | 2 | T38913 |
| 12 | 30 | 88.2 | 1136 | 2 | T26953 |
| 13 | 30 | 88.2 | 3147 | 2 | T21328 |
| 14 | 29 | 85.3 | 58 | 2 | PQ0098 |
| 15 | 29 | 85.3 | 379 | 2 | AG0585 |
| 16 | 29 | 85.3 | 435 | 2 | S13171 |
| 17 | 29 | 85.3 | 719 | 2 | S51739 |
| 18 | 29 | 85.3 | 792 | 2 | AB0704 |
| 19 | 29 | 85.3 | 792 | 2 | E85778 |
| 20 | 29 | 85.3 | 792 | 2 | A90930 |
| 21 | 29 | 85.3 | 792 | 2 | S20554 |
| 22 | 29 | 85.3 | 1274 | 1 | I40487 |
| 23 | 29 | 85.3 | 1391 | 2 | T20406 |
| 24 | 28 | 82.4 | 107 | 2 | A49442 |
| 25 | 28 | 82.4 | 122 | 2 | PQ0791 |
| 26 | 28 | 82.4 | 122 | 2 | PQ0792 |
| 27 | 28 | 82.4 | 122 | 2 | PQ0793 |
| 28 | 28 | 82.4 | 251 | 2 | F89929 |
| 29 | 28 | 82.4 | 348 | 2 | A40578 |
| 30 | 28 | 82.4 | 349 | 2 | A40551 |
| 31 | 28 | 82.4 | 376 | 2 | S57177 |
| 32 | 28 | 82.4 | 384 | 2 | F32252 |
| 33 | 28 | 82.4 | 436 | 2 | A83500 |
| 34 | 28 | 82.4 | 498 | 1 | PWNTB |
| 35 | 28 | 82.4 | 498 | 1 | PWNTB9 |
| 36 | 28 | 82.4 | 498 | 1 | PWNTBB |
| 37 | 28 | 82.4 | 498 | 1 | PWNTBC |
| 38 | 28 | 82.4 | 498 | 1 | PWNTBZ |
| 39 | 28 | 82.4 | 508 | 2 | T05473 |
| 40 | 28 | 82.4 | 558 | 2 | B81711 |
| 41 | 28 | 82.4 | 587 | 1 | VCLJSA |
| 42 | 28 | 82.4 | 706 | 2 | T01351 |
| 43 | 28 | 82.4 | 1532 | 2 | A61262 |
| 44 | 28 | 82.4 | 2470 | 2 | I50726 |
| 45 | 27 | 79.4 | 122 | 2 | D70730 |
| 46 | 27 | 79.4 | 244 | 1 | VCCVSV |
| 47 | 27 | 79.4 | 244 | 1 | VCCVZ |
| 48 | 27 | 79.4 | 244 | 2 | S04805 |
| 49 | 27 | 79.4 | 244 | 2 | T10112 |
| 50 | 27 | 79.4 | 255 | 2 | H90130 |
| 51 | 27 | 79.4 | 259 | 2 | A83174 |
| 52 | 27 | 79.4 | 261 | 2 | D55587 |
| 53 | 27 | 79.4 | 279 | 2 | C96986 |
| 54 | 27 | 79.4 | 292 | 2 | F97082 |
| 55 | 27 | 79.4 | 295 | 2 | E70022 |
| 56 | 27 | 79.4 | 307 | 2 | E69036 |
| 57 | 27 | 79.4 | 309 | 2 | B95356 |
| 58 | 27 | 79.4 | 313 | 1 | H69510 |
| 59 | 27 | 79.4 | 329 | 1 | G69210 |
| 60 | 27 | 79.4 | 346 | 2 | AC3619 |
| 61 | 27 | 79.4 | 357 | 2 | A99272 |
| 62 | 27 | 79.4 | 376 | 2 | A81786 |
| 63 | 27 | 79.4 | 382 | 2 | AH2056 |
| 64 | 27 | 79.4 | 387 | 2 | G86429 |
| 65 | 27 | 79.4 | 400 | 2 | C90214 |
| 66 | 27 | 79.4 | 401 | 2 | B83414 |
| 67 | 27 | 79.4 | 402 | 2 | T12745 |
| 68 | 27 | 79.4 | 403 | 2 | T08471 |
| 69 | 27 | 79.4 | 421 | 2 | E64329 |
| 70 | 27 | 79.4 | 437 | 2 | A11142 |
| 71 | 27 | 79.4 | 451 | 2 | E90171 |
| 72 | 27 | 79.4 | 483 | 2 | E90159 |
| 73 | 27 | 79.4 | 515 | 2 | JC7533 |
| 74 | 27 | 79.4 | 543 | 2 | A97096 |
| 75 | 27 | 79.4 | 543 | 2 | H97096 |
| 76 | 27 | 79.4 | 554 | 2 | B50017 |
| 77 | 27 | 79.4 | 554 | 2 | H86772 |
| 78 | 27 | 79.4 | 640 | 2 | D70850 |
| 79 | 27 | 79.4 | 652 | 2 | E70705 |
| 80 | 27 | 79.4 | 747 | 2 | B90216 |
| 81 | 27 | 79.4 | 841 | 1 | S39365 |
| 82 | 27 | 79.4 | 857 | 2 | S33821 |
| 83 | 27 | 79.4 | 987 | 2 | D79029 |
| 84 | 27 | 79.4 | 1014 | 2 | S37405 |
| 85 | 27 | 79.4 | 1039 | 2 | C84745 |
| 86 | 27 | 79.4 | 1068 | 2 | T48756 |
| 87 | 27 | 79.4 | 1153 | 1 | RWHULB |
| 88 | 27 | 79.4 | 1154 | 2 | S69206 |
| 89 | 27 | 79.4 | 1249 | 2 | H71404 |
| 90 | 27 | 79.4 | 1624 | 2 | C70867 |
| 91 | 27 | 79.4 | 1844 | 1 | R8WPTM |
| 92 | 27 | 79.4 | 1844 | 2 | S01956 |
| 93 | 27 | 79.4 | 1985 | 2 | S19151 |
| 94 | 27 | 79.4 | 2415 | 1 | A39086 |
| 95 | 27 | 79.4 | 3591 | 1 | S21010 |
| 96 | 26 | 76.5 | 41 | 2 | S26936 |
| 97 | 26 | 76.5 | 56 | 2 | S46471 |
| 98 | 26 | 76.5 | 71 | 2 | I49258 |
| 99 | 26 | 76.5 | 86 | 1 | TNLJNR |
| 100 | 26 | 76.5 | 86 | 1 | TNLJNR |
| 101 | 26 | 76.5 | 86 | 2 | JC5591 |
| 102 | 26 | 76.5 | 86 | 2 | S54381 |

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deoxyhypusine synt
Probable ABC trans
conserved hypothet
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inorganic phosphat
cell division prot
hypothetical prote
hypothetical prote
glycerate kinase,
hypothetical prote
hypothetical prote
harpin - Erwinia a
hypothetical prote
gelsoin, ovarian
inorganic phosphat
hypothetical prote
inulinase (EC 3.2.
malic enzyme limpo
malic enzyme limpo
alpha-acetolactate
alpha-acetolactate
probable oxidoredu
probable malate ox
glutamate synthase
outer membrane uuh
median body protei
ribonucleotide red
cytotoxic necrotiz
hypothetical prote
probable Helix-tur
genome polyprotein
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tat protein - huma

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|-----|----|------|-----|---|--------|---------------------|-----|----|------|------|---|--------|----------------------|
| 103 | 26 | 76.5 | 87 | 2 | T01665 | tat protein - huma | 176 | 26 | 76.5 | 428 | 2 | B81531 | conserved hypot |
| 104 | 26 | 76.5 | 96 | 2 | S26924 | Ig heavy chain V r | 177 | 26 | 76.5 | 430 | 2 | T50296 | conserved hypot |
| 105 | 26 | 76.5 | 101 | 2 | T09446 | tat protein - huma | 178 | 26 | 76.5 | 432 | 2 | D72008 | CR850 hypot |
| 106 | 26 | 76.5 | 104 | 2 | A1904 | ferredoxin [impor | 179 | 26 | 76.5 | 432 | 2 | B86616 | glucosyltransfer |
| 107 | 26 | 76.5 | 119 | 2 | S18555 | Ig heavy chain V r | 180 | 26 | 76.5 | 438 | 2 | T45602 | hypothetical prote |
| 108 | 26 | 76.5 | 124 | 2 | A49002 | Ig heavy chain V r | 181 | 26 | 76.5 | 447 | 2 | T12978 | glycylpeptide N-te |
| 109 | 26 | 76.5 | 125 | 1 | MHUMC | Ig heavy chain V-I | 182 | 26 | 76.5 | 451 | 2 | A38099 | 4-aminobutyrate tr |
| 110 | 26 | 76.5 | 125 | 2 | T24982 | hypothetical prote | 183 | 26 | 76.5 | 457 | 2 | G75036 | phosphoribosylam |
| 111 | 26 | 76.5 | 130 | 2 | A00745 | flagellar protein | 184 | 26 | 76.5 | 458 | 2 | E75397 | phosphate transpor |
| 112 | 26 | 76.5 | 130 | 2 | C55546 | flagellar protein | 185 | 26 | 76.5 | 466 | 2 | T10234 | amidease homolog T1 |
| 113 | 26 | 76.5 | 133 | 2 | H70646 | hypothetical prote | 186 | 26 | 76.5 | 471 | 2 | H90502 | probable 4-aminobu |
| 114 | 26 | 76.5 | 138 | 2 | S31513 | Ig heavy chain - h | 187 | 26 | 76.5 | 474 | 2 | H71126 | cytochrome d ubiqu |
| 115 | 26 | 76.5 | 168 | 2 | E83757 | hypothetical prote | 188 | 26 | 76.5 | 480 | 2 | A12308 | cytochrome d oxida |
| 116 | 26 | 76.5 | 169 | 2 | S67636 | probable membrane | 189 | 26 | 76.5 | 483 | 2 | S75271 | guanosine pentapho |
| 117 | 26 | 76.5 | 174 | 2 | A90905 | probable repressor | 190 | 26 | 76.5 | 484 | 2 | F64554 | guanosine-5'-triph |
| 118 | 26 | 76.5 | 182 | 2 | A02946 | keratin, 59K type | 191 | 26 | 76.5 | 484 | 2 | F71954 | steroid 15beta-mon |
| 119 | 26 | 76.5 | 188 | 2 | D70820 | hypothetical prote | 192 | 26 | 76.5 | 504 | 2 | A32140 | glycine betaine tr |
| 120 | 26 | 76.5 | 194 | 2 | G64033 | hypothetical prote | 193 | 26 | 76.5 | 502 | 2 | E83980 | lysine-tRNA ligase |
| 121 | 26 | 76.5 | 204 | 2 | A1961 | ATP-dependent Clp | 194 | 26 | 76.5 | 506 | 2 | G84980 | l-lysine-tRNA ligase |
| 122 | 26 | 76.5 | 212 | 2 | D85712 | hypothetical prote | 195 | 26 | 76.5 | 516 | 2 | JC8015 | l-lysine-tRNA ligase |
| 123 | 26 | 76.5 | 220 | 2 | AC0982 | probable outer mem | 196 | 26 | 76.5 | 516 | 2 | JE0266 | l-lysine-tRNA ligase |
| 124 | 26 | 76.5 | 242 | 2 | F84362 | hypothetical prote | 197 | 26 | 76.5 | 530 | 2 | S38092 | DnaK-type molecula |
| 125 | 26 | 76.5 | 243 | 2 | AH0777 | probable permease | 198 | 26 | 76.5 | 532 | 2 | AE1964 | hypothetical prote |
| 126 | 26 | 76.5 | 243 | 2 | T24981 | hypothetical prote | 199 | 26 | 76.5 | 539 | 2 | S75727 | hypothetical prote |
| 127 | 26 | 76.5 | 246 | 2 | G82819 | acetoacetyl-CoA re | 200 | 26 | 76.5 | 539 | 2 | T00149 | malolactate enzyme |
| 128 | 26 | 76.5 | 253 | 1 | I40444 | Spo0A activation i | 201 | 26 | 76.5 | 541 | 2 | T13496 | hypothetical prote |
| 129 | 26 | 76.5 | 253 | 2 | G97357 | chromosome partiti | 202 | 26 | 76.5 | 541 | 2 | G64441 | hypothetical prote |
| 130 | 26 | 76.5 | 292 | 2 | E90180 | conserved hypot | 203 | 26 | 76.5 | 550 | 2 | G90842 | probable sulfate t |
| 131 | 26 | 76.5 | 294 | 2 | S32947 | hupK protein - Rho | 204 | 26 | 76.5 | 550 | 2 | D85700 | probable sulfate t |
| 132 | 26 | 76.5 | 297 | 1 | S61359 | stearyl-CoA 9-des | 205 | 26 | 76.5 | 550 | 2 | C64867 | probable sulfate t |
| 133 | 26 | 76.5 | 300 | 2 | G87707 | transcription regu | 206 | 26 | 76.5 | 553 | 2 | A82505 | sulfate permease f |
| 134 | 26 | 76.5 | 305 | 2 | D84963 | nitrogen assimilati | 207 | 26 | 76.5 | 556 | 2 | C87472 | steroid monooxygen |
| 135 | 26 | 76.5 | 305 | 2 | F85823 | nitrogen assimilati | 208 | 26 | 76.5 | 560 | 2 | AD0359 | probable membrane |
| 136 | 26 | 76.5 | 305 | 2 | H50976 | nitrogen assimilati | 209 | 26 | 76.5 | 561 | 2 | AG0720 | probable sulphate |
| 137 | 26 | 76.5 | 310 | 2 | T52453 | ATP-dependent Clp | 210 | 26 | 76.5 | 596 | 1 | JU0345 | major capsid prote |
| 138 | 26 | 76.5 | 309 | 2 | F82979 | probable transcrip | 211 | 26 | 76.5 | 648 | 2 | B81686 | conserved hypot |
| 139 | 26 | 76.5 | 310 | 2 | T52041 | probable ATP-depen | 212 | 26 | 76.5 | 649 | 2 | B96729 | hypothetical prote |
| 140 | 26 | 76.5 | 315 | 2 | T23597 | hypothetical prote | 213 | 26 | 76.5 | 653 | 2 | F70864 | probable oxidoredu |
| 141 | 26 | 76.5 | 316 | 2 | E82082 | conserved hypot | 214 | 26 | 76.5 | 672 | 2 | G87386 | TPR domain protein |
| 142 | 26 | 76.5 | 323 | 2 | T52297 | squamosa promoter | 215 | 26 | 76.5 | 689 | 2 | F81286 | probable polysacch |
| 143 | 26 | 76.5 | 330 | 2 | E84270 | mevalonate kinase | 216 | 26 | 76.5 | 695 | 2 | S70103 | probable membrane |
| 144 | 26 | 76.5 | 336 | 1 | FLYB3 | flagellin - Lym | 217 | 26 | 76.5 | 710 | 2 | A90011 | hypothetical prote |
| 145 | 26 | 76.5 | 336 | 2 | I40088 | flagellin - Lym | 218 | 26 | 76.5 | 864 | 1 | S63229 | probable multifunc |
| 146 | 26 | 76.5 | 336 | 2 | I40081 | flagellin - Lym | 219 | 26 | 76.5 | 873 | 2 | T16282 | hypothetical prote |
| 147 | 26 | 76.5 | 336 | 2 | S37728 | flagellin - Lym | 220 | 26 | 76.5 | 879 | 2 | D96902 | MDR-type permease |
| 148 | 26 | 76.5 | 336 | 2 | I40079 | flagellin - Lym | 221 | 26 | 76.5 | 901 | 2 | G89810 | conserved hypot |
| 149 | 26 | 76.5 | 336 | 2 | A38450 | flagellin - Lym | 222 | 26 | 76.5 | 903 | 2 | T20804 | hypothetical prote |
| 150 | 26 | 76.5 | 336 | 2 | S70256 | flagellin - Lym | 223 | 26 | 76.5 | 953 | 2 | F87466 | TonB-dependent rec |
| 151 | 26 | 76.5 | 336 | 2 | S70256 | flagellin - Lym | 224 | 26 | 76.5 | 981 | 2 | T46330 | hypothetical prote |
| 152 | 26 | 76.5 | 336 | 2 | I40134 | flagellin - Lym | 225 | 26 | 76.5 | 1093 | 2 | T18275 | 1-phosphatidylinos |
| 153 | 26 | 76.5 | 336 | 2 | I40140 | flagellin - Lym | 226 | 26 | 76.5 | 1238 | 2 | T32625 | hypothetical prote |
| 154 | 26 | 76.5 | 336 | 2 | I40092 | flagellar filament | 227 | 26 | 76.5 | 1342 | 2 | A31946 | xanthine dehydroge |
| 155 | 26 | 76.5 | 336 | 2 | I40077 | flagellin - Lym | 228 | 26 | 76.5 | 1509 | 2 | B89985 | hypothetical prote |
| 156 | 26 | 76.5 | 336 | 2 | I40075 | flagellin - Lym | 229 | 26 | 76.5 | 1592 | 2 | A38175 | glucosyltransferas |
| 157 | 26 | 76.5 | 336 | 2 | I40135 | flagellin - Lym | 230 | 26 | 76.5 | 1891 | 2 | T13594 | hypothetical prote |
| 158 | 26 | 76.5 | 336 | 2 | I40041 | flagellin - Borrel | 231 | 26 | 76.5 | 1893 | 2 | A56158 | eye development pr |
| 159 | 26 | 76.5 | 336 | 2 | I40204 | flagellin - Borrel | 232 | 26 | 76.5 | 1920 | 2 | T13893 | gene hindsight pro |
| 160 | 26 | 76.5 | 340 | 2 | S23953 | hlyE protein - Rho | 233 | 26 | 76.5 | 5188 | 2 | B85547 | probable RTX fami |
| 161 | 26 | 76.5 | 347 | 2 | C40858 | GA-binding protein | 234 | 26 | 76.5 | 5291 | 2 | F90696 | hypothetical prote |
| 162 | 26 | 76.5 | 361 | 2 | J00374 | lignin peroxidase | 235 | 25 | 73.5 | 38 | 2 | E82858 | hypothetical prote |
| 163 | 26 | 76.5 | 367 | 2 | E03349 | interferon-inducib | 236 | 25 | 73.5 | 40 | 2 | H95063 | hypothetical prote |
| 164 | 26 | 76.5 | 377 | 2 | G86724 | acetylornithine tr | 237 | 25 | 73.5 | 53 | 2 | AC2486 | hypothetical prote |
| 165 | 26 | 76.5 | 378 | 2 | G70435 | hypothetical prote | 238 | 25 | 73.5 | 57 | 2 | C36491 | phosphoprotein pho |
| 166 | 26 | 76.5 | 379 | 2 | T23592 | hypothetical prote | 239 | 25 | 73.5 | 72 | 2 | B90762 | hypothetical prote |
| 167 | 26 | 76.5 | 380 | 1 | VCVGR | coat protein - Cym | 240 | 25 | 73.5 | 95 | 2 | S55439 | hypothetical prote |
| 168 | 26 | 76.5 | 380 | 2 | S05457 | coat protein - Cym | 241 | 25 | 73.5 | 96 | 2 | S26923 | Ig heavy chain V r |
| 169 | 26 | 76.5 | 382 | 2 | B40858 | GA-binding protein | 242 | 25 | 73.5 | 102 | 2 | T45338 | hypothetical prote |
| 170 | 26 | 76.5 | 386 | 2 | G70674 | probable dioxygena | 243 | 25 | 73.5 | 106 | 2 | S77325 | farredoxin [3Fe-2S |
| 171 | 26 | 76.5 | 390 | 1 | S58814 | cell division prot | 244 | 25 | 73.5 | 106 | 2 | H83754 | multidrug resistan |
| 172 | 26 | 76.5 | 390 | 2 | JC6014 | cell division prot | 245 | 25 | 73.5 | 121 | 2 | A36005 | Ig heavy chain V r |
| 173 | 26 | 76.5 | 390 | 2 | C90573 | cell division prot | 246 | 25 | 73.5 | 137 | 2 | F69436 | conserved hypot |
| 174 | 26 | 76.5 | 401 | 2 | E69501 | sugar transporter | 247 | 25 | 73.5 | 143 | 2 | H82385 | conserved hypot |
| 175 | 26 | 76.5 | 404 | 2 | D84533 | hypothetical prote | 248 | 25 | 73.5 | 160 | 2 | T14931 | hypothetical prote |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|--------|---------------------|-----|----|------|-----|---|--------|---------------------|
| 249 | 25 | 73.5 | 178 | 2 | T36549 | hypothetical prote | 322 | 25 | 73.5 | 382 | 2 | AG3533 | spermidine/putresc |
| 250 | 25 | 73.5 | 184 | 2 | S63441 | probable membrane | 323 | 25 | 73.5 | 384 | 2 | AG1948 | hypothetical prote |
| 251 | 25 | 73.5 | 187 | 2 | T48941 | hypothetical prote | 324 | 25 | 73.5 | 387 | 2 | A56017 | transcription fact |
| 252 | 25 | 73.5 | 190 | 2 | S28605 | GTP-binding protei | 325 | 25 | 73.5 | 392 | 2 | T51772 | acetyl-CoA C-acety |
| 253 | 25 | 73.5 | 193 | 2 | G71292 | hypothetical prote | 326 | 25 | 73.5 | 392 | 2 | T33014 | hypothetical prote |
| 254 | 25 | 73.5 | 195 | 2 | C95974 | hypothetical prote | 327 | 25 | 73.5 | 393 | 2 | S75810 | rod shape-determin |
| 255 | 25 | 73.5 | 196 | 2 | AC0488 | two-component syst | 328 | 25 | 73.5 | 395 | 2 | C85942 | hypothetical prote |
| 256 | 25 | 73.5 | 205 | 2 | S55041 | proteasome endopep | 329 | 25 | 73.5 | 396 | 2 | C85942 | probable carbamoyl |
| 257 | 25 | 73.5 | 208 | 2 | S40468 | proteasome subunit | 330 | 25 | 73.5 | 396 | 2 | G91096 | probable carbamoyl |
| 258 | 25 | 73.5 | 208 | 2 | B75359 | endopeptidase-rela | 331 | 25 | 73.5 | 401 | 2 | G82210 | amino acid ABC tra |
| 259 | 25 | 73.5 | 210 | 2 | T05541 | heat shock protein | 332 | 25 | 73.5 | 409 | 2 | T20847 | hypothetical prote |
| 260 | 25 | 73.5 | 227 | 2 | T15772 | hypothetical prote | 333 | 25 | 73.5 | 409 | 2 | C87538 | conserved hypothet |
| 261 | 25 | 73.5 | 232 | 2 | D70754 | hypothetical prote | 334 | 25 | 73.5 | 415 | 2 | S53020 | G-box-binding prot |
| 262 | 25 | 73.5 | 233 | 2 | FV0001 | recF protein - Pse | 335 | 25 | 73.5 | 415 | 2 | T37167 | probable oxidoredu |
| 263 | 25 | 73.5 | 233 | 2 | B64525 | trbI protein - Hel | 336 | 25 | 73.5 | 415 | 2 | S43484 | heterogeneous nucl |
| 264 | 25 | 73.5 | 238 | 2 | S05572 | hypothetical prote | 337 | 25 | 73.5 | 417 | 2 | E69804 | multidrug resistan |
| 265 | 25 | 73.5 | 239 | 2 | AH1323 | alpha-acetolactate | 338 | 25 | 73.5 | 420 | 2 | AF1270 | isocitrate dehydrog |
| 266 | 25 | 73.5 | 239 | 2 | AI1694 | alpha-acetolactate | 339 | 25 | 73.5 | 420 | 2 | AH1632 | isocitrate dehydrog |
| 267 | 25 | 73.5 | 246 | 2 | S74961 | hypothetical prote | 340 | 25 | 73.5 | 422 | 2 | C89953 | isocitrate dehydrog |
| 268 | 25 | 73.5 | 249 | 4 | T44821 | bacteriorhodopsin | 341 | 25 | 73.5 | 422 | 2 | G84044 | isocitrate dehydrog |
| 269 | 25 | 73.5 | 252 | 2 | S74884 | bacteriorhodopsin | 342 | 25 | 73.5 | 423 | 1 | I40382 | isocitrate dehydrog |
| 270 | 25 | 73.5 | 253 | 2 | B84157 | centromere-like fu | 343 | 25 | 73.5 | 430 | 2 | G87324 | hypothetical prote |
| 271 | 25 | 73.5 | 253 | 2 | AG0262 | probable exported | 344 | 25 | 73.5 | 433 | 2 | F86163 | hypothetical prote |
| 272 | 25 | 73.5 | 259 | 4 | T44820 | bacteriorhodopsin | 345 | 25 | 73.5 | 434 | 2 | G86163 | hypothetical prote |
| 273 | 25 | 73.5 | 261 | 2 | A69142 | hypothetical prote | 346 | 25 | 73.5 | 445 | 2 | S37779 | porin precursor, m |
| 274 | 25 | 73.5 | 262 | 1 | RAHSB | bacteriorhodopsin | 347 | 25 | 73.5 | 449 | 2 | JN0644 | naphthalene 1,2-di |
| 275 | 25 | 73.5 | 262 | 2 | H84300 | bacteriorhodopsin | 348 | 25 | 73.5 | 449 | 2 | JS0071 | naphthalene dioxys |
| 276 | 25 | 73.5 | 264 | 2 | E95410 | probable ABC trans | 349 | 25 | 73.5 | 449 | 2 | C55217 | polycyclic aromati |
| 277 | 25 | 73.5 | 265 | 2 | S16346 | hypothetical prote | 350 | 25 | 73.5 | 452 | 2 | B89799 | glycerol-3-phospha |
| 278 | 25 | 73.5 | 265 | 2 | AD1288 | aminoglycoside N3' | 351 | 25 | 73.5 | 454 | 2 | AH3555 | atrazine chlorohyd |
| 279 | 25 | 73.5 | 277 | 2 | B70364 | cytochrome c-type | 352 | 25 | 73.5 | 457 | 2 | AD0950 | oxygen-independent |
| 280 | 25 | 73.5 | 278 | 2 | A69098 | phosphate-binding | 353 | 25 | 73.5 | 458 | 2 | T31237 | trab protein homol |
| 281 | 25 | 73.5 | 278 | 2 | E83773 | transcription regu | 354 | 25 | 73.5 | 459 | 1 | F65191 | coproporphyrinogen |
| 282 | 25 | 73.5 | 286 | 2 | F96720 | unknown protein, 5 | 355 | 25 | 73.5 | 459 | 2 | E91227 | coproporphyrinogen |
| 283 | 25 | 73.5 | 287 | 2 | AI2038 | carboxyphosphoen | 356 | 25 | 73.5 | 459 | 2 | D86074 | O2-independent cop |
| 284 | 25 | 73.5 | 288 | 2 | A55737 | PD-1 protein - hum | 357 | 25 | 73.5 | 459 | 2 | F83895 | metal-tetracycline |
| 285 | 25 | 73.5 | 289 | 2 | S04648 | ampr protein - Rho | 358 | 25 | 73.5 | 462 | 2 | S27632 | naphthalene 1,2-di |
| 286 | 25 | 73.5 | 290 | 2 | AG0159 | probable LysR-fam | 359 | 25 | 73.5 | 462 | 2 | C69676 | alkaline phosphata |
| 287 | 25 | 73.5 | 290 | 2 | G95397 | probable LysR-fam | 360 | 25 | 73.5 | 466 | 2 | F95876 | hypothetical prote |
| 288 | 25 | 73.5 | 291 | 2 | G82314 | hypothetical prote | 361 | 25 | 73.5 | 468 | 2 | B84942 | phosphogluconate d |
| 289 | 25 | 73.5 | 298 | 2 | B53305 | transcription acti | 362 | 25 | 73.5 | 468 | 2 | G89930 | phosphogluconate d |
| 290 | 25 | 73.5 | 301 | 2 | F96019 | probable transcrip | 363 | 25 | 73.5 | 469 | 2 | A72377 | 6-phosphogluconate |
| 291 | 25 | 73.5 | 304 | 2 | F85725 | probable adhesin, l | 364 | 25 | 73.5 | 469 | 2 | AC3650 | phosphogluconate d |
| 292 | 25 | 73.5 | 304 | 2 | C90892 | probable adhesin, l | 365 | 25 | 73.5 | 470 | 1 | S14628 | phosphogluconate d |
| 293 | 25 | 73.5 | 307 | 1 | PARBA2 | phosphoprotein pho | 366 | 25 | 73.5 | 470 | 2 | D84863 | hypothetical prote |
| 294 | 25 | 73.5 | 307 | 2 | S28173 | phosphoprotein pho | 367 | 25 | 73.5 | 476 | 2 | AE2764 | phosphogluconate d |
| 295 | 25 | 73.5 | 311 | 1 | C69101 | conserved hypothet | 368 | 25 | 73.5 | 476 | 2 | D97545 | 6-phosphogluconate |
| 296 | 25 | 73.5 | 314 | 2 | T08933 | hypothetical prote | 369 | 25 | 73.5 | 476 | 2 | AC2465 | 6-phosphogluconate |
| 297 | 25 | 73.5 | 315 | 2 | T34502 | hypothetical prote | 370 | 25 | 73.5 | 476 | 2 | T46067 | hypothetical prote |
| 298 | 25 | 73.5 | 317 | 2 | S18583 | regulatory protein | 371 | 25 | 73.5 | 479 | 2 | A81714 | 6-phosphogluconate |
| 299 | 25 | 73.5 | 317 | 2 | G70608 | hypothetical prote | 372 | 25 | 73.5 | 480 | 2 | A71561 | probable 6-phospho |
| 300 | 25 | 73.5 | 317 | 2 | T45172 | hypothetical prote | 373 | 25 | 73.5 | 480 | 2 | S57842 | acute myeloid leuk |
| 301 | 25 | 73.5 | 318 | 2 | D75210 | hypothetical prote | 374 | 25 | 73.5 | 482 | 2 | S76127 | hypothetical prote |
| 302 | 25 | 73.5 | 320 | 2 | S18324 | lamin C - mouse (f | 375 | 25 | 73.5 | 484 | 2 | T01658 | phosphogluconate d |
| 303 | 25 | 73.5 | 323 | 2 | C86369 | protein F508.11 [i | 376 | 25 | 73.5 | 486 | 2 | S57786 | phosphogluconate d |
| 304 | 25 | 73.5 | 325 | 2 | G64055 | aerobic respiratio | 377 | 25 | 73.5 | 486 | 2 | H81377 | exopolysphatase |
| 305 | 25 | 73.5 | 325 | 2 | B87721 | protein F56A6.1 [i | 378 | 25 | 73.5 | 491 | 2 | T76943 | hypothetical prote |
| 306 | 25 | 73.5 | 325 | 2 | T33082 | hypothetical prote | 379 | 25 | 73.5 | 493 | 2 | T35685 | hypothetical prote |
| 307 | 25 | 73.5 | 328 | 1 | B64478 | hypothetical prote | 380 | 25 | 73.5 | 498 | 2 | G56938 | sensory transducti |
| 308 | 25 | 73.5 | 328 | 2 | B65086 | hydrogenase (EC 1, | 381 | 25 | 73.5 | 507 | 2 | S15476 | transmembrane glyc |
| 309 | 25 | 73.5 | 328 | 2 | A85959 | hydrogenase-2 smal | 382 | 25 | 73.5 | 507 | 2 | T19136 | hypothetical prote |
| 310 | 25 | 73.5 | 329 | 2 | A91114 | hydrogenase-2 smal | 383 | 25 | 73.5 | 515 | 2 | S72987 | acetolactate synth |
| 311 | 25 | 73.5 | 329 | 2 | T15910 | hypothetical prote | 384 | 25 | 73.5 | 516 | 2 | H82973 | choline transporte |
| 312 | 25 | 73.5 | 334 | 2 | T36475 | probable DNA-bindi | 385 | 25 | 73.5 | 518 | 2 | S34565 | gene G protein - h |
| 313 | 25 | 73.5 | 335 | 2 | T47274 | cyanide insensitiv | 386 | 25 | 73.5 | 519 | 2 | T23739 | hypothetical prote |
| 314 | 25 | 73.5 | 336 | 2 | AH0546 | probable terminal | 387 | 25 | 73.5 | 521 | 2 | T38466 | probable NRAMP-fam |
| 315 | 25 | 73.5 | 351 | 2 | S76667 | hypothetical prote | 388 | 25 | 73.5 | 523 | 2 | E72314 | alkaline phosphata |
| 316 | 25 | 73.5 | 361 | 2 | A87132 | probable alcohol d | 389 | 25 | 73.5 | 524 | 1 | PAHUH | alkaline phosphata |
| 317 | 25 | 73.5 | 363 | 2 | F65070 | hypothetical prote | 390 | 25 | 73.5 | 524 | 2 | A29600 | alkaline phosphata |
| 318 | 25 | 73.5 | 365 | 2 | S21056 | recF protein - Pse | 391 | 25 | 73.5 | 524 | 2 | A40172 | alkaline phosphata |
| 319 | 25 | 73.5 | 370 | 2 | E90423 | acyl-CoA dehydroge | 392 | 25 | 73.5 | 524 | 2 | A28114 | alkaline phosphata |
| 320 | 25 | 73.5 | 376 | 2 | B71981 | DNA transformation | 393 | 25 | 73.5 | 524 | 2 | S00289 | alkaline phosphata |
| 321 | 25 | 73.5 | 378 | 2 | C87425 | aldose 1-epimerase | 394 | 25 | 73.5 | 524 | 2 | S66467 | alkaline phosphata |

395 25 73.5 532 2 S12076 alkaline phosphata
396 25 73.5 535 1 PARUA alkaline phosphata
397 25 73.5 538 2 A11902 metabolite export
398 25 73.5 541 1 MMBYH2 glucose transport
399 25 73.5 546 2 S48313 hexose transport p
400 25 73.5 547 2 AC0405 fumarate hydratase
401 25 73.5 548 1 B44511 fumarate hydratase
402 25 73.5 548 1 UFECAQ fumarate hydratase
403 25 73.5 548 2 H91266 fumarase B (import
404 25 73.5 548 2 F30918 fumarase A (import
405 25 73.5 548 2 C85767 fumarase A (seimila
406 25 73.5 548 2 B86107 hypothetical prote
407 25 73.5 548 2 AB0691 fumarate hydratase
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411 25 73.5 550 2 G64996 hypothetical prote
412 25 73.5 553 2 AP2662 two component sens
413 25 73.5 555 2 E37444 probable two-compo
414 25 73.5 558 2 G36932 uncharacterized me
415 25 73.5 560 2 S46734 hypothetical prote
416 25 73.5 572 2 S73541 phosphotransferase
417 25 73.5 575 1 VCLJHD env polyprotein pr
418 25 73.5 599 2 G81550 GTP-binding protei
419 25 73.5 604 2 T47479 receptor-like prot
420 25 73.5 617 1 F48556 hemagglutinin - me
421 25 73.5 617 1 HNNZED hemagglutinin - me
422 25 73.5 617 1 HNNZHA hemagglutinin - me
423 25 73.5 620 2 JU0273 hemagglutinin - me
424 25 73.5 637 2 P69869 heavy metal-transp
425 25 73.5 643 2 I50539 intermediate filam
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428 25 73.5 652 2 T45499 probable DNA recom
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431 25 73.5 686 2 E71895 probable heavy-met
432 25 73.5 696 2 A12849 GDFP family prote
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435 25 73.5 705 2 S70029 probable transmem
436 25 73.5 714 2 S37345 pilQ protein - Pse
437 25 73.5 714 2 A83016 type 4 fimbrial bi
438 25 73.5 719 2 S55119 hypothetical prote
439 25 73.5 731 2 T34217 hypothetical prote
440 25 73.5 781 2 F82584 catalase/peroxidas
441 25 73.5 789 2 S58235 endo-1,4-beta-xyla
442 25 73.5 810 2 B84185 cytochrome-like pr
443 25 73.5 814 2 T05537 probable serine/th
444 25 73.5 815 2 T00740 hypothetical prote
445 25 73.5 818 2 AG2278 cation-transportin
446 25 73.5 821 2 S58333 probable membrane
447 25 73.5 821 2 AD1148 probable secreted
448 25 73.5 828 2 F96535 hypothetical prote
449 25 73.5 840 1 K1QAP0 pyruvate, phosphat
450 25 73.5 845 2 J65256 adipocyte transcri
451 25 73.5 850 2 F95260 ABC transporter, p
452 25 73.5 850 2 A38126 conserved hypoteth
453 25 73.5 883 2 C86729 hypothetical prote
454 25 73.5 921 2 G83902 hypothetical prote
455 25 73.5 922 2 S15204 pertactin - Bordet
456 25 73.5 925 2 T16235 hypothetical prote
457 25 73.5 1058 2 AG2541 cation efflux syst
458 25 73.5 1146 2 C83304 hypothetical prote
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460 25 73.5 1178 1 A47255 pyruvate carboxyla
461 25 73.5 1178 1 JC2460 pyruvate carboxyla
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463 25 73.5 1195 2 T43735 pyruvate carboxyla
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465 25 73.5 1222 2 G72614 probable reverse g
466 25 73.5 1230 2 F82857 PilY1 protein homo
467 25 73.5 1395 2 T00068 hypothetical prote

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470 25 73.5 1469 2 T50210 probable ABC trans
471 25 73.5 1500 2 A42210 alpha-1-macroglobu
472 25 73.5 1502 2 S45429 probable membrane
473 25 73.5 1506 2 S52957 bimD protein - Eme
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475 25 73.5 1886 2 S04921 nuclear pore prote
476 25 73.5 2054 2 T46612 multi PDZ domain p
477 25 73.5 2055 2 T30259 multiple PDZ domai
478 25 73.5 2092 2 S30026 genome polyprotein
479 25 73.5 2149 2 S18676 genome polyprotein
480 25 73.5 2512 1 XYCHFA enoyl-[acyl-carrie
481 25 73.5 4660 2 T42737 gp330 protein prec
482 25 73.5 4936 2 AH2515 hypothetical prote
483 24 70.6 22 2 S39557 light harvesting c
484 24 70.6 103 2 B25913 Ig heavy chain pre
485 24 70.6 113 2 F72746 hypothetical prote
486 24 70.6 116 2 S26328 Ig heavy chain V r
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490 24 70.6 136 2 G72524 hypothetical prote
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507 24 70.6 201 2 G97513 NADH dehydrogenase
508 24 70.6 201 2 AB2732 NADH ubiquinone ox
509 24 70.6 205 2 AG2461 hypothetical prote
510 24 70.6 209 2 C71647 hypothetical prote
511 24 70.6 209 2 H97864 hypothetical prote
512 24 70.6 216 1 HLHUG class II histocomp
513 24 70.6 217 2 F71953 hypothetical prote
514 24 70.6 223 2 C86827 cation transport A
515 24 70.6 224 2 A60032 cerebellin-like gl
516 24 70.6 227 2 G81014 conserved hypoteth
517 24 70.6 229 2 S57854 glutenin low molec
518 24 70.6 232 2 S07504 purine nucleoside
519 24 70.6 236 2 G90007 helix-destabilizin
520 24 70.6 236 2 C82578 conserved hypoteth
521 24 70.6 238 1 JC2297 CD63 antigen - rab
522 24 70.6 238 2 S75336 hypothetical prote
523 24 70.6 238 2 S03906 45K antigen - shue
524 24 70.6 239 2 T20255 hypothetical prote
525 24 70.6 239 2 T50631 hypothetical prote
526 24 70.6 241 2 F81835 hypothetical prote
527 24 70.6 241 2 B81129 conserved hypoteth
528 24 70.6 242 2 G97082 uncharacterized me
529 24 70.6 243 2 T51746 MHC class II alpha
530 24 70.6 243 2 F72719 hypothetical prote
531 24 70.6 244 2 E81690 probable sodium-tr
532 24 70.6 246 2 H95408 probable short cha
533 24 70.6 247 2 AG2570 chromosome partiti
534 24 70.6 248 2 F69868 glucose 1-dehydrog
535 24 70.6 250 2 G81447 major antigenic pe
536 24 70.6 251 2 A13185 dehydrogenase Act5
537 24 70.6 251 2 AG2972 conserved hypoteth
538 24 70.6 251 2 D98310 hypothetical prote
539 24 70.6 252 2 C85708 probable colonizat
540 24 70.6 252 2 D90850 probable colonizat

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|--------|--------------------|-----|----|------|-----|---|--------|--------------------|
| 541 | 24 | 70.6 | 252 | 2 | AB2274 | hypothetical prote | 614 | 24 | 70.6 | 348 | 2 | C82862 | conjugal transfer |
| 542 | 24 | 70.6 | 253 | 2 | S49371 | repB protein - Cam | 615 | 24 | 70.6 | 349 | 1 | A54679 | opsin, blue-sensit |
| 543 | 24 | 70.6 | 255 | 2 | C86591 | chromosome partiti | 616 | 24 | 70.6 | 349 | 2 | H75299 | conserved hypotet |
| 544 | 24 | 70.6 | 256 | 2 | F72034 | ParA chromosome pa | 617 | 24 | 70.6 | 352 | 2 | AH2097 | sorbitol dehydroge |
| 545 | 24 | 70.6 | 256 | 2 | D86544 | NADH (ubiquinone) | 618 | 24 | 70.6 | 354 | 2 | D96522 | Fl1A17.19 (impor |
| 546 | 24 | 70.6 | 256 | 2 | H72078 | probable sodium-tr | 619 | 24 | 70.6 | 357 | 2 | T40410 | hypothetical prote |
| 547 | 24 | 70.6 | 256 | 2 | S49368 | repB protein - Cam | 620 | 24 | 70.6 | 359 | 2 | H96969 | aspartate semialde |
| 548 | 24 | 70.6 | 258 | 2 | H95326 | probable (imported | 621 | 24 | 70.6 | 362 | 2 | S78515 | single-stranded nu |
| 549 | 24 | 70.6 | 258 | 2 | H95983 | 3-hydroxybutyrate | 622 | 24 | 70.6 | 365 | 2 | T06615 | hypothetical prote |
| 550 | 24 | 70.6 | 259 | 2 | G39999 | hypothetical prote | 623 | 24 | 70.6 | 365 | 2 | S42471 | hnRNP protein E2 - |
| 551 | 24 | 70.6 | 259 | 2 | S18148 | hypothetical prote | 624 | 24 | 70.6 | 368 | 2 | H96990 | probable membrane |
| 552 | 24 | 70.6 | 260 | 1 | D47031 | orf2 3' of bah - S | 625 | 24 | 70.6 | 369 | 2 | H69112 | hypothetical prote |
| 553 | 24 | 70.6 | 261 | 1 | S25079 | monensin polyketid | 626 | 24 | 70.6 | 372 | 2 | T36008 | probable transaldo |
| 554 | 24 | 70.6 | 261 | 2 | AE3064 | hydroxybutyrate de | 627 | 24 | 70.6 | 375 | 2 | A95867 | probable pyrroloqu |
| 555 | 24 | 70.6 | 261 | 2 | C98222 | d-beta-hydroxybuty | 628 | 24 | 70.6 | 376 | 2 | S73941 | oligopeptide trans |
| 556 | 24 | 70.6 | 261 | 2 | S35196 | hypothetical prote | 629 | 24 | 70.6 | 376 | 2 | AG1410 | cell division prot |
| 557 | 24 | 70.6 | 261 | 2 | S54815 | urdamycin polyketi | 630 | 24 | 70.6 | 376 | 2 | T51342 | RNA helicase RH10 |
| 558 | 24 | 70.6 | 262 | 2 | S69225 | nogalamycin polyke | 631 | 24 | 70.6 | 377 | 2 | A43333 | pyrroloquinoline q |
| 559 | 24 | 70.6 | 271 | 2 | T41026 | probable methyltra | 632 | 24 | 70.6 | 380 | 2 | S20457 | pqqE protein - Kle |
| 560 | 24 | 70.6 | 272 | 1 | S05397 | granaticin polyket | 633 | 24 | 70.6 | 381 | 2 | E69352 | conserved hypotet |
| 561 | 24 | 70.6 | 277 | 2 | I40842 | hypothetical prote | 634 | 24 | 70.6 | 382 | 2 | G86847 | hypothetical prote |
| 562 | 24 | 70.6 | 279 | 1 | HLHMSG | class II histocomp | 635 | 24 | 70.6 | 383 | 2 | D71084 | hypothetical prote |
| 563 | 24 | 70.6 | 280 | 2 | S04362 | class II histocomp | 636 | 24 | 70.6 | 384 | 2 | G75102 | group II decarboxy |
| 564 | 24 | 70.6 | 280 | 2 | H89800 | hypothetical prote | 637 | 24 | 70.6 | 384 | 2 | B70690 | hypothetical prote |
| 565 | 24 | 70.6 | 284 | 2 | T22671 | hypothetical prote | 638 | 24 | 70.6 | 385 | 1 | S76874 | probable hydro-ly |
| 566 | 24 | 70.6 | 284 | 2 | AG3231 | conjugal transfer | 639 | 24 | 70.6 | 387 | 2 | AH1050 | conserved hypotet |
| 567 | 24 | 70.6 | 285 | 2 | S20853 | glutenin low molec | 640 | 24 | 70.6 | 388 | 2 | AH1183 | antibiotic resista |
| 568 | 24 | 70.6 | 286 | 2 | T05910 | glutenin low molec | 641 | 24 | 70.6 | 388 | 2 | AF1541 | antibiotic resista |
| 569 | 24 | 70.6 | 289 | 2 | D90494 | tatC-like protein, | 642 | 24 | 70.6 | 388 | 2 | A84445 | hypothetical prote |
| 570 | 24 | 70.6 | 290 | 1 | B64657 | conserved hypotet | 643 | 24 | 70.6 | 389 | 1 | C64923 | chloramphenicol re |
| 571 | 24 | 70.6 | 290 | 2 | G71859 | hypothetical prote | 644 | 24 | 70.6 | 389 | 2 | F90924 | probable transport |
| 572 | 24 | 70.6 | 291 | 2 | G86903 | cell shape determi | 645 | 24 | 70.6 | 389 | 2 | B85773 | probable transport |
| 573 | 24 | 70.6 | 291 | 2 | H84609 | hypothetical prote | 646 | 24 | 70.6 | 389 | 2 | AH3003 | penicillin-binding |
| 574 | 24 | 70.6 | 292 | 2 | A97034 | transcription regu | 647 | 24 | 70.6 | 394 | 2 | AB1068 | probable membrane |
| 575 | 24 | 70.6 | 295 | 2 | S56296 | probable membrane | 648 | 24 | 70.6 | 395 | 2 | D69312 | molybdopterin oxid |
| 576 | 24 | 70.6 | 296 | 2 | T31062 | hypothetical prote | 649 | 24 | 70.6 | 395 | 2 | T51021 | related to hydroxy |
| 577 | 24 | 70.6 | 297 | 2 | B85765 | probable transcrip | 650 | 24 | 70.6 | 396 | 2 | T40010 | hypothetical prote |
| 578 | 24 | 70.6 | 297 | 2 | E64915 | probable transcrip | 651 | 24 | 70.6 | 398 | 2 | A99280 | penicillin-binding |
| 579 | 24 | 70.6 | 297 | 2 | E90916 | probable transcrip | 652 | 24 | 70.6 | 399 | 2 | E86480 | 43.6K hypothetical |
| 580 | 24 | 70.6 | 297 | 2 | B87567 | integral membrane | 653 | 24 | 70.6 | 402 | 2 | E71279 | hypothetical prote |
| 581 | 24 | 70.6 | 300 | 2 | A69635 | transcription acti | 654 | 24 | 70.6 | 405 | 2 | D71337 | conserved hypotet |
| 582 | 24 | 70.6 | 301 | 2 | S51132 | ADP,ATP carrier pr | 655 | 24 | 70.6 | 408 | 2 | B75635 | phosphoenolpyruvat |
| 583 | 24 | 70.6 | 301 | 2 | A83017 | probable transcrip | 656 | 24 | 70.6 | 409 | 2 | T03788 | hypothetical prote |
| 584 | 24 | 70.6 | 304 | 2 | T06505 | glutenin low molec | 657 | 24 | 70.6 | 410 | 2 | D64158 | hypothetical prote |
| 585 | 24 | 70.6 | 304 | 2 | E91230 | hypothetical prote | 658 | 24 | 70.6 | 414 | 1 | C8ECFW | cell division prot |
| 586 | 24 | 70.6 | 304 | 2 | D86077 | hypothetical prote | 659 | 24 | 70.6 | 414 | 2 | AD0518 | cell division prot |
| 587 | 24 | 70.6 | 305 | 2 | T28063 | hypothetical prote | 660 | 24 | 70.6 | 414 | 2 | E90640 | cell division prot |
| 588 | 24 | 70.6 | 307 | 2 | H71160 | hypothetical prote | 661 | 24 | 70.6 | 414 | 2 | B85491 | cell division prot |
| 589 | 24 | 70.6 | 310 | 2 | D70139 | conserved hypotet | 662 | 24 | 70.6 | 417 | 2 | E82966 | tryptophan permeas |
| 590 | 24 | 70.6 | 311 | 2 | T09656 | oryR protein homol | 663 | 24 | 70.6 | 417 | 2 | JC7092 | paul protein - fis |
| 591 | 24 | 70.6 | 311 | 2 | D87164 | probable LysR-fam | 664 | 24 | 70.6 | 418 | 2 | T51129 | hypothetical prote |
| 592 | 24 | 70.6 | 314 | 2 | B83536 | probable transcrip | 665 | 24 | 70.6 | 418 | 2 | B83686 | hypothetical prote |
| 593 | 24 | 70.6 | 315 | 2 | E69400 | 3-hydroxyacyl-CoA | 666 | 24 | 70.6 | 422 | 2 | AD0484 | GntP family permea |
| 594 | 24 | 70.6 | 316 | 2 | S75062 | transcription regu | 667 | 24 | 70.6 | 423 | 2 | H86195 | hypothetical prote |
| 595 | 24 | 70.6 | 317 | 2 | C75012 | hypothetical prote | 668 | 24 | 70.6 | 423 | 2 | T19030 | hypothetical prote |
| 596 | 24 | 70.6 | 317 | 2 | E95239 | conserved hypotet | 669 | 24 | 70.6 | 425 | 2 | C35128 | stage IV sporulati |
| 597 | 24 | 70.6 | 317 | 2 | E98103 | conserved hypotet | 670 | 24 | 70.6 | 430 | 2 | H91259 | hypothetical prote |
| 598 | 24 | 70.6 | 318 | 2 | A69653 | transmembrane lipo | 671 | 24 | 70.6 | 430 | 2 | S52700 | NUP42 protein - ye |
| 599 | 24 | 70.6 | 320 | 2 | H84092 | phage-related prot | 672 | 24 | 70.6 | 430 | 2 | D86100 | hypothetical prote |
| 600 | 24 | 70.6 | 323 | 2 | T06506 | glutenin low molec | 673 | 24 | 70.6 | 433 | 2 | G86812 | D-xylose proton-sy |
| 601 | 24 | 70.6 | 323 | 2 | T25459 | hypothetical prote | 674 | 24 | 70.6 | 434 | 2 | B72410 | alkaline phosphata |
| 602 | 24 | 70.6 | 326 | 2 | C91035 | probable hydrogena | 675 | 24 | 70.6 | 437 | 2 | A34800 | Opaque-2 protein - |
| 603 | 24 | 70.6 | 326 | 2 | E75902 | hypothetical prote | 676 | 24 | 70.6 | 439 | 2 | C69392 | hypothetical prote |
| 604 | 24 | 70.6 | 328 | 2 | T19815 | hypothetical prote | 677 | 24 | 70.6 | 440 | 2 | F69791 | conserved hypotet |
| 605 | 24 | 70.6 | 329 | 2 | S73345 | sn-glycerol-3-phos | 678 | 24 | 70.6 | 443 | 2 | JQ2134 | nitrate transport |
| 606 | 24 | 70.6 | 331 | 2 | AD1220 | Salmonella enteric | 679 | 24 | 70.6 | 448 | 2 | B81439 | probable transmemb |
| 607 | 24 | 70.6 | 331 | 2 | AG1573 | highly Salmonella | 680 | 24 | 70.6 | 449 | 2 | H81835 | probable glutamate |
| 608 | 24 | 70.6 | 334 | 2 | T04572 | hypothetical prote | 681 | 24 | 70.6 | 449 | 2 | H81128 | probable glutamate |
| 609 | 24 | 70.6 | 337 | 2 | T06720 | hypothetical prote | 682 | 24 | 70.6 | 453 | 2 | H71732 | cytochrome D ubiqu |
| 610 | 24 | 70.6 | 340 | 2 | H81742 | major outer membra | 683 | 24 | 70.6 | 454 | 2 | F75580 | probable sugar tra |
| 611 | 24 | 70.6 | 341 | 2 | AB0974 | L-threonine 3-dehy | 684 | 24 | 70.6 | 454 | 2 | D70904 | probable meel prot |
| 612 | 24 | 70.6 | 346 | 2 | T51551 | quinone oxidoreduc | 685 | 24 | 70.6 | 456 | 2 | G91251 | probable DNA circu |
| 613 | 24 | 70.6 | 348 | 1 | COHUB | opsin, blue-sensit | 686 | 24 | 70.6 | 456 | 2 | H97735 | hypothetical prote |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|--------|---------------------|-----|----|------|-----|---|--------|---------------------|
| 687 | 24 | 70.6 | 457 | 2 | H83662 | DNA repair protein | 760 | 24 | 70.6 | 615 | 1 | H64769 | preprotein translo |
| 688 | 24 | 70.6 | 459 | 2 | T30219 | hypothetical prote | 761 | 24 | 70.6 | 615 | 2 | AG0552 | protein-export mem |
| 689 | 24 | 70.6 | 459 | 2 | AF1397 | two-component sens | 762 | 24 | 70.6 | 615 | 2 | C90886 | protein-export mem |
| 690 | 24 | 70.6 | 459 | 2 | A11772 | two-component sens | 763 | 24 | 70.6 | 615 | 2 | G85536 | protein-export mem |
| 691 | 24 | 70.6 | 460 | 2 | S06022 | regulatory protein | 764 | 24 | 70.6 | 624 | 2 | B82108 | flagellar hook-aa |
| 692 | 24 | 70.6 | 460 | 2 | C96736 | probable ketoacyl- | 765 | 24 | 70.6 | 634 | 2 | D83615 | hypothetical prote |
| 693 | 24 | 70.6 | 462 | 2 | H37292 | UDP-N-acetylmuram | 766 | 24 | 70.6 | 635 | 2 | F96660 | protein F2K1.10 [|
| 694 | 24 | 70.6 | 463 | 2 | G11191 | probable DNA damag | 767 | 24 | 70.6 | 638 | 2 | I53169 | cycloeratin 2 - hu |
| 695 | 24 | 70.6 | 464 | 2 | T23632 | dihydroliipoamide d | 768 | 24 | 70.6 | 641 | 2 | T49477 | phenol hydroxylase |
| 696 | 24 | 70.6 | 464 | 2 | S12591 | beta-l-adrenergic | 769 | 24 | 70.6 | 647 | 2 | E90259 | amino acid transpo |
| 697 | 24 | 70.6 | 465 | 2 | A47023 | S-layer protein - | 770 | 24 | 70.6 | 647 | 2 | S61011 | hypothetical prote |
| 698 | 24 | 70.6 | 466 | 2 | AH0476 | NAD(P) transehydrog | 771 | 24 | 70.6 | 648 | 2 | T47896 | hypothetical prote |
| 699 | 24 | 70.6 | 466 | 2 | S36794 | beta-l-adrenergic | 772 | 24 | 70.6 | 651 | 2 | E83443 | hypothetical prote |
| 700 | 24 | 70.6 | 466 | 2 | D84906 | probable beta-keto | 773 | 24 | 70.6 | 654 | 2 | S21552 | Mx protein homolog |
| 701 | 24 | 70.6 | 467 | 2 | AH0585 | conserved hypothet | 774 | 24 | 70.6 | 657 | 2 | E96812 | protein F3F9.10 [i |
| 702 | 24 | 70.6 | 473 | 2 | T15986 | hypothetical prote | 775 | 24 | 70.6 | 657 | 2 | S64073 | hypothetical prote |
| 703 | 24 | 70.6 | 473 | 2 | A47284 | myocyte enhancer-b | 776 | 24 | 70.6 | 660 | 2 | A40098 | hypothetical prote |
| 704 | 24 | 70.6 | 474 | 2 | T35220 | probable integral | 777 | 24 | 70.6 | 661 | 2 | F70751 | hypothetical prote |
| 705 | 24 | 70.6 | 474 | 2 | A35276 | sensor histidine k | 778 | 24 | 70.6 | 662 | 2 | A33481 | interferon-induced |
| 706 | 24 | 70.6 | 476 | 2 | T36395 | probable transcrip | 779 | 24 | 70.6 | 666 | 1 | D69103 | DNA helicase (EC 3 |
| 707 | 24 | 70.6 | 477 | 1 | QRHUB1 | beta-l-adrenergic | 780 | 24 | 70.6 | 672 | 2 | F36891 | transfer complex p |
| 708 | 24 | 70.6 | 477 | 2 | B28988 | hypothetical prote | 781 | 24 | 70.6 | 728 | 2 | B83805 | GRP pyrophosphokin |
| 709 | 24 | 70.6 | 479 | 2 | A48565 | phosphogluconate d | 782 | 24 | 70.6 | 731 | 2 | D95235 | penicillin-binding |
| 710 | 24 | 70.6 | 479 | 2 | T50726 | hypothetical prote | 783 | 24 | 70.6 | 731 | 2 | E98099 | peptidoglycan glyc |
| 711 | 24 | 70.6 | 479 | 2 | S26223 | cruciferin precurs | 784 | 24 | 70.6 | 734 | 2 | C69691 | GRP pyrophosphokin |
| 712 | 24 | 70.6 | 480 | 2 | I53053 | beta l adrenergic | 785 | 24 | 70.6 | 740 | 2 | T12223 | NADH2 dehydrogenas |
| 713 | 24 | 70.6 | 482 | 2 | B69803 | metabolite transpo | 786 | 24 | 70.6 | 740 | 2 | B86638 | GRP diphosphokinase |
| 714 | 24 | 70.6 | 487 | 2 | H97304 | uncharacterized co | 787 | 24 | 70.6 | 740 | 2 | D97180 | relA/Spot protein, |
| 715 | 24 | 70.6 | 490 | 2 | S49792 | probable membrane | 788 | 24 | 70.6 | 749 | 2 | A70812 | hypothetical glyci |
| 716 | 24 | 70.6 | 491 | 2 | A55927 | pre-B cell enhanci | 789 | 24 | 70.6 | 754 | 2 | E69745 | hypothetical prote |
| 717 | 24 | 70.6 | 492 | 2 | P86384 | probable protein f | 790 | 24 | 70.6 | 764 | 2 | H82737 | malate oxidoreduct |
| 718 | 24 | 70.6 | 493 | 2 | F70841 | probable lpda prot | 791 | 24 | 70.6 | 765 | 2 | A69440 | conserved hypothet |
| 719 | 24 | 70.6 | 493 | 2 | A85433 | sugar transporter | 792 | 24 | 70.6 | 765 | 2 | T01330 | hypothetical prote |
| 720 | 24 | 70.6 | 493 | 2 | H86392 | hypothetical prote | 793 | 24 | 70.6 | 770 | 2 | JC7728 | xylin 1,4-beta-xy |
| 721 | 24 | 70.6 | 494 | 2 | I52658 | neurofilament-66 - | 794 | 24 | 70.6 | 774 | 2 | S25284 | protein kinase nek |
| 722 | 24 | 70.6 | 494 | 2 | B84230 | hypothetical prote | 795 | 24 | 70.6 | 778 | 2 | AD0432 | aerobic respiratio |
| 723 | 24 | 70.6 | 497 | 2 | S27785 | acetyl-CoA acetyl | 796 | 24 | 70.6 | 782 | 1 | FAHUP | gelsoin precursor |
| 724 | 24 | 70.6 | 497 | 2 | T52308 | very-long-chain fa | 797 | 24 | 70.6 | 783 | 2 | T38313 | hypothetical prote |
| 725 | 24 | 70.6 | 501 | 2 | S54576 | probable membrane | 798 | 24 | 70.6 | 793 | 2 | B65113 | hypothetical outer |
| 726 | 24 | 70.6 | 502 | 2 | D86765 | hypothetical prote | 799 | 24 | 70.6 | 793 | 2 | S59067 | penton long fiber |
| 727 | 24 | 70.6 | 503 | 2 | JC5078 | glutamate transpor | 800 | 24 | 70.6 | 801 | 2 | T07617 | proteinase TMP - t |
| 728 | 24 | 70.6 | 503 | 2 | T50791 | hypothetical prote | 801 | 24 | 70.6 | 805 | 2 | T08932 | hypothetical prote |
| 729 | 24 | 70.6 | 504 | 2 | A80404 | probable sugar ABC | 802 | 24 | 70.6 | 812 | 2 | AC2349 | hypothetical prote |
| 730 | 24 | 70.6 | 505 | 2 | A41023 | alpha-interneixin - | 803 | 24 | 70.6 | 827 | 2 | B95969 | probable H+/K+-exc |
| 731 | 24 | 70.6 | 505 | 2 | F95345 | FixL Oxygen regula | 804 | 24 | 70.6 | 835 | 2 | B82051 | penicillin-binding |
| 732 | 24 | 70.6 | 505 | 2 | S39984 | nitrogen fixation | 805 | 24 | 70.6 | 851 | 2 | A86200 | hypothetical prote |
| 733 | 24 | 70.6 | 509 | 2 | A35540 | cruciferin 1 precu | 806 | 24 | 70.6 | 877 | 2 | S58824 | probable membrane |
| 734 | 24 | 70.6 | 516 | 2 | J50301 | inulinase (EC 3.2. | 807 | 24 | 70.6 | 879 | 2 | AC1308 | pyruvate phosphate |
| 735 | 24 | 70.6 | 518 | 2 | T29633 | hypothetical prote | 808 | 24 | 70.6 | 879 | 2 | AC1680 | pyruvate phosphate |
| 736 | 24 | 70.6 | 528 | 2 | B88989 | protein F02C9.2 [i | 809 | 24 | 70.6 | 891 | 1 | DEEC | acetaldehyde dehyd |
| 737 | 24 | 70.6 | 529 | 2 | S62468 | probable membrane | 810 | 24 | 70.6 | 891 | 2 | D85704 | hypothetical prote |
| 738 | 24 | 70.6 | 535 | 2 | S33957 | VAM1 protein - yea | 811 | 24 | 70.6 | 891 | 2 | E90846 | acetaldehyde dehyd |
| 739 | 24 | 70.6 | 538 | 2 | A70836 | hypothetical prote | 812 | 24 | 70.6 | 891 | 2 | AG0265 | alcohol dehydrogen |
| 740 | 24 | 70.6 | 541 | 2 | T28069 | hypothetical prote | 813 | 24 | 70.6 | 892 | 2 | AE0650 | alcohol dehydrogen |
| 741 | 24 | 70.6 | 542 | 2 | B81910 | probable ABC-trans | 814 | 24 | 70.6 | 894 | 2 | D82127 | alcohol dehydrogen |
| 742 | 24 | 70.6 | 542 | 2 | E81105 | ABC transporter, A | 815 | 24 | 70.6 | 917 | 2 | T04661 | hypothetical prote |
| 743 | 24 | 70.6 | 542 | 2 | T14632 | hypothetical prote | 816 | 24 | 70.6 | 919 | 2 | E83212 | probable sensor/re |
| 744 | 24 | 70.6 | 552 | 1 | TVMV73 | transforming prote | 817 | 24 | 70.6 | 920 | 2 | C70668 | probable mmp17 pro |
| 745 | 24 | 70.6 | 561 | 2 | A30777 | probable two-compo | 818 | 24 | 70.6 | 926 | 2 | AE1130 | conserved hypothet |
| 746 | 24 | 70.6 | 575 | 2 | A81067 | acetylactate synth | 819 | 24 | 70.6 | 947 | 1 | KIZMPO | pyruvate, phosphat |
| 747 | 24 | 70.6 | 575 | 2 | F81801 | hypothetical prote | 820 | 24 | 70.6 | 947 | 1 | T02979 | pyruvate, phosphat |
| 748 | 24 | 70.6 | 586 | 2 | T51211 | hypothetical prote | 821 | 24 | 70.6 | 949 | 1 | S55478 | pyruvate, phosphat |
| 749 | 24 | 70.6 | 588 | 2 | D72062 | single-stranded-DN | 822 | 24 | 70.6 | 953 | 2 | S56650 | pyruvate, phosphat |
| 750 | 24 | 70.6 | 588 | 2 | G86560 | ssDNA exonuclease | 823 | 24 | 70.6 | 953 | 2 | S12894 | pyruvate, phosphat |
| 751 | 24 | 70.6 | 589 | 2 | T38738 | major facilitator | 824 | 24 | 70.6 | 954 | 2 | A10438 | probable exported |
| 752 | 24 | 70.6 | 594 | 2 | D84859 | probable MAP kinase | 825 | 24 | 70.6 | 955 | 2 | S56649 | pyruvate, phosphat |
| 753 | 24 | 70.6 | 595 | 1 | TVCHRL | transforming prote | 826 | 24 | 70.6 | 956 | 1 | S53257 | pyruvate, phosphat |
| 754 | 24 | 70.6 | 595 | 2 | B97415 | hypothetical prote | 827 | 24 | 70.6 | 960 | 2 | A71420 | pyruvate, phosphat |
| 755 | 24 | 70.6 | 595 | 2 | AF2632 | conserved hypothet | 828 | 24 | 70.6 | 972 | 2 | AB3640 | pyruvate, phosphat |
| 756 | 24 | 70.6 | 595 | 2 | C88468 | protein C05D11.7 [| 829 | 24 | 70.6 | 977 | 2 | I52657 | seizure-related pr |
| 757 | 24 | 70.6 | 598 | 2 | S10893 | transforming prote | 830 | 24 | 70.6 | 979 | 2 | G85167 | ABC transporter li |
| 758 | 24 | 70.6 | 612 | 2 | S55084 | probable membrane | 831 | 24 | 70.6 | 979 | 2 | A70848 | probable membrane |
| 759 | 24 | 70.6 | 613 | 2 | T09105 | holocytochrome c-t | 832 | 24 | 70.6 | 985 | 2 | T29910 | hypothetical prote |

| | | | | | | | | | | | | | |
|-----|----|------|------|---|--------|----------------------|-----|----|------|-----|---|--------|---------------------|
| 833 | 24 | 70.6 | 993 | 2 | D96812 | protein F3P9.12 (i | 906 | 23 | 67.6 | 100 | 2 | S77878 | hypothetical prote |
| 834 | 24 | 70.6 | 1001 | 2 | C86181 | hypothetical prote | 907 | 23 | 67.6 | 105 | 2 | T14666 | hypothetical prote |
| 835 | 24 | 70.6 | 1002 | 2 | T19226 | hypothetical prote | 908 | 23 | 67.6 | 106 | 2 | AE2230 | sulfur-regulated p |
| 836 | 24 | 70.6 | 1004 | 2 | T00795 | 26S proteasome reg | 909 | 23 | 67.6 | 107 | 2 | B72525 | hypothetical prote |
| 837 | 24 | 70.6 | 1007 | 2 | T01437 | hypothetical prote | 910 | 23 | 67.6 | 108 | 2 | A71353 | probable anti-sigm |
| 838 | 24 | 70.6 | 1016 | 2 | H73356 | exonuclease ABC c | 911 | 23 | 67.6 | 112 | 2 | S58139 | gene 9 protein - p |
| 839 | 24 | 70.6 | 1020 | 2 | T18260 | 1-phosphatidylinos | 912 | 23 | 67.6 | 116 | 2 | JA5188 | sporulation-specifi |
| 840 | 24 | 70.6 | 1028 | 2 | C88364 | protein C13B4.1 (i | 913 | 23 | 67.6 | 116 | 2 | A48042 | stage II sporulati |
| 841 | 24 | 70.6 | 1043 | 2 | AB0370 | multidrug efflux p | 914 | 23 | 67.6 | 116 | 2 | H83841 | anti-sigma F facto |
| 842 | 24 | 70.6 | 1048 | 1 | XPBEA9 | large structural p | 915 | 23 | 67.6 | 116 | 2 | C65214 | hypothetical 13.0 |
| 843 | 24 | 70.6 | 1066 | 2 | S50237 | TATA box-binding p | 916 | 23 | 67.6 | 116 | 2 | F86099 | hypothetical prote |
| 844 | 24 | 70.6 | 1087 | 2 | C84263 | transmembrane olig | 917 | 23 | 67.6 | 116 | 2 | B91259 | hypothetical prote |
| 845 | 24 | 70.6 | 1091 | 1 | IJCHNL | neural cell adhesi | 918 | 23 | 67.6 | 117 | 1 | H64868 | ychN protein - Esc |
| 846 | 24 | 70.6 | 1093 | 2 | I38533 | AF17 protein - hum | 919 | 23 | 67.6 | 117 | 2 | A37165 | sporulation locus |
| 847 | 24 | 70.6 | 1106 | 2 | S38783 | integrin alpha cha | 920 | 23 | 67.6 | 117 | 2 | D90844 | hypothetical prote |
| 848 | 24 | 70.6 | 1133 | 1 | EGRT | epidermal growth f | 921 | 23 | 67.6 | 117 | 2 | C85702 | hypothetical prote |
| 849 | 24 | 70.6 | 1135 | 2 | I61186 | alpha-7 integrin - | 922 | 23 | 67.6 | 117 | 2 | A72474 | hypothetical prote |
| 850 | 24 | 70.6 | 1137 | 2 | JC5950 | integrin alpha-7 c | 923 | 23 | 67.6 | 119 | 1 | A55646 | stage II sporulati |
| 851 | 24 | 70.6 | 1140 | 2 | A34728 | hypothetical prote | 924 | 23 | 67.6 | 120 | 2 | A72617 | hypothetical prote |
| 852 | 24 | 70.6 | 1177 | 1 | D71416 | probable PDR5-like | 925 | 23 | 67.6 | 121 | 2 | S28799 | hypothetical prote |
| 853 | 24 | 70.6 | 1196 | 1 | GNMVRV | HIV-1 retropepsin | 926 | 23 | 67.6 | 123 | 2 | H75149 | hypothetical prote |
| 854 | 24 | 70.6 | 1196 | 1 | GNMVG | HIV-1 retropepsin | 927 | 23 | 67.6 | 123 | 2 | T14949 | hypothetical prote |
| 855 | 24 | 70.6 | 1198 | 2 | T28678 | polyketide synthas | 928 | 23 | 67.6 | 127 | 2 | A71085 | hypothetical prote |
| 856 | 24 | 70.6 | 1199 | 1 | GNMVM | HIV-1 retropepsin | 929 | 23 | 67.6 | 129 | 2 | H83408 | hypothetical prote |
| 857 | 24 | 70.6 | 1204 | 2 | S70393 | pol polyprotein - | 930 | 23 | 67.6 | 135 | 2 | C82766 | conserved hypotet |
| 858 | 24 | 70.6 | 1204 | 2 | S35475 | pol polyprotein - | 931 | 23 | 67.6 | 136 | 2 | B95333 | hypothetical prote |
| 859 | 24 | 70.6 | 1207 | 2 | T23754 | hypothetical prote | 932 | 23 | 67.6 | 137 | 2 | S54219 | flagellar basal bo |
| 860 | 24 | 70.6 | 1241 | 2 | S01827 | period clock prote | 933 | 23 | 67.6 | 138 | 2 | I46634 | rearranged T-cell |
| 861 | 24 | 70.6 | 1276 | 2 | S75801 | probable phytochro | 934 | 23 | 67.6 | 141 | 2 | S43320 | cold-regulated pro |
| 862 | 24 | 70.6 | 1324 | 2 | S52863 | DNA-binding protei | 935 | 23 | 67.6 | 147 | 1 | G2HUCS | lg heavy chain pre |
| 863 | 24 | 70.6 | 1326 | 2 | S63395 | secretory phosphol | 936 | 23 | 67.6 | 147 | 2 | I46625 | rearranged T-cell |
| 864 | 24 | 70.6 | 1335 | 2 | S07245 | seaxanthine dehydrog | 937 | 23 | 67.6 | 148 | 2 | AC3074 | cell division prot |
| 865 | 24 | 70.6 | 1337 | 2 | T13948 | atypical protein k | 938 | 23 | 67.6 | 148 | 2 | F98212 | cell division prot |
| 866 | 24 | 70.6 | 1338 | 2 | T02206 | hypothetical prote | 939 | 23 | 67.6 | 150 | 2 | A83217 | conserved hypotet |
| 867 | 24 | 70.6 | 1347 | 2 | T45632 | helicase homolog F | 940 | 23 | 67.6 | 156 | 2 | F86626 | hypothetical prote |
| 868 | 24 | 70.6 | 1360 | 2 | T34302 | cell polarity prot | 941 | 23 | 67.6 | 157 | 2 | F82071 | conserved hypotet |
| 869 | 24 | 70.6 | 1366 | 2 | S36851 | L-shaped tail fibe | 942 | 23 | 67.6 | 158 | 2 | B81172 | riboflavin synthas |
| 870 | 24 | 70.6 | 1452 | 2 | T29107 | polymorphic antiag | 943 | 23 | 67.6 | 160 | 2 | T33883 | hypothetical prote |
| 871 | 24 | 70.6 | 1452 | 2 | A56395 | secretory phosphol | 944 | 23 | 67.6 | 160 | 2 | E82069 | conserved hypotet |
| 872 | 24 | 70.6 | 1589 | 2 | T13606 | hypothetical prote | 945 | 23 | 67.6 | 161 | 2 | T05496 | hypothetical prote |
| 873 | 24 | 70.6 | 1597 | 1 | BVPFSL | sol protein, large | 946 | 23 | 67.6 | 162 | 2 | C83401 | hypothetical prote |
| 874 | 24 | 70.6 | 1597 | 2 | T08428 | gene small optic l | 947 | 23 | 67.6 | 162 | 2 | T16223 | hypothetical prote |
| 875 | 24 | 70.6 | 1718 | 2 | T14603 | hypothetical prote | 948 | 23 | 67.6 | 163 | 2 | S01152 | RAB21 protein - ri |
| 876 | 24 | 70.6 | 1784 | 2 | T10532 | gag-pol polyprotei | 949 | 23 | 67.6 | 163 | 2 | T08261 | hypothetical prote |
| 877 | 24 | 70.6 | 1910 | 2 | AF0394 | probable adhesin h | 950 | 23 | 67.6 | 165 | 2 | T03392 | probable dehydrin |
| 878 | 24 | 70.6 | 1951 | 2 | B43963 | RNA viral polymera | 951 | 23 | 67.6 | 166 | 2 | B55216 | chemotaxis methyl |
| 879 | 24 | 70.6 | 1976 | 2 | I58555 | sodium channel pro | 952 | 23 | 67.6 | 166 | 2 | A97174 | chemotaxis protein |
| 880 | 24 | 70.6 | 1999 | 2 | AB2018 | hypothetical prote | 953 | 23 | 67.6 | 166 | 2 | F96024 | conserved hypotet |
| 881 | 24 | 70.6 | 2005 | 2 | A46269 | sodium channel alp | 954 | 23 | 67.6 | 166 | 2 | C84742 | hypothetical prote |
| 882 | 24 | 70.6 | 2005 | 2 | B25019 | sodium channel pro | 955 | 23 | 67.6 | 168 | 2 | B86861 | hypothetical prote |
| 883 | 24 | 70.6 | 2150 | 2 | S13553 | hypothetical prote | 956 | 23 | 67.6 | 170 | 2 | A12857 | probable acetyltra |
| 884 | 24 | 70.6 | 2151 | 1 | S16449 | genome polyprotein | 957 | 23 | 67.6 | 170 | 2 | G97634 | hypothetical prote |
| 885 | 24 | 70.6 | 2471 | 2 | T03820 | probable histidine | 958 | 23 | 67.6 | 171 | 1 | LWY1 | H+-transporting tw |
| 886 | 24 | 70.6 | 2609 | 2 | T40399 | probable transport | 959 | 23 | 67.6 | 173 | 1 | S09613 | shikimate kinase (|
| 887 | 24 | 70.6 | 2783 | 2 | T31433 | inositol 1,4,5-tri | 960 | 23 | 67.6 | 175 | 2 | S03755 | fagG protein precu |
| 888 | 24 | 70.6 | 3104 | 2 | S20473 | fatty-acid synthas | 961 | 23 | 67.6 | 175 | 2 | B53859 | ADP-ribosylation f |
| 889 | 24 | 70.6 | 3507 | 2 | T34513 | hypothetical prote | 962 | 23 | 67.6 | 177 | 2 | B72580 | hypothetical prote |
| 890 | 24 | 70.6 | 3716 | 2 | E70969 | probable PPS prote | 963 | 23 | 67.6 | 181 | 2 | S62651 | feritin - signal |
| 891 | 24 | 70.6 | 5138 | 2 | B96695 | hypothetical prote | 964 | 23 | 67.6 | 184 | 2 | F96925 | bioY protein precu |
| 892 | 23 | 67.6 | 15 | 2 | S66443 | NAD(P) transhydrog | 965 | 23 | 67.6 | 184 | 2 | AH1112 | putative secreted, |
| 893 | 23 | 67.6 | 18 | 2 | B33660 | osteoclast functio | 966 | 23 | 67.6 | 185 | 2 | C71174 | hypothetical prote |
| 894 | 23 | 67.6 | 19 | 2 | I49039 | T-cell receptor be | 967 | 23 | 67.6 | 186 | 2 | S30596 | transcription fact |
| 895 | 23 | 67.6 | 54 | 2 | PC1135 | purQ protein - Lac | 968 | 23 | 67.6 | 189 | 2 | B70924 | conserved hypotet |
| 896 | 23 | 67.6 | 73 | 2 | T14887 | hypothetical prote | 969 | 23 | 67.6 | 191 | 2 | D82821 | NADH-ubiquinone ox |
| 897 | 23 | 67.6 | 80 | 2 | S77759 | probable phosphotr | 970 | 23 | 67.6 | 192 | 2 | AB2545 | hypothetical prote |
| 898 | 23 | 67.6 | 87 | 2 | T34648 | probable SIR2 fami | 971 | 23 | 67.6 | 193 | 2 | H97224 | protease subunits |
| 899 | 23 | 67.6 | 90 | 2 | A96505 | probable glycine-r | 972 | 23 | 67.6 | 194 | 2 | S73713 | MG319 homolog H08 |
| 900 | 23 | 67.6 | 91 | 2 | F64375 | hypothetical prote | 973 | 23 | 67.6 | 194 | 2 | T72242 | conserved hypotet |
| 901 | 23 | 67.6 | 91 | 2 | H97856 | hypothetical prote | 974 | 23 | 67.6 | 195 | 2 | F85519 | hypothetical prote |
| 902 | 23 | 67.6 | 93 | 2 | AF1018 | probable membrane | 975 | 23 | 67.6 | 195 | 2 | C90669 | hypothetical prote |
| 903 | 23 | 67.6 | 93 | 2 | T14766 | hypothetical prote | 976 | 23 | 67.6 | 195 | 2 | E64755 | yagZ protein - Esc |
| 904 | 23 | 67.6 | 96 | 2 | S55012 | NADH2 dehydrogenas | 977 | 23 | 67.6 | 195 | 2 | A13153 | hypothetical prote |
| 905 | 23 | 67.6 | 98 | 2 | T10994 | NADH2 dehydrogenas | 978 | 23 | 67.6 | 196 | 2 | H64968 | acetyl CoA acetyl |

979 23 67.6 197 2 E82960 conserved hypothet
980 23 67.6 199 2 A10694 probable rekr-fami
981 23 67.6 199 2 F90923 hypothetrical prote
982 23 67.6 199 2 T49450 hypothetrical prote
983 23 67.6 199 2 B85772 hypothetrical prote
984 23 67.6 199 2 AC0290 TetR-family transc
985 23 67.6 199 2 C54922 conserved hypothet
986 23 67.6 202 2 S36293 T-cell receptor ga
987 23 67.6 204 2 JC4796 intracellular memb
988 23 67.6 208 2 D84985 endopeptidase Clp
989 23 67.6 210 2 C87251 conserved hypothet
990 23 67.6 211 2 AB2645 conserved hypothet
991 23 67.6 212 2 S37973 DNA-directed RNA p
992 23 67.6 212 2 AG1050 conserved hypothet
993 23 67.6 213 2 C83772 hypothetrical prote
994 23 67.6 215 2 T35768 hypothetrical prote
995 23 67.6 216 2 E86700 phosphoserine phos
996 23 67.6 216 2 A00545 hypothetrical prote
997 23 67.6 219 2 AD0495 probable lipoprote
998 23 67.6 219 2 AC2051 hypothetrical prote
999 23 67.6 221 1 WZBE58 gene 58 protein -
1000 23 67.6 225 2 G70340 Mg(2+) transport A

ALIGNMENTS

RESULT 1
S11740
Ig heavy chain precursor V-D-J region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S11740
R:Hayakawa, K.; Carmarck, C.E.; Hyman, R.; Hardy, R.R.
A:Submitted to the EMBL Data Library, May 1990
A:Description: Natural autoantibodies to thymocytes: Origin, VH genes, fine specificities
A:Reference number: S11740
A:Accession: S11740
A:Molecule type: mRNA
A:Residues: 1-122 <EMBL>
A:Cross-references: UNIPARC:UPI000011D0B5; EMBL:X53097; NID:G52368; PIDN:CAA37261.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:22-106/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 34; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
|||
DB 38 TSGMGVS 44

RESULT 2
PT0174
Ig heavy chain precursor V region (IdB5.7) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996
C:Accession: PT0174
R:Perfetti, V.; Borden, P.; Tao, M.H.; Morrison, S.L.; Kabat, E.A.
Mol. Immunol. 28, 505-515, 1991
A:Title: Specificity and variable region cDNA sequence of an isogenic monoclonal anti-
A:Reference number: PT0174; MUID:91287738; PMID:1712074
A:Accession: PT0174
A:Molecule type: mRNA
A:Residues: 1-143 <PER>
A:Cross-references: UNIPARC:UPI0000176976
A:Experimental source: strain BALB/c
C:Comment: IdB5.7 is an antibody to anti-alpha (1-6) dextran.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-118/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 34; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
|||
DB 50 TSGMGVS 56

RESULT 3
S73091
hypothetical protein c0624 - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C>Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C:Accession: S73091
R:Sensen, C.W.; Klenk, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penny, S.
Mol. Microbiol. 22, 175-191, 1996
A:Title: Organizational characteristics and information content of an archaeal genome: 1
A:Reference number: S73076; MUID:97055432; PMID:8899719
A:Accession: S73091
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1068 <SEN>
A:Cross-references: UNIPROT:P95871; UNIPARC:UPI00001373B1; EMBL:Y08256; NID:G1707679; P
A:Experimental source: strain P2
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1996
C:Superfamily: tricorn protease

Query Match 91.2%; Score 31; DB 2; Length 1068;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
|||
DB 97 TSGMGVS 103

RESULT 4
A39808
proteoglycan core protein, cartilage - bovine (fragments)
N:Alternate names: aggrecan; aggregating cartilage proteoglycan
C:Species: Bos primigenius taurus (cattle)
C>Date: 20-Mar-1992 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C:Accession: A34234; A27752; A39808; A27751; E29164; B27751; D27751; E27751; F2
R:Antonsson, P.; Heinegard, D.; Oldberg, A.
J. Biol. Chem. 264, 16170-16173, 1989
A:Title: The keratan sulfate-enriched region of bovine cartilage proteoglycan consists
A:Reference number: A34234; MUID:89380219; PMID:2528543
A:Accession: A34234
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 128-621 <ANT>
A:Cross-references: UNIPROT:P13608; UNIPARC:UPI0000177421; GB:J05028
R:Oldberg, A.; Antonsson, P.; Heinegard, D.
Biochem. J. 243, 255-259, 1987
A:Title: The partial amino acid sequence of bovine cartilage proteoglycan, deduced from a
A:Reference number: A27752; MUID:87270630; PMID:3111460
A:Accession: A27752
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 622-1340 <OLD>
A:Cross-references: UNIPARC:UPI0000087C64
R:Sandy, J.D.; Boynton, R.E.; Flannery, C.R.
J. Biol. Chem. 266, 8198-8205, 1991
A:Title: Analysis of the catabolism of aggrecan in cartilage explants by quantitation of
A:Reference number: A39808; MUID:91217051; PMID:2022637
A:Accession: A39808
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-28; 59-82; 131-137; 'QSET', 142-149; 196-207; 226-249; 1137-1143; 1252-1267; 1274-1
A:Cross-references: UNIPARC:UPI0000177422; UNIPARC:UPI0000177423; UNIPARC:UPI0000177424,
429; UNIPARC:UPI000017742A

R:Perin, J.P.; Bonnet, F.; Jolles, P.
 FEBS Lett. 206, 73-77, 1986
 A:Title: Structural relationship between link proteins and proteoglycan monomers.
 A:Reference number: A27751; MUID:87005253; PMID:3530809
 A:Accession: A27751
 A:Molecule type: protein
 A:Residues: 29-58;74-130;174-175,'A',177-204;208-225 <PER>
 A:Cross-references: UNIPARC:UPI000017742B; UNIPARC:UPI000017742C; UNIPARC:UPI000017742D;
 R:Perin, J.P.; Bonnet, F.; Jolles, J.; Jolles, P.
 FEBS Lett. 176, 37-42, 1984
 A:Title: Sequence data concerning the protein core of the cartilage proteoglycan monomer
 A:Reference number: A91327; MUID:85027710; PMID:6489519
 A:Accession: E29164
 A:Molecule type: protein
 A:Residues: 1230-1249 <PE2>
 A:Cross-references: UNIPARC:UPI000017742F
 C:Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EC
 C:Keywords: glycoprotein
 F:8-28/Domain: link protein repeat homology (fragment) <LNK1>
 F:29-58/Domain: link protein repeat homology (fragment) <LNK2>
 F:80-146/Domain: link protein repeat homology (fragments) <LNK3>
 F:167-248/Domain: link protein repeat homology <LNK4>
 F:1130-1250/Domain: C-type lectin homology <LCH>
 F:1257-1313/Domain: complement factor H repeat homology <FHD>
 Query Match 91.2%; Score 31; DB 2; Length 1340;
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TSGMGVS 7
 |||:||||
 Db 990 TSLGLVS 996
 RESULT 5
 T42630
 aggrecan - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T42630
 R:Hering, T.M.; Kollar, J.; Huynh, T.D.
 submitted to the EMBL Data Library, September 1996
 A:Description: Complete coding sequence of bovine aggrecan: comparative structural analy
 A:Reference number: Z22182
 A:Accession: T42630
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-2327 <HER>
 A:Cross-references: UNIPROT:P13608; UNIPARC:UPI000002B0E1; EMBL:U76615; NID:gl730259; PI
 A:Experimental source: articular chondrocytes
 C:Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EC
 C:Keywords: cartilage; chondroitin sulfate proteoglycan; extracellular matrix; glycopro
 Query Match 91.2%; Score 31; DB 2; Length 2327;
 Best Local Similarity 85.7%; Pred. No. 3.3e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TSGMGVS 7
 |||:||||
 Db 1977 TSLGLVS 1983
 RESULT 6
 B90784
 hypothetical protein ECs1242 [imported] - Escherichia coli (strain O157:H7, substrain RI
 C:Species: Escherichia coli
 C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 C:Accession: B90784
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
 DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
 A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: B90784
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-2793 <HAY>
 A:Cross-references: UNIPROT:Q8X2Q2; UNIPARC:UPI000002D2A88; GB:BA000007; PIDN:BA834665.1
 A:Experimental source: strain O157:H7, substrain RIMD 0509952
 C:Genetics:
 A:Gene: ECs1242

Query Match 91.2%; Score 31; DB 2; Length 2793;
 Best Local Similarity 85.7%; Pred. No. 3.9e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
 |||:||||
 Db 391 TAGMGVS 397

RESULT 7

D85644

hypothetical protein Z1495 [imported] - Escherichia coli (strain O157:H7, substrain EDL
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C:Accession: D85644
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe
 iller, L.; Grothbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: D85644
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-2806 <STO>
 A:Cross-references: UNIPROT:Q8X470; UNIPARC:UPI000009BB7E; GB:AE005174; NID:gl2514354;
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: Z1495

Query Match 91.2%; Score 31; DB 2; Length 2806;
 Best Local Similarity 85.7%; Pred. No. 3.9e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
 |||:||||
 Db 404 TAGMGVS 410

RESULT 8

S26465

IG heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S26465
 R:Kavaler, J.
 submitted to the EMBL Data Library, April 1991
 A:Reference number: S26459
 A:Accession: S26465
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-113 <KAV>
 A:Cross-references: UNIPARC:UPI0000115F69; EMBL:X59115; NID:G51928; PIDN:CAA41841.1; PI
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:6-90/Domain: immunoglobulin homology <IMM>

Query Match 88.2%; Score 30; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGV 6
 |||:||||
 Db 22 TSGMGV 27

```
RESULT 9
H75057
hypothetical protein PAB0965 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: H75057
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: H75057
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-188 <KAW>
A:Cross-references: UNIPROT:Q9UYQ5; UNIPARC:UPI0000063447; GB:AJ248287; GB:AL096836; NID
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB0965
C:Superfamily: hypothetical protein MJ0224

Query Match      88.2%; Score 30; DB 2; Length 188;
Best Local Similarity 85.7%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7
| | | | |
Db 148 TDGMGVS 154

RESULT 10
D70478
conserved hypothetical protein aq_2082 - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: D70478
R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: D70478
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-537 <AQF>
A:Cross-references: UNIPROT:O67856; UNIPARC:UPI0000056784; GB:AE000771; NID:G2984286; PI
A:Experimental source: strain VFS
C:Genetics:
A:Gene: aq_2082

Query Match      88.2%; Score 30; DB 2; Length 537;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSGMGV 6
| | | | |
Db 354 TSGMGV 359

RESULT 11
T38913
translation initiation factor if-2 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T38913
R:Pearson, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, February 1996
A:Reference number: Z21817
A:Accession: T38913
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-1079 <PEA>
A:Cross-references: UNIPROT:Q10251; UNIPARC:UPI000012D2C8; EMBL:Z69728; PIDN:CAA93574.1;
```

```
A:Experimental source: strain 972h-; cosmid c56F8
C:Genetics:
A:Gene: SPDB:SPAC56F8.03
A:Map position: 1
F:485-612/Domain: translation elongation factor Tu homology <ETU>
```

```
Query Match      88.2%; Score 30; DB 2; Length 1079;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 TSGMGVS 7
| | | | |
Db 829 TSGIGVS 835
```

```
RESULT 12
T26953
hypothetical protein Y47D3B.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26953
R:Matthews, L.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z20290
A:Accession: T26953
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-1136 <WIL>
A:Cross-references: UNIPROT:Q9XX01; UNIPARC:UPI000016411B; EMBL:AL031635; PIDN:CAA21041.1;
A:Experimental source: clone Y47D3B
C:Genetics:
A:Gene: CESP:Y47D3B.5
A:Map position: 3
A:Introns: 35/2; 95/3; 132/3; 175/2; 206/2; 266/1; 312/2; 386/1; 433/3; 508/3; 531/2; 59
```

```
Query Match      88.2%; Score 30; DB 2; Length 1136;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 TSGMGVS 7
| | | | |
Db 956 TSGMGVS 962
```

```
RESULT 13
T21328
hypothetical protein F25C8.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
C:Accession: T21328
R:Matthews, L.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19407
A:Accession: T21328
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-3147 <WIL>
A:Cross-references: UNIPROT:Q9XV66; UNIPARC:UPI0000164296; EMBL:Z81512; PIDN:CAB04172.1;
A:Experimental source: clone F25C8
C:Genetics:
A:Gene: CESP:F25C8.3
A:Map position: 5
A:Introns: 32/2; 57/2; 73/3; 113/3; 157/3; 366/1; 456/1; 509/1; 638/1; 773/2; 848/1; 902
```

```
Query Match      88.2%; Score 30; DB 2; Length 3147;
Best Local Similarity 85.7%; Pred. No. 7.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 TSGMGVS 7
| | | | |
Db 2748 TEGMGVS 2754
```



```
RESULT 14
PQ0098
citB protein - Salmonella typhimurium (fragment)
C:Species: Salmonella typhimurium
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: PQ0098
R:Shimamoto, T.; Izawa, H.; Daimon, H.; Iehiguro, N.; Shinagawa, M.; Sakano, Y.; Tsuda,
J. Biochem. 110, 22-28, 1991
A>Title: Cloning and nucleotide sequence of the gene (citA) encoding a citrate carrier
A:Reference number: JQ0576; MUID:92041761; PMID:1718953
A:Accession: PQ0098
A:Molecule type: DNA
A:Residues: 1-58 <SHI>
A:Cross-references: UNIPROT:P37463; UNIPARC:UPI0000170314; GB:D90203; NID:g217050; PIDN:
A:Experimental source: strain LT2
C:Genetics:
A:Gene: citB
C:Superfamily: Escherichia coli plasmid pWR60 hypothetical 42K protein

Query Match      85.3%; Score 29; DB 2; Length 58;
Best Local Similarity 83.3%; Pred. No. 19;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGV 6
DB 4 TSGMGI 9

RESULT 15
AG0585
citrate utilization protein B [imported] - Salmonella enterica subsp. enterica serovar Typh
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A>Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AG0585
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AG0585
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-379 <PAR>
A:Cross-references: UNIPARC:UPI000005A149; GB:AL513382; PIDN:CAD05153.1; PID:g16501926;
A:Genetics:
A:Gene: citB
C:Superfamily: Escherichia coli plasmid pWR60 hypothetical 42K protein

Query Match      85.3%; Score 29; DB 2; Length 379;
Best Local Similarity 83.3%; Pred. No. 13e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGV 6
DB 325 TSGMGI 330

RESULT 16
I39171
cyclin A/CDK2-associated p45 - human
C:Species: Homo sapiens (man)
C>Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 21-Jul-2000
C:Accession: I39171
R:Zhang, H.; Kobayashi, R.; Galaktionov, K.; Beach, D.
Cell 82, 915-925, 1995
A>Title: p19Skp1 and p45Skp2 are essential elements of the cyclin A-CDK2 S phase kinase.
A:Reference number: I39170; MUID:96016087; PMID:7553852
A:Accession: I39171
A>Status: preliminary
```

```
A:Molecule type: mRNA
A:Residues: 1-435 <RES>
A:Cross-references: UNIPARC:UPI0000035C93; EMBL:U33761; NID:g995825; PIDN:AAC50242.1; P;
C:Genetics:
A:Gene: Skp2
C:Keywords: cell cycle control

Query Match      85.3%; Score 29; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SGMGVS 7
DB 46 SGMGVS 51

RESULT 17
SS1739
transcription repressor ABBP1 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S60227; SS1739
R:He, G.P.; Muise, A.; Li, A.W.; Ro, H.S.
Nature 378, 92-96, 1995
A>Title: A eukaryotic transcriptional repressor with carboxypeptidase activity.
A:Reference number: S60227; MUID:96061010; PMID:7477299
A:Accession: S60227
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-719 <HE2>
A:Cross-references: UNIPROT:Q61281; UNIPARC:UPI0000039DD1; EMBL:X80478; NID:g607131; P;

Query Match      85.3%; Score 29; DB 2; Length 719;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGV 6
DB 422 TSGMGI 427

RESULT 18
AB0704
pyruvate, water dikinase (EC 2.7.9.2) - Salmonella enterica subsp. enterica serovar Typh
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A>Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AB0704
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AB0704
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-792 <PAR>
A:Cross-references: UNIPARC:UPI0000059DD6; GB:AL513382; PIDN:CAD02003.1; PID:g16502841;
A:Genetics:
A:Gene: ppsA
C:Superfamily: Escherichia coli pyruvate, water dikinase; phosphotransferase system enzym
C:Keywords: transferase

Query Match      85.3%; Score 29; DB 2; Length 792;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SGMGVS 7
DB 39 SGMGVS 44
```

```

RESULT 19
E85778
phosphoenolpyruvate synthase [imported] - Escherichia coli (strain O157:H7, substrain ED
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: E85778
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouisis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: E85778
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-792 <STO>
A:Cross-references: UNIPROT:Q8XEC4; UNIPARC:UPI00000D0268; GB:AE005174; NID:G12515710; E
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
C:Superfamily: Escherichia coli pyruvate,water dikinase; phosphotransferase system enzym
Query Match 85.3%; Score 29; DB 2; Length 792;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 SGMGVS 7
Db 39 SGMGVS 44

RESULT 20
A90930
phosphoenolpyruvate synthase [imported] - Escherichia coli (strain O157:H7, substrain RI
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: A90930
R:Hayashi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: A90930
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-792 <HAY>
A:Cross-references: UNIPROT:Q8XEC4; UNIPARC:UPI0000165476; GB:BA0000007; PIDN:BAB35832.1;
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: EC82409
C:Superfamily: Escherichia coli pyruvate,water dikinase; phosphotransferase system enzym
Query Match 85.3%; Score 29; DB 2; Length 792;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 SGMGVS 7
Db 39 SGMGVS 44

RESULT 21
S20554
pyruvate, water dikinase (EC 2.7.9.2) ppsA [validated] - Escherichia coli (strain K-12)
N:Alternate names: phosphoenolpyruvate synthase
C:Species: Escherichia coli
A:Variety: strain K12
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C:Accession: S20554; F64928; S14838
R:Niersbach, M.; Kreuzaler, F.; Geerse, R.H.; Postma, P.W.; Hirsch, H.J.
Mol. Gen. Genet. 231, 332-336, 1992
A:Title: Cloning and nucleotide sequence of the Escherichia coli K-12 ppsA gene, encodin
A:Reference number: S20554; MUID:92140374; PMID:1310524

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A:Accession: S20554
A:Molecule type: DNA
A:Residues: 1-792 <NIE>
A:Cross-references: UNIPROT:P23538; UNIPARC:UPI00001680C9; EMBL:X59381; NID:G42480; PIDN
A:Experimental source: strain K-12, substrain DH1
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: F64928
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-792 <BLAT>
A:Cross-references: UNIPARC:UPI00001680C9; GB:AE000265; GB:U00096; NID:G2367122; PIDN:AA
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: ppsA
C:Function:
A:Description: EC 2.7.9.2 [validated, MUID:66071519]; catalyzes the ATP-dependent conver
A:Pathway: gluconeogenesis
C:Superfamily: Escherichia coli pyruvate,water dikinase; phosphotransferase system enzym
C:Keywords: phosphoprotein; transferase
Query Match 85.3%; Score 29; DB 2; Length 792;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 SGMGVS 7
Db 39 SGMGVS 44

RESULT 22
I40487
surfactin synthetase / competence protein srfAC - Bacillus subtilis
N:Alternate names: surfactin synthetase srfA3
C:Species: Bacillus subtilis
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: I40487; S46969; D69718; S34987
R:Cosmina, P.; Rodriguez, F.; de Ferra, F.; Grandi, G.; Perego, M.; Venema, G.; van Sind
Mol. Microbiol. 8, 821-831, 1993
A:Title: Sequence and analysis of the genetic locus responsible for surfactin synthesis
A:Reference number: I40485; MUID:93360813; PMID:8355609
A:Accession: I40487
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1274 <RES>
A:Cross-references: UNIPROT:Q08787; UNIPARC:UPI000005FF05; EMBL:X70356; NID:G396480; PID
A:Experimental source: ATCC 21332
R:Fabret, C.; Quentin, Y.; Guisepi, A.; Bueuttil, J.; Haiech, J.; Denizot, F.
submitted to the EMBL Data Library, March 1993
A:Reference number: S46967
A:Accession: S46969
A:Molecule type: DNA
A:Residues: 1-25, 'A', 27-32, 'S', 34-646 <FAB>
A:Cross-references: UNIPARC:UPI00000B4D29; EMBL:X72672; NID:G516358; PID:G516361
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrati, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377

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A:Accession: D69718
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1274 <KUN>
 A:Cross-references: UNIPARC:UPI000005FF05; GB:Z99105; GB:AL009126; NID:92632457; PIDN:CA
 A:Experimental source: strain 168
 C:Genetics:

A:Gene: srfAC; srfA3
 C:Superfamily: peptidase synthetase ppsE; acetate-CoA ligase homology; acyl carrier protein
 C:Keywords: antibiotic biosynthesis; carrier protein; phosphopantetheine; phosphoprotein
 F:510-954/Domain: acetate-CoA ligase homology <ACL1>
 F:971-1038/Domain: acyl carrier protein homology <ACP1>
 F:1003/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

Query Match 85.3%; Score 29; DB 1; Length 1274;
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQMGVS 7
 |||||
 DB 809 SQMGVS 814

RESULT 23
 T20406
 Hypothetical protein E01G6.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T20406
 R:Illoyd, C.
 submitted to the EMBL Data Library, February 1996

A:Reference number: Z19270
 A:Accession: T20406
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-1391 <WIL>
 A:Cross-references: UNIPROT:Q19021; UNIPARC:UPI000007DCB8; EMBL:Z69717; PIDN:CAA93531.1;
 A:Experimental source: clone E01G6
 C:Genetics:
 A:Gene: CESP:E01G6.1
 A:Map position: X
 A:Introns: 44/1; 84/3; 175/1; 389/2; 423/1; 501/1; 1358/1

Query Match 85.3%; Score 29; DB 2; Length 1391;
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQMGVS 7
 |||||
 DB 878 SQMGVS 883

RESULT 24
 A49442
 Ig heavy chain V region (50.1) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
 C:Accession: A49442
 R:Stura, E.A.; Stanfield, R.L.; Fieser, G.G.; Silver, S.; Roguska, M.; Hincapie, L.M.; S
 Proteins 14, 499-508, 1992
 A:Title: Crystallization, sequence, and preliminary crystallographic data for an antipep
 A:Reference number: A49442; MUID:93066166; PMID:1438187
 A:Accession: A49442

A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-107 <STU>
 A:Cross-references: UNIPARC:UPI00001768FD
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:7-31/Domain: immunoglobulin homology <IMM>

Query Match 82.4%; Score 28; DB 2; Length 107;
 Best Local Similarity 85.7%; Pred. No. 60;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TSGMGVS 7
 |||||
 DB 23 TYGMGVS 29

RESULT 25

PQ0791
 H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain - tomato chloroplast
 N:Alternate names: ATPase beta chain
 C:Species: chloroplast Lycopersicon esculentum (tomato)
 C:Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 31-Dec-2004
 C:Accession: PQ0791
 R:Kawagoe, Y.; Kikuta, Y.
 Theor. Appl. Genet. 81, 13-20, 1991

A:Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.).
 A:Reference number: JQ2306
 A:Accession: PQ0791
 A:Molecule type: DNA
 A:Residues: 1-122 <KAW>
 A:Cross-references: UNIPROT:Q9SCB5; UNIPARC:UPI0000175B6D
 C:Genetics:

A:Genome: chloroplast
 C:Superfamily: H(+)-transporting ATP synthase; H+-transporting ATP synthase alpha chain
 C:Keywords: ATP biosynthesis; chloroplast; hydrolase; membrane-associated complex; thyl-

Query Match 82.4%; Score 28; DB 2; Length 122;
 Best Local Similarity 85.7%; Pred. No. 69;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
 |||||
 DB 7 TSGSGVS 13

RESULT 26

PQ0792
 H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain - potato chloroplast (cv. 150
 C:Species: chloroplast Solanum tuberosum (potato)
 C:Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 31-Dec-2004
 C:Accession: PQ0792
 R:Kawagoe, Y.; Kikuta, Y.
 Theor. Appl. Genet. 81, 13-20, 1991

A:Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.).
 A:Reference number: JQ2306
 A:Accession: PQ0792
 A:Molecule type: DNA
 A:Residues: 1-122 <KAW>
 A:Cross-references: UNIPROT:Q7M2H0; UNIPARC:UPI0000175E7D
 C:Genetics:

A:Gene: atpB
 A:Genome: chloroplast
 C:Superfamily: H(+)-transporting ATP synthase; H+-transporting ATP synthase alpha chain
 C:Keywords: ATP biosynthesis; chloroplast; hydrolase; thylakoid

Query Match 82.4%; Score 28; DB 2; Length 122;
 Best Local Similarity 85.7%; Pred. No. 69;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
 |||||
 DB 7 TSGSGVS 13

RESULT 27

PQ0793
 H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain - potato chloroplast (fragmen
 N:Alternate names: ATPase beta chain
 C:Species: chloroplast Solanum tuberosum (potato)
 C:Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 31-Dec-2004
 C:Accession: PQ0793; PQ0794
 R:Kawagoe, Y.; Kikuta, Y.

Theor. Appl. Genet. 81, 13-20, 1991
A:Title: Chloroplast DNA evolution in potato (*Solanum tuberosum* L.).
A:Reference number: JQ2306
A:Accession: PQ0793
A:Molecule type: DNA
A:Residues: 1-122 <KWI>
A:Cross-references: UNIPROT:Q7M2H1; UNIPARC:UPI00000175E7C
A:Experimental source: cv. W553-4
A:Accession: PQ0794
A:Molecule type: DNA
A:Residues: 1-122 <KW2>
A:Cross-references: UNIPARC:UPI00000175E7C
A:Experimental source: cv. I. Cobbler
C:Genetics:
A:Gene: atpB
A:Genome: chloroplast
C:Superfamily: H(+)-transporting ATP synthase; H+-transporting ATP synthase alpha chain
C:Keywords: ATP biosynthesis; chloroplast; hydrolase; thylakoid

Query Match 82.4%; Score 28; DB 2; Length 122;
Best Local Similarity 85.7%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7
| | | | |
Db 7 TSGSGVS 13

RESULT 28
F89929
hypothetical protein SA1333 [imported] - *Staphylococcus aureus* (strain N315)
C:Species: *Staphylococcus aureus*
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: F89929
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: F89929
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-251 <KUP>
A:Cross-references: UNIPROT:Q99TZ1; UNIPARC:UPI000000CA987; GB:BA0000018; PID:g13701301; F
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA1333

Query Match 82.4%; Score 28; DB 2; Length 122;
Best Local Similarity 85.7%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7
| | | | |
Db 7 TSGSGVS 13

RESULT 29
A40578
beta IG-M2 protein precursor - mouse
C:Species: *Mus musculus* (house mouse)
C:Date: 06-Mar-1992 #sequence_revision 06-Mar-1992 #text_change 31-Dec-2004
C:Accession: A40578; A53228
R:Brunner, A.; Chinn, J.; Neubauer, M.; Purchio, A.F.
DNA Cell Biol. 10, 293-300, 1991
A:Title: Identification of a gene family regulated by transforming growth factor-beta.
A:Reference number: A40578; MUID:91229699; PMID:2029337
A:Accession: A40578
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-348 <BRU>
A:Cross-references: UNIPROT:P29568; UNIPARC:UPI0000028AEF; GB:M80263; NID:g201945; PIDN:

Query Match 82.4%; Score 28; DB 2; Length 251;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7
| | | | |
Db 12 TSGGLS 18

RESULT 30
A40551
connective tissue growth factor - human
C:Species: *Homo sapiens* (man)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 31-Dec-2004
C:Accession: A40551; S44205
R:Bradham, D.M.; Igarashi, A.; Potter, R.L.; Grotendorst, G.R.
J. Cell Biol. 114, 1285-1294, 1991
A:Title: Connective tissue growth factor: a cysteine-rich mitogen secreted by human vasc
A:Reference number: A40551; MUID:91373462; PMID:1654338
A:Accession: A40551
A:Molecule type: mRNA
A:Residues: 1-349 <BRA>
A:Cross-references: UNIPROT:P29279; UNIPARC:UPI000003FD13; GB:M92934; GB:M36965; GB:S562
R:Oemar, B.S.; Werner, A.; Yang, Z.; Garnier, J.M.; Gentz, R.; Luescher, T.F.
submitted to the EMBL Data Library, April 1994
A:Description: Differential cloning and expression of human connective tissue growth fac
A:Reference number: S44205
A:Accession: S44205
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-349 <OEM>
A:Cross-references: UNIPARC:UPI000003FD13; EMBL:X78947; NID:g474933; PID:g474934
C:Superfamily: IGFBP-related protein, CNN type

Query Match 82.4%; Score 28; DB 2; Length 349;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7
| | | | |
Db 212 TCGMGIS 218

RESULT 31
S57177
branched-chain-amino-acid transaminase (EC 2.6.1.42) BAT2, cytosolic - yeast (*Saccharomy*
N:Alternate names: protein J2209; protein YJR148w; TWT2 protein
C:Species: *Saccharomyces cerevisiae*
C:Date: 23-Aug-1995 #sequence_revision 08-Sep-1995 #text_change 05-Oct-2004
C:Accession: S57177; S61565
R:Scarcez, T.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S57169
A:Accession: S57177
A:Molecule type: DNA
A:Residues: 1-376 <SCA>
A:Cross-references: UNIPROT:P47176; UNIPARC:UPI0000052E2B; EMBL:Z49648; NID:g1015896; PI
R:Kispal, G.; Lill, R.; Neupert, N.
submitted to the EMBL Data Library, April 1995
A:Reference number: S61565

R:Ryseck, R.P.; Macdonald-Bravo, H.; Mattei, M.G.; Bravo, R.
Cell Growth Differ. 2, 225-233, 1991
A:Title: Structure, mapping, and expression of fisp-12, a growth factor-inducible gene
A:Reference number: A53228; MUID:91363290; PMID:1888698
A:Accession: A53228
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-160, 'K', 162-348 <RYS>
A:Cross-references: UNIPARC:UPI000003FD12; GB:M70641; NID:g193313; PIDN:AAA37627.1; PID:
C:Genetics:
A:Gene: fisp-12
C:Superfamily: IGFBP-related protein, CNN type

Query Match 82.4%; Score 28; DB 2; Length 348;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7
| | | | |
Db 211 TCGMGIS 217

RESULT 30
A40551
connective tissue growth factor - human
C:Species: *Homo sapiens* (man)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 31-Dec-2004
C:Accession: A40551; S44205
R:Bradham, D.M.; Igarashi, A.; Potter, R.L.; Grotendorst, G.R.
J. Cell Biol. 114, 1285-1294, 1991
A:Title: Connective tissue growth factor: a cysteine-rich mitogen secreted by human vasc
A:Reference number: A40551; MUID:91373462; PMID:1654338
A:Accession: A40551
A:Molecule type: mRNA
A:Residues: 1-349 <BRA>
A:Cross-references: UNIPROT:P29279; UNIPARC:UPI000003FD13; GB:M92934; GB:M36965; GB:S562
R:Oemar, B.S.; Werner, A.; Yang, Z.; Garnier, J.M.; Gentz, R.; Luescher, T.F.
submitted to the EMBL Data Library, April 1994
A:Description: Differential cloning and expression of human connective tissue growth fac
A:Reference number: S44205
A:Accession: S44205
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-349 <OEM>
A:Cross-references: UNIPARC:UPI000003FD13; EMBL:X78947; NID:g474933; PID:g474934
C:Superfamily: IGFBP-related protein, CNN type

Query Match 82.4%; Score 28; DB 2; Length 348;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7
| | | | |
Db 211 TCGMGIS 217

RESULT 30
A40551
connective tissue growth factor - human
C:Species: *Homo sapiens* (man)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 31-Dec-2004
C:Accession: A40551; S44205
R:Bradham, D.M.; Igarashi, A.; Potter, R.L.; Grotendorst, G.R.
J. Cell Biol. 114, 1285-1294, 1991
A:Title: Connective tissue growth factor: a cysteine-rich mitogen secreted by human vasc
A:Reference number: A40551; MUID:91373462; PMID:1654338
A:Accession: A40551
A:Molecule type: mRNA
A:Residues: 1-349 <BRA>
A:Cross-references: UNIPROT:P29279; UNIPARC:UPI000003FD13; GB:M92934; GB:M36965; GB:S562
R:Oemar, B.S.; Werner, A.; Yang, Z.; Garnier, J.M.; Gentz, R.; Luescher, T.F.
submitted to the EMBL Data Library, April 1994
A:Description: Differential cloning and expression of human connective tissue growth fac
A:Reference number: S44205
A:Accession: S44205
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-349 <OEM>
A:Cross-references: UNIPARC:UPI000003FD13; EMBL:X78947; NID:g474933; PID:g474934
C:Superfamily: IGFBP-related protein, CNN type

Query Match 82.4%; Score 28; DB 2; Length 349;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7
| | | | |
Db 212 TCGMGIS 218

RESULT 31
S57177
branched-chain-amino-acid transaminase (EC 2.6.1.42) BAT2, cytosolic - yeast (*Saccharomy*
N:Alternate names: protein J2209; protein YJR148w; TWT2 protein
C:Species: *Saccharomyces cerevisiae*
C:Date: 23-Aug-1995 #sequence_revision 08-Sep-1995 #text_change 05-Oct-2004
C:Accession: S57177; S61565
R:Scarcez, T.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S57169
A:Accession: S57177
A:Molecule type: DNA
A:Residues: 1-376 <SCA>
A:Cross-references: UNIPROT:P47176; UNIPARC:UPI0000052E2B; EMBL:Z49648; NID:g1015896; PI
R:Kispal, G.; Lill, R.; Neupert, N.
submitted to the EMBL Data Library, April 1995
A:Reference number: S61565

A:Accession: S61565
A:Molecule type: mRNA
A:Residues: 'NSARV', 2-147, 'MA', 150-169, 'LWVLIIT', 176, 'LDLRSDWKPLIMQELAQEA', 199-206, 'VR
A:Cross-references: UNIPARC:UPI0000168EA4; EMBL:X86568; NID:g1107862; PIDN:CAA60376.1; B
C:Genetics:
A:Gene: SGD:BAT2; TWT2
A:Cross-references: MIPS:YJR148w; SGD:S0003909
A:Map position: 10R
C:Superfamily: branched-chain amino acid aminotransferase, BCAT1 type
C:Keywords: aminotransferase; cytosol

Query Match 82.4%; Score 28; DB 2; Length 376;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7
|:|:|:|
Db 151 TAGLGVS 157

RESULT 32
F32252
gene III protein - Acinetobacter calcoaceticus
C:Species: Acinetobacter calcoaceticus
C:Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 09-Jul-2004
C:Accession: F32252; T01635; T01636
R:Goosen, N.; Horeman, H.P.A.; Huinen, R.G.M.; van de Putte, P.
J. Bacteriol. 171, 447-455, 1989
A:Title: Acinetobacter calcoaceticus genes involved in biosynthesis of the coenzyme pyrri
A:Reference number: A32252; MUID:89123056; PMID:2536663
A:Accession: F32252
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-384 <GOO>
A:Cross-references: UNIPROT:P07782; UNIPARC:UPI0000132133; GB:X06452; NID:G38740; PIDN:C
A:Experimental source: strain LMD 79.41
C:Function:
A:Description: involved in synthesis of coenzyme pyrrolo-quinoline-quinone (PQQ)

Query Match 82.4%; Score 28; DB 2; Length 384;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7
|:|:|:|
Db 90 TSGMGLT 96

RESULT 33
AE3500
phosphate transport system permease protein pstA [imported] - Brucella melitensis (strai
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AE3500
R:DeIvecchio, V.G.; Kapatal, R.J.; Patra, G.; Mujar, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltman, E.; Selkov, E.; Elizer, P.H.; Hagius, S.; O'Callaghan, D.; Letese
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A:Reference number: AD3252; PMID:11756688
A:Accession: AE3500
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-436 <KUR>
A:Cross-references: UNIPROT:Q8VE91; UNIPARC:UPI00000582A6; GB:AE008917; PIDN:AAL53168.1;
A:Experimental source: strain 16W
C:Genetics:
A:Gene: BME11987
A:Map position: 1

Query Match 82.4%; Score 28; DB 2; Length 436;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7
|:|:|:|
Db 211 TSLGLVA 217

RESULT 34
PWNTB
H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain - common tobacco chloroplast
N:Alternate names: CFI-beta; coupling factor-1 beta; proton-ATPase beta subunit
C:Species: chloroplast Nicotiana tabacum (common tobacco)
C:Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 31-Dec-2004
C:Accession: A01027; S15726; A43264
R:Shinozaki, K.; Deno, H.; Kato, A.; Sugiyama, M.
Gene 24, 147-155, 1983
A:Title: Overlap and cotranscription of the genes for the beta and epsilon subunits of t
A:Reference number: A91502; MUID:84059075; PMID:6227526
A:Accession: A01027
A:Molecule type: DNA
A:Residues: 1-498 <SHI>
A:Cross-references: UNIPROT:P00826; UNIPARC:UPI000012648D; EMBL:X00507; NID:g343480; PID
A:Experimental source: variety BY4
R:Avni, A.; Anderson, J.D.; Rochaix, J.D.; Edelman, M.
submitted to the EMBL Data Library, July 1991
A:Description: The receptor site for tentoxin sensitivity in chloroplasts.
A:Reference number: S15722
A:Accession: S15726
A:Molecule type: DNA
A:Residues: 1-498 <AVN>
A:Cross-references: UNIPARC:UPI000012648D; EMBL:X61319; NID:g11788; PIDN:CAA43612.1; P
R:Avni, A.; Anderson, J.D.; Holland, N.; Rochaix, J.D.; Gromet-Elhanan, Z.; Edelman, M.
Science 257, 1245-1247, 1992
A:Title: Tentoxin sensitivity of chloroplasts determined by codon 83 of beta subunit of
A:Reference number: A43264; MUID:92390714; PMID:1387730
A:Accession: A43264
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-76, 'V', 78-153, 'K', 155-498 <AV2>
A:Cross-references: UNIPARC:UPI0000172E12
A:Experimental source: var. Xanthi, tentoxin-resistant
A:Note: sequence extracted from NCBI backbone (NCBI:P112485)
A:Note: variants of Nicotiana sp. and engineered sequences with Glu-83 showed tentoxin r
C:Genetics:
A:Genome: chloroplast
C:Superfamily: H(+)-transporting ATP synthase; H+-transporting ATP synthase alpha chain
C:Keywords: ATP biosynthesis; chloroplast; hydrolase; membrane-associated complex; nucle
P:172-179/Region: nucleotide-binding motif A (P-loop)
F:198-374/Domain: H+-transporting ATP synthase alpha chain homology <ATP>

Query Match 82.4%; Score 28; DB 1; Length 498;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7
|:|:|:|
Db 7 TSGSGVS 13

RESULT 35
PWNTB9
H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain - tobacco chloroplast
C:Species: chloroplast Nicotiana sp. (tobacco)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 31-Dec-2004
C:Accession: S15725
R:Avni, A.; Anderson, J.D.; Rochaix, J.D.; Edelman, M.
submitted to the EMBL Data Library, July 1991
A:Description: The receptor site for tentoxin sensitivity in chloroplasts.
A:Reference number: S15722
A:Accession: S15725
A:Molecule type: DNA
A:Residues: 1-498 <AVN>
A:Cross-references: UNIPROT:P26531; UNIPARC:UPI00000126468; EMBL:X61317; NID:g11765; PIDN
C:Genetics:
A:Gene: atpB

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A:Genome: chloroplast
C:Superfamily: H(+)-transporting ATP synthase; H+-transporting ATP synthase alpha chain
C:Keywords: ATP biosynthesis; chloroplast; hydrolase; membrane-associated complex; nucle
F:172-179/Region: nucleotide-binding motif A (P-loop)
F:198-374/Domain: H+-transporting ATP synthase alpha chain homology <ATP>

  Query Match      82.4%; Score 28; DB 1; Length 498;
  Best Local Similarity 85.7%; Pred. No. 2.9e+02;
  Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1 TSGMGVS 7
    |||||
Db  7 TSGSGVS 13

RESULT 36
PWNTBB
H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain - Bigelow's tobacco chloroplast
C:Species: chloroplast Nicotiana bigelovii (Bigelow's tobacco)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 31-Dec-2004
C:Accession: S15722
R:Avni, A.; Anderson, J.D.; Rochhaix, J.D.; Edelman, M.
submitted to the EMBL Data Library, July 1991
A:Description: The receptor site for tentoxin sensitivity in chloroplasts.
A:Reference number: S15722
A:Accession: S15722
A:Molecule type: DNA
A:Residues: 1-498 <AVN>
A:Cross-references: UNIPROT:P26529; UNIPARC:UPI0000126466; EMBL:X61316; NID:g11745; PIDN
C:Genetics:
A:Gene: atpB
A:Genome: chloroplast
C:Superfamily: H(+)-transporting ATP synthase; H+-transporting ATP synthase alpha chain
C:Keywords: ATP biosynthesis; chloroplast; hydrolase; membrane-associated complex; nucle
F:172-179/Region: nucleotide-binding motif A (P-loop)
F:198-374/Domain: H+-transporting ATP synthase alpha chain homology <ATP>

  Query Match      82.4%; Score 28; DB 1; Length 498;
  Best Local Similarity 85.7%; Pred. No. 2.9e+02;
  Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1 TSGMGVS 7
    |||||
Db  7 TSGSGVS 13

RESULT 37
PWNTBC
H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain - curled-leaved tobacco chloroplast
C:Species: chloroplast Nicotiana plumbaginifolia (curled-leaved tobacco)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 31-Dec-2004
C:Accession: S15723
R:Avni, A.; Anderson, J.D.; Rochhaix, J.D.; Edelman, M.
submitted to the EMBL Data Library, July 1991
A:Description: The receptor site for tentoxin sensitivity in chloroplasts.
A:Reference number: S15722
A:Accession: S15723
A:Molecule type: DNA
A:Residues: 1-498 <AVN>
A:Cross-references: UNIPROT:P26529; UNIPARC:UPI0000126466; EMBL:X61320; NID:g11756; PIDN
C:Genetics:
A:Gene: atpB
A:Genome: chloroplast
C:Superfamily: H(+)-transporting ATP synthase; H+-transporting ATP synthase alpha chain
C:Keywords: ATP biosynthesis; chloroplast; hydrolase; membrane-associated complex; nucle
F:172-179/Region: nucleotide-binding motif A (P-loop)
F:198-374/Domain: H+-transporting ATP synthase alpha chain homology <ATP>

  Query Match      82.4%; Score 28; DB 1; Length 498;
  Best Local Similarity 85.7%; Pred. No. 2.9e+02;
  Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1 TSGMGVS 7
    |||||
Db  7 TSGSGVS 13

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Db  7 TSGSGVS 13
    |||||

RESULT 38
PWNTBZ
H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain - Aztec tobacco chloroplast
C:Species: chloroplast Nicotiana rustica (Aztec tobacco)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 31-Dec-2004
C:Accession: S15724
R:Avni, A.; Anderson, J.D.; Rochhaix, J.D.; Edelman, M.
submitted to the EMBL Data Library, July 1991
A:Description: The receptor site for tentoxin sensitivity in chloroplasts.
A:Reference number: S15722
A:Accession: S15724
A:Molecule type: DNA
A:Residues: 1-498 <AVN>
A:Cross-references: UNIPROT:P26530; UNIPARC:UPI0000126467; EMBL:X61318; NID:g11763; PIDN
C:Genetics:
A:Gene: atpB
A:Genome: chloroplast
C:Superfamily: H(+)-transporting ATP synthase; H+-transporting ATP synthase alpha chain
C:Keywords: ATP biosynthesis; chloroplast; hydrolase; membrane-associated complex; nucle
F:172-179/Region: nucleotide-binding motif A (P-loop)
F:198-374/Domain: H+-transporting ATP synthase alpha chain homology <ATP>

  Query Match      82.4%; Score 28; DB 1; Length 498;
  Best Local Similarity 85.7%; Pred. No. 2.9e+02;
  Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1 TSGMGVS 7
    |||||
Db  7 TSGSGVS 13

RESULT 39
T05473
hypothetical protein T805.120 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T05473
R:Bevan, M.; Wedler, H.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schuelle
submitted to the Protein Sequence Database, February 1998
A:Reference number: Z15417
A:Accession: T05473
A:Molecule type: DNA
A:Residues: 1-508 <BEV>
A:Cross-references: UNIPROT:O49714; UNIPARC:UPI00000A0E02; EMBL:AL021890
C:Genetics:
A:Map position: 4
A:Introns: 111/3; 322/2; 341/2; 434/1; 473/3; 482/1
A:Note: T805.120

  Query Match      82.4%; Score 28; DB 2; Length 508;
  Best Local Similarity 83.3%; Pred. No. 3e+02;
  Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  2 SGMGVS 7
    |||||
Db  76 SGMGIS 81

RESULT 40
B81711
conserved hypothetical protein TC0355 [imported] - Chlamydia muridarum (strain Nigg)
C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: B81711
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

```

A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: B81711
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-558 <TEXT>
A;Cross-references: UNIPROT:Q9PKV6; UNIPARC:UPI00000578C2; GB:AE002303; GB:AE002160; NID
A;Experimental source: strain Nigg (MoPh)
C;Genetics:
A;Gene: TC0355

Query Match 82.4%; Score 28; DB 2; Length 558;
Best Local Similarity 71.4%; Pred. No. 3.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
|||:|
Db 324 TSLGLVT 330

RESULT 41

VCLJSA

env polyprotein - simian AIDS retrovirus SRV-1
N;Alternate names: coat polyprotein
N;Contains: coat protein gp20; coat protein gp70
C;Species: simian AIDS retrovirus SRV-1
A;Note: host Macaca mulatta (rhesus macaque)
C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 16-Jul-1999
C;Accession: A04000
R;Power, M.D.; Marx, P.A.; Bryant, M.L.; Gardner, M.B.; Barr, P.J.; Luciw, P.A.
Science 231, 1567-1572, 1986
A;Title: Nucleotide sequence of SRV-1, a type D simian acquired immune deficiency syndro
A;Reference number: A94711; MUID:86151668; PMID:3006247
A;Accession: A04000
A;Molecule type: DNA

A;Residues: 1-587 <POW>
A;Cross-references: UNIPARC:UPI000012A05B; GB:M11841; NID:g334746; PIDN:AAA47733.1; PID:
C;Comment: The env polyprotein contains coat protein gp70 and coat protein gp20; however
C;Genetics:
A;Gene: env
C;Superfamily: type C retrovirus env polyprotein
C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein
F;120,237,266,271,277,280,295,308,322,328,340,358,488,565/Binding site: carbohydrate (As

Query Match 82.4%; Score 28; DB 1; Length 587;
Best Local Similarity 71.4%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
|||:|
Db 416 TAGLGVS 422

RESULT 42

T01351

subtilisin-like proteinase homolog F6N15.3 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01351
R;Ryan, E.; Edwards, J.; Pape, K.
submitted to the EMBL Data Library, May 1998
A;Description: The sequence of A. thaliana F6N15.
A;Reference number: Z14297
A;Accession: T01351

A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: DNA

A;Residues: 1-706 <RYA>
A;Cross-references: UNIPROT:O81324; UNIPARC:UPI00000488CB; EMBL:AF069299; NID:g3193311;
A;Experimental source: cultivar Columbia
C;Genetics:

A;Map position: 4

A;Introns: 10/2; 43/1; 91/1; 126/2; 297/3; 330/2; 418/2; 454/3; 526/1
A;Note: F6N15.3
C;Superfamily: subtilisin-like proteinase ag12; subtilisin homology

Query Match 82.4%; Score 28; DB 2; Length 706;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SGMGVS 7
|||:|
Db 297 SGMGIS 302

RESULT 43

A61262

collagen alpha 1(XVII) chain - human (fragment)
N;Alternate names: bullous pemphigoid 180K autoantigen BPAG2; bullous pemphigoid antigen
C;Species: Homo sapiens (man)
C;Date: 12-May-1994 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
C;Accession: I56325; I55345; A61262
R;Giudice, G.J.; Emery, D.J.; Diaz, L.A.
J. Invest. Dermatol. 99, 243-250, 1992
A;Title: Cloning and primary structural analysis of the Bullous pemphigoid autoantigen,
A;Reference number: I56325; MUID:92381323; PMID:1324962
A;Accession: I56325
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-1532 <RES>
A;Cross-references: UNIPROT:Q9UMD9; UNIPARC:UPI000006F72A; GB:M63730; NID:gl79520; PIDN:AAA51839.1; PID:
R;Li, K.H.; Sawamura, D.; Giudice, G.J.; Diaz, L.A.; Mattei, M.G.; Chu, M.L.; Uitto, J.
J. Biol. Chem. 266, 24064-24069, 1991
A;Title: Genomic organization of collagen domains and chromosomal assignment of humar
A;Reference number: I55345; MUID:92084712; PMID:1748679
A;Accession: I55345
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA

A;Residues: 543-890, 'P' <RE2>
A;Cross-references: UNIPARC:UPI000006F72A; GB:M63730; NID:gl79520; PIDN:AAA51839.1; PID:
R;Giudice, G.J.; Squiquera, H.L.; Elias, P.M.; Diaz, L.A.
J. Clin. Invest. 87, 734-738, 1991
A;Title: Identification of two collagen domains within the bullous pemphigoid autoantigen
A;Reference number: A61262; MUID:91123476; PMID:1846881
A;Accession: A61262

A;Molecule type: mRNA
A;Residues: 543-890, 'P' <GIU>
A;Cross-references: UNIPARC:UPI000006F72A
C;Genetics:
A;Gene: GDB:COL17A1; BPAG2: BP180
A;Cross-references: GDB:I31396; OMIM:113811
A;Map position: 10q24.3-10q24.3

Query Match 82.4%; Score 28; DB 2; Length 1532;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
|||:|
Db 1105 TSGYGSV 1111

RESULT 44

I50726

cation-independent mannose-6-phosphate receptor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50726

R;Zhou, M.; Ma, Z.; Sly, W.S.
Proc. Natl. Acad. Sci. U.S.A. 92, 9762-9766, 1995

A;Title: Cloning and expression of the cDNA of chicken cation-independent mannose-6-phos
A;Reference number: I50726; MUID:96003859; PMID:7568213
A;Accession: I50726

A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-2470 <ZHO>

A;Cross-references: UNIPROT:Q90681; UNIPARC:UPI00000FB0C6; EMBL:U35037; NID:gl019118; PI
C;Superfamily: mannose 6-phosphate receptor, cation-independent; fibronectin type II rep

F:1882-1921/Domain: fibronectin type II repeat homology <2F1>

Query Match 82.4%; Score 28; DB 2; Length 2470;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7
||| |||

Db 1837 TSGSGVS 1843

RESULT 45

D70730

hypothetical protein RV2272 - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: D70730
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70730
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-122 <COL>
A;Cross-references: UNIPROT:Q50691; UNIPARC:UPI000013B91E; GB:Z77163; GB:AL123456; NID:959364
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: RV2272

Query Match 79.4%; Score 27; DB 2; Length 122;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSGMGV 6
||| |||

Db 70 TSGMGL 75

RESULT 46

VCCSV

coat protein - maize streak virus (Nigerian isolate)

C;Species: maize streak virus
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C;Accession: A04173
R;Mullineaux, P.M.; Donson, J.; Morris-Kreinich, B.A.M.; Boulton, M.I.; Davies, J.W.
EMBO J. 3, 3063-3068, 1984
A;Title: The nucleotide sequence of maize streak virus DNA.
A;Reference number: A90997; MUID:85126910; PMID:6526009
A;Accession: A04173
A;Molecule type: DNA
A;Residues: 1-244 <MUL>
A;Cross-references: UNIPROT:P06448; UNIPARC:UPI000000039D; GB:X01633; GB:X02026; NID:959365
C;Superfamily: maize streak virus coat protein
C;Keywords: coat protein

Query Match 79.4%; Score 27; DB 1; Length 244;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSGMGV 6
||| |||

Db 191 TSGLGV 196

RESULT 47

VCCVZ

coat protein - maize streak virus (Kenyan isolate)

C;Species: maize streak virus
A;Note: host Zea mays (maize)

C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 09-Jul-2004
C;Accession: A04172

R;Howell, S.H.

Nucleic Acids Res. 12, 7359-7375, 1984

A;Title: Physical structure and genetic organisation of the genome of maize streak virus

A;Reference number: A93538; MUID:85037917; PMID:6493977

A;Accession: A04172

A;Molecule type: DNA

A;Residues: 1-244 <HOW>

A;Cross-references: UNIPROT:P03569; UNIPARC:UPI0000127D6A; GB:X01089; NID:959364; PIDN:C

C;Superfamily: maize streak virus coat protein

C;Keywords: coat protein

Query Match 79.4%; Score 27; DB 1; Length 244;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSGMGV 6
||| |||

Db 191 TSGLGV 196

RESULT 48

S04805

coat protein - maize streak virus (South African isolate)

C;Species: maize streak virus
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S04805

R;Lazarowitz, S.G.

Nucleic Acids Res. 16, 229-249, 1988

A;Title: Infectivity and complete nucleotide sequence of the genome of a South African isolate
A;Reference number: S04804; MUID:88124198; PMID:2829117
A;Accession: S04805
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-244 <LAZ>
A;Cross-references: UNIPROT:P14986; UNIPARC:UPI0000127D6B; EMBL:X00514; NID:959365; PIDN:C

Query Match 79.4%; Score 27; DB 2; Length 244;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSGMGV 6
||| |||

Db 191 TSGLGV 196

RESULT 49

T10112

capsid protein - maize streak virus (isolate SP2)

C;Species: maize streak virus
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10112

R;Inard, M.; Granier, M.; Frutos, R.; Reynaud, B.; Peterschmitt, M.

J. Gen. Virol. 79, 3091-3099, 1998

A;Title: Quasiespecies nature of three related maize streak virus isolates obtained through serial passage
A;Reference number: Z16955; MUID:99094636; PMID:9880027
A;Accession: T10112
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-244 <ISN>

A;Cross-references: UNIPROT:O73473; UNIPARC:UPI000000F721F; EMBL:AJ225008; NID:92980718;

C;Genetics:

A;Gene: CP

C;Superfamily: maize streak virus coat protein

C;Keywords: capsid protein

Query Match 79.4%; Score 27; DB 2; Length 244;

Best Local Similarity 83.3%; Pred. No. 2.3e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSGMGV 6

Db 191 TSGMGVS 196

RESULT 50
H90130
60S ribosomal protein L1 [imported] - Giardia theta nucleomorph
C:Species: nucleomorph Giardia theta
A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H90130
R:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reid
Nature 410, 1091-1096, 2001
A:Title: The highly reduced genome of an enslaved algal nucleus.
A:Reference number: A99082; MUID:11323671; PMID:11323671
A:Accession: H90130
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-255 <DOU>
A:Cross-references: UNIPROT:Q98S44; UNIPARC:UPI000009423E; GB:AF083031; NID:gl3794362; F
C:Genetics:
A:Gene: rpl1
A:Map position: 3
A:Genome: nucleomorph
C:Superfamily: rat ribosomal protein L4
C:Keywords: nucleomorph

Query Match 79.4%; Score 27; DB 2; Length 255;
Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
|:|:|:|
Db 52 TAGMGTS 58

Search completed: February 23, 2006, 09:51:34
Job time : 23.9077 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2006, 09:29:53 ; Search time 60.3077 Seconds
(without alignments)
81.892 Million cell updates/sec

Title: US-10-723-872-22

Perfect score: 34

Sequence: 1 TSGMGVS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 34 | 100.0 | 254 | 2 | Q6CON5 YARROWIA |
| 2 | 31 | 91.2 | 15 | 2 | Q9WTA3 GLUCONACT |
| 3 | 31 | 91.2 | 197 | 2 | Q5HXS1 GLUCONACT |
| 4 | 31 | 91.2 | 219 | 2 | Q4R0Z9 BILHA |
| 5 | 31 | 91.2 | 285 | 2 | Q4IDB8 GIBZE |
| 6 | 31 | 91.2 | 292 | 2 | Q898J4 CLOTE |
| 7 | 31 | 91.2 | 498 | 2 | Q6EW72 NYMAL |
| 8 | 31 | 91.2 | 511 | 2 | Q8BVH0 MOUSE |
| 9 | 31 | 91.2 | 616 | 2 | Q9BGH2 PIG |
| 10 | 31 | 91.2 | 643 | 2 | Q8BV16 MOUSE |
| 11 | 31 | 91.2 | 1068 | 1 | TRI SULSO |
| 12 | 31 | 91.2 | 2149 | 2 | Q6XL68 BOVIN |
| 13 | 31 | 91.2 | 2327 | 2 | Q6XL66 BOVIN |
| 14 | 31 | 91.2 | 2364 | 1 | PGCA BOVIN |
| 15 | 31 | 91.2 | 2365 | 2 | Q6XL67 BOVIN |
| 16 | 31 | 91.2 | 2576 | 2 | Q7Y2T1_9CAUD |
| 17 | 31 | 91.2 | 2793 | 2 | Q8X2Q2 ECO57 |
| 18 | 31 | 91.2 | 2806 | 2 | Q776K5_9CAUD |
| 19 | 31 | 91.2 | 2806 | 2 | Q7Y392 stx1 conver |
| 20 | 31 | 91.2 | 2806 | 2 | Q9TK19 BpVT2 |
| 21 | 31 | 91.2 | 2806 | 2 | Q9TKJ1 bacterioph |
| 22 | 31 | 91.2 | 2806 | 2 | Q9KXAE ECO57 |
| 23 | 31 | 91.2 | 2806 | 2 | Q8X470 ECO57 |
| 24 | 30 | 88.2 | 118 | 2 | Q811U5 MOUSE |
| 25 | 30 | 88.2 | 188 | 2 | Q8YUQ5 PYRAB |
| 26 | 30 | 88.2 | 253 | 2 | Q8YU22 ENTFA |
| 27 | 30 | 88.2 | 345 | 2 | Q82MA4 STEAW |
| 28 | 30 | 88.2 | 404 | 2 | Q4RXV0 TETNG |
| 29 | 30 | 88.2 | 417 | 2 | Q6H4T2 ORYSA |
| 30 | 30 | 88.2 | 434 | 2 | Q57TW1_9TRYP |
| 31 | 30 | 88.2 | 449 | 2 | Q7QUW4_GIALA |

| | | | | | |
|-----|------|------|---|---------------|---------------------|
| 32 | 88.2 | 472 | 2 | Q6AER2 LEIXX | Q6aer2 leifsonia x |
| 33 | 88.2 | 537 | 2 | Q67856 AQUAE | Q67856 aquifex aeo |
| 34 | 88.2 | 580 | 2 | Q4T137 TETNG | Q4t137 tetraodon n |
| 35 | 88.2 | 814 | 2 | Q8TR2_9PROT | Q8tr2 uncultured |
| 36 | 88.2 | 814 | 2 | Q8SFA3_9BACT | Q8sfa3 uncultured |
| 37 | 88.2 | 1033 | 2 | Q6Z4T5 ORYSA | Q6z4t5 oryza sativ |
| 38 | 88.2 | 1035 | 2 | Q6Z4T3 ORYSA | Q6z4t3 oryza sativ |
| 39 | 88.2 | 1045 | 2 | Q54XP6 DICTDI | Q54xp6 dictyosteli |
| 40 | 88.2 | 1050 | 2 | Q4T9N9 TETNG | Q4t9n9 tetraodon n |
| 41 | 88.2 | 1079 | 1 | IF2P SCHPO | Q10251 schizosacch |
| 42 | 88.2 | 1088 | 2 | Q9XX01 CAEEL | Q9xx01 caenorhabdi |
| 43 | 88.2 | 1100 | 2 | Q61BN8 CAEEL | Q61bn8 caenorhabdi |
| 44 | 88.2 | 1136 | 2 | Q6EUT8 CAEEL | Q6eut8 caenorhabdi |
| 45 | 88.2 | 1175 | 2 | Q474Y4 GEOSL | Q474y4 geobacter s |
| 46 | 88.2 | 1689 | 2 | Q6Y5E0_9VIRU | Q6y5e0 crmean-con |
| 47 | 88.2 | 2125 | 2 | Q51YX7 MAGGR | Q51yx7 magnaporthe |
| 48 | 88.2 | 3175 | 2 | Q7JKT8 CAEEL | Q7jkt8 caenorhabdi |
| 49 | 88.2 | 3184 | 2 | Q9XV66 CAEEL | Q9xv66 caenorhabdi |
| 50 | 85.3 | 156 | 2 | Q71EF6 BACSU | Q71ef6 bacillus su |
| 51 | 85.3 | 194 | 2 | Q84IM9 CLOLM | Q84im9 clostridium |
| 52 | 85.3 | 197 | 2 | Q4Z619 PLABE | Q4z619 plasmodium |
| 53 | 85.3 | 227 | 1 | KCV XANAC | Q8pk76 xanthomonas |
| 54 | 85.3 | 236 | 2 | Q6L0J5 PICTO | Q6l0j5 picrophilus |
| 55 | 85.3 | 250 | 2 | Q88Q79 PSEPK | Q88q79 pseudomonas |
| 56 | 85.3 | 251 | 2 | Q89302_9FLAV | Q89302 yellow feve |
| 57 | 85.3 | 253 | 2 | Q4KAF4_PSEF5 | Q4kaf4 pseudomonas |
| 58 | 85.3 | 255 | 2 | Q4LUE5_9BURK | Q4lue5 burkholderi |
| 59 | 85.3 | 331 | 2 | Q7WEP2_BORBR | Q7wef2 bordetella |
| 60 | 85.3 | 343 | 1 | NOV XENLA | P51609 xenopus lae |
| 61 | 85.3 | 343 | 2 | Q6INN3 XENLA | Q6inn3 xenopus lae |
| 62 | 85.3 | 347 | 2 | Q7W335 BORPA | Q7w335 bordetella |
| 63 | 85.3 | 379 | 1 | CIT2 SALTY | P37463 salmonella |
| 64 | 85.3 | 379 | 2 | Q8Z8F6_SALTI | Q8z8f6 salmonella |
| 65 | 85.3 | 379 | 2 | Q5PC12_SALPA | Q5pci2 salmonella |
| 66 | 85.3 | 389 | 2 | Q58AS1_9BURK | Q58as1 ralstonia m |
| 67 | 85.3 | 392 | 2 | Q8PUN6 WETMA | Q8pun6 methanosarc |
| 68 | 85.3 | 396 | 2 | Q7MR64 WOLSU | Q7mr64 wolinnella s |
| 69 | 85.3 | 416 | 2 | Q58HZ9_CHICK | Q58hz9 gallus gall |
| 70 | 85.3 | 424 | 1 | SKP2_HUMAN | Q13309 homo sapien |
| 71 | 85.3 | 424 | 1 | SKP2_MOUSE | Q92023 mus musculu |
| 72 | 85.3 | 424 | 2 | Q56Z99_MOUSE | Q56z99 mus musculu |
| 73 | 85.3 | 443 | 2 | Q5ZM99_CHICK | Q5zm99 gallus gall |
| 74 | 85.3 | 575 | 2 | Q5L9E5_BACFN | Q5l9e5 bacteroides |
| 75 | 85.3 | 575 | 2 | Q64PM9_BACFR | Q64pm9 bacteroides |
| 76 | 85.3 | 578 | 1 | SYK PORGI | Q7muv7 porphyromon |
| 77 | 85.3 | 655 | 2 | Q89FK3_BRAJA | Q89fk3 bradyrhizob |
| 78 | 85.3 | 719 | 2 | Q61281_MOUSE | Q61281 mus musculu |
| 79 | 85.3 | 748 | 2 | Q5NC19_MOUSE | Q5nc19 mus musculu |
| 80 | 85.3 | 791 | 1 | PFSA ECOLI | P23538 escherichia |
| 81 | 85.3 | 792 | 2 | Q57PT7_SALCH | Q57pt7 salmonella |
| 82 | 85.3 | 792 | 2 | Q7ADG6_ECO57 | Q7adg6 escherichia |
| 83 | 85.3 | 792 | 2 | Q8F333_ECOL6 | Q8fh33 escherichia |
| 84 | 85.3 | 792 | 2 | Q8Z6J0_SALTI | Q8z6j0 salmonella |
| 85 | 85.3 | 792 | 2 | Q8ZPS3_SALTY | Q8zps3 salmonella |
| 86 | 85.3 | 792 | 2 | Q5PH78_SALPA | Q5ph78 salmonella |
| 87 | 85.3 | 792 | 2 | Q83L32_SHIFL | Q83l32 shigella fl |
| 88 | 85.3 | 792 | 2 | Q8XEC4_ECO57 | Q8xec4 escherichia |
| 89 | 85.3 | 1128 | 2 | Q88442_MOUSE | Q88442 mus musculu |
| 90 | 85.3 | 1128 | 2 | Q640N1_MOUSE | Q640n1 mus musculu |
| 91 | 85.3 | 1144 | 2 | Q5NKT4_PANTR | Q5nkt4 pan troglod |
| 92 | 85.3 | 1274 | 1 | SRFAC_BACSU | Q8r787 bacillus su |
| 93 | 85.3 | 1278 | 2 | Q70KJ4_BACAM | Q70kj4 bacillus am |
| 94 | 85.3 | 1391 | 2 | Q19021_CAEL | Q19021 caenorhabdi |
| 95 | 85.3 | 2302 | 2 | Q5CRG7_CRYPV | Q5crg7 cryptospori |
| 96 | 82.4 | 64 | 2 | Q6Z9F0_ORYSA | Q6z9f0 oryza sativ |
| 97 | 82.4 | 100 | 2 | Q9UDL6_HUMAN | Q9udl6 homo sapien |
| 98 | 82.4 | 122 | 2 | Q7M2H0_SOLTU | Q7m2h0 solanum tub |
| 99 | 82.4 | 122 | 2 | Q7M2H1_SOLTU | Q7m2h1 solanum tub |
| 100 | 82.4 | 128 | 2 | Q9R2C0_RAT | Q9r2c0 ratus norv |
| 101 | 82.4 | 165 | 2 | Q69LX0_ORYSA | Q69lx0 oryza sativ |
| 102 | 82.4 | 177 | 2 | Q6BQ11_DEBHA | Q6bq11 debaryomyce |
| 103 | 82.4 | 181 | 2 | Q5HAX7_EHRRW | Q5hax7 ehrlichia r |
| 104 | 82.4 | 182 | 2 | Q6XC19_9HYPO | Q6xc19 hypocrea sp |

| | | | | | | | | | | | | | | | | | |
|-----|----|------|----|---|--------------|--------|-------|-------|-----|----|------|----|---|--------------|--------|-------|-------|
| 835 | 26 | 76.5 | 71 | 2 | Q5UGB7_9HIV1 | Q5ugb7 | human | immun | 908 | 26 | 76.5 | 71 | 2 | Q8ATV7_9HIV1 | Q8atv7 | human | immun |
| 836 | 26 | 76.5 | 71 | 2 | Q5UGC2_9HIV1 | Q5ugc2 | human | immun | 909 | 26 | 76.5 | 71 | 2 | Q8ATV9_9HIV1 | Q8atv9 | human | immun |
| 837 | 26 | 76.5 | 71 | 2 | Q5UGC3_9HIV1 | Q5ugc3 | human | immun | 910 | 26 | 76.5 | 71 | 2 | Q8ATW0_9HIV1 | Q8atw0 | human | immun |
| 838 | 26 | 76.5 | 71 | 2 | Q5UGD0_9HIV1 | Q5ugd0 | human | immun | 911 | 26 | 76.5 | 71 | 2 | Q8ATW1_9HIV1 | Q8atw1 | human | immun |
| 839 | 26 | 76.5 | 71 | 2 | Q5UGD1_9HIV1 | Q5ugd1 | human | immun | 912 | 26 | 76.5 | 71 | 2 | Q8ATW2_9HIV1 | Q8atw2 | human | immun |
| 840 | 26 | 76.5 | 71 | 2 | Q5UGD4_9HIV1 | Q5ugd4 | human | immun | 913 | 26 | 76.5 | 71 | 2 | Q8ATW4_9HIV1 | Q8atw4 | human | immun |
| 841 | 26 | 76.5 | 71 | 2 | Q5UGD5_9HIV1 | Q5ugd5 | human | immun | 914 | 26 | 76.5 | 71 | 2 | Q8ATW5_9HIV1 | Q8atw5 | human | immun |
| 842 | 26 | 76.5 | 71 | 2 | Q5UGB0_9HIV1 | Q5uge0 | human | immun | 915 | 26 | 76.5 | 71 | 2 | Q8ATW6_9HIV1 | Q8atw6 | human | immun |
| 843 | 26 | 76.5 | 71 | 2 | Q5UGB1_9HIV1 | Q5uge1 | human | immun | 916 | 26 | 76.5 | 71 | 2 | Q8ATW8_9HIV1 | Q8atw8 | human | immun |
| 844 | 26 | 76.5 | 71 | 2 | Q5UGB2_9HIV1 | Q5uge2 | human | immun | 917 | 26 | 76.5 | 71 | 2 | Q8ATW9_9HIV1 | Q8atw9 | human | immun |
| 845 | 26 | 76.5 | 71 | 2 | Q5UGB3_9HIV1 | Q5uge3 | human | immun | 918 | 26 | 76.5 | 71 | 2 | Q8ATX0_9HIV1 | Q8atx0 | human | immun |
| 846 | 26 | 76.5 | 71 | 2 | Q5UGB4_9HIV1 | Q5uge4 | human | immun | 919 | 26 | 76.5 | 71 | 2 | Q8ATX2_9HIV1 | Q8atx2 | human | immun |
| 847 | 26 | 76.5 | 71 | 2 | Q5UGB5_9HIV1 | Q5uge5 | human | immun | 920 | 26 | 76.5 | 71 | 2 | Q8ATX3_9HIV1 | Q8atx3 | human | immun |
| 848 | 26 | 76.5 | 71 | 2 | Q5UGB6_9HIV1 | Q5uge6 | human | immun | 921 | 26 | 76.5 | 71 | 2 | Q8ATX5_9HIV1 | Q8atx5 | human | immun |
| 849 | 26 | 76.5 | 71 | 2 | Q5UGB7_9HIV1 | Q5uge7 | human | immun | 922 | 26 | 76.5 | 71 | 2 | Q8ATX9_9HIV1 | Q8atx9 | human | immun |
| 850 | 26 | 76.5 | 71 | 2 | Q5UGB8_9HIV1 | Q5uge8 | human | immun | 923 | 26 | 76.5 | 71 | 2 | Q8ATY1_9HIV1 | Q8aty1 | human | immun |
| 851 | 26 | 76.5 | 71 | 2 | Q5UGB9_9HIV1 | Q5uge9 | human | immun | 924 | 26 | 76.5 | 71 | 2 | Q8ATY2_9HIV1 | Q8aty2 | human | immun |
| 852 | 26 | 76.5 | 71 | 2 | Q5UGP2_9HIV1 | Q5ugf2 | human | immun | 925 | 26 | 76.5 | 71 | 2 | Q8ATY3_9HIV1 | Q8aty3 | human | immun |
| 853 | 26 | 76.5 | 71 | 2 | Q5UGF3_9HIV1 | Q5ugf3 | human | immun | 926 | 26 | 76.5 | 71 | 2 | Q8ATY5_9HIV1 | Q8aty5 | human | immun |
| 854 | 26 | 76.5 | 71 | 2 | Q5UGF4_9HIV1 | Q5ugf4 | human | immun | 927 | 26 | 76.5 | 71 | 2 | Q8ATY6_9HIV1 | Q8aty6 | human | immun |
| 855 | 26 | 76.5 | 71 | 2 | Q5UGF5_9HIV1 | Q5ugf5 | human | immun | 928 | 26 | 76.5 | 71 | 2 | Q8ATY9_9HIV1 | Q8aty9 | human | immun |
| 856 | 26 | 76.5 | 71 | 2 | Q5UGF6_9HIV1 | Q5ugf6 | human | immun | 929 | 26 | 76.5 | 71 | 2 | Q8ATZ0_9HIV1 | Q8atz0 | human | immun |
| 857 | 26 | 76.5 | 71 | 2 | Q5UGF7_9HIV1 | Q5ugf7 | human | immun | 930 | 26 | 76.5 | 71 | 2 | Q9B8K8_9HIV1 | Q9b8k8 | human | immun |
| 858 | 26 | 76.5 | 71 | 2 | Q5UGF8_9HIV1 | Q5ugf8 | human | immun | 931 | 26 | 76.5 | 71 | 2 | Q9B8L2_9HIV1 | Q9b8l2 | human | immun |
| 859 | 26 | 76.5 | 71 | 2 | Q5UGF9_9HIV1 | Q5ugf9 | human | immun | 932 | 26 | 76.5 | 71 | 2 | Q9B8L5_9HIV1 | Q9b8l5 | human | immun |
| 860 | 26 | 76.5 | 71 | 2 | Q5UGG6_9HIV1 | Q5ugg6 | human | immun | 933 | 26 | 76.5 | 71 | 2 | Q9B8L7_9HIV1 | Q9b8l7 | human | immun |
| 861 | 26 | 76.5 | 71 | 2 | Q5UGG7_9HIV1 | Q5ugg7 | human | immun | 934 | 26 | 76.5 | 71 | 2 | Q9B8M9_9HIV1 | Q9b8m9 | human | immun |
| 862 | 26 | 76.5 | 71 | 2 | Q5UGG8_9HIV1 | Q5ugg8 | human | immun | 935 | 26 | 76.5 | 71 | 2 | Q9B8N1_9HIV1 | Q9b8n1 | human | immun |
| 863 | 26 | 76.5 | 71 | 2 | Q5UGG9_9HIV1 | Q5ugg9 | human | immun | 936 | 26 | 76.5 | 71 | 2 | Q9B8N4_9HIV1 | Q9b8n4 | human | immun |
| 864 | 26 | 76.5 | 71 | 2 | Q5UGH2_9HIV1 | Q5ugh2 | human | immun | 937 | 26 | 76.5 | 71 | 2 | Q9B8P4_9HIV1 | Q9b8p4 | human | immun |
| 865 | 26 | 76.5 | 71 | 2 | Q5UGH5_9HIV1 | Q5ugh5 | human | immun | 938 | 26 | 76.5 | 71 | 2 | Q9B8P8_9HIV1 | Q9b8p8 | human | immun |
| 866 | 26 | 76.5 | 71 | 2 | Q5UGH6_9HIV1 | Q5ugh6 | human | immun | 939 | 26 | 76.5 | 71 | 2 | Q9B8Q1_9HIV1 | Q9b8q1 | human | immun |
| 867 | 26 | 76.5 | 71 | 2 | Q5UGH9_9HIV1 | Q5ugh9 | human | immun | 940 | 26 | 76.5 | 71 | 2 | Q9B8Q4_9HIV1 | Q9b8q4 | human | immun |
| 868 | 26 | 76.5 | 71 | 2 | Q5UGI0_9HIV1 | Q5ugi0 | human | immun | 941 | 26 | 76.5 | 71 | 2 | Q9B8Q7_9HIV1 | Q9b8q7 | human | immun |
| 869 | 26 | 76.5 | 71 | 2 | Q66MQ3_9HIV1 | Q66mq3 | human | immun | 942 | 26 | 76.5 | 71 | 2 | Q9B8R1_9HIV1 | Q9b8r1 | human | immun |
| 870 | 26 | 76.5 | 71 | 2 | Q66MQ5_9HIV1 | Q66mq5 | human | immun | 943 | 26 | 76.5 | 71 | 2 | Q9B8R4_9HIV1 | Q9b8r4 | human | immun |
| 871 | 26 | 76.5 | 71 | 2 | Q66MQ7_9HIV1 | Q66mq7 | human | immun | 944 | 26 | 76.5 | 71 | 2 | Q9B8S7_9HIV1 | Q9b8s7 | human | immun |
| 872 | 26 | 76.5 | 71 | 2 | Q66MR3_9HIV1 | Q66mr3 | human | immun | 945 | 26 | 76.5 | 71 | 2 | Q9B8T2_9HIV1 | Q9b8t2 | human | immun |
| 873 | 26 | 76.5 | 71 | 2 | Q66MR7_9HIV1 | Q66mr7 | human | immun | 946 | 26 | 76.5 | 71 | 2 | Q9B8T6_9HIV1 | Q9b8t6 | human | immun |
| 874 | 26 | 76.5 | 71 | 2 | Q66MR9_9HIV1 | Q66mr9 | human | immun | 947 | 26 | 76.5 | 71 | 2 | Q9B8T8_9HIV1 | Q9b8t8 | human | immun |
| 875 | 26 | 76.5 | 71 | 2 | Q66MS3_9HIV1 | Q66ms3 | human | immun | 948 | 26 | 76.5 | 71 | 2 | Q9B8T9_9HIV1 | Q9b8t9 | human | immun |
| 876 | 26 | 76.5 | 71 | 2 | Q66MS5_9HIV1 | Q66ms5 | human | immun | 949 | 26 | 76.5 | 71 | 2 | Q9B8T9_9HIV1 | Q9b8t9 | human | immun |
| 877 | 26 | 76.5 | 71 | 2 | Q66MS7_9HIV1 | Q66ms7 | human | immun | 950 | 26 | 76.5 | 71 | 2 | Q9B8T9_9HIV1 | Q9b8t9 | human | immun |
| 878 | 26 | 76.5 | 71 | 2 | Q66MS9_9HIV1 | Q66ms9 | human | immun | 951 | 26 | 76.5 | 71 | 2 | Q9B8T9_9HIV1 | Q9b8t9 | human | immun |
| 879 | 26 | 76.5 | 71 | 2 | Q61UE7_9HIV1 | Q61ue7 | human | immun | 952 | 26 | 76.5 | 71 | 2 | Q9B8T9_9HIV1 | Q9b8t9 | human | immun |
| 880 | 26 | 76.5 | 71 | 2 | Q71875_9HIV1 | Q71875 | human | immun | 953 | 26 | 76.5 | 71 | 2 | Q9B8T9_9HIV1 | Q9b8t9 | human | immun |
| 881 | 26 | 76.5 | 71 | 2 | Q71886_9HIV1 | Q71886 | human | immun | 954 | 26 | 76.5 | 71 | 2 | Q9B8T9_9HIV1 | Q9b8t9 | human | immun |
| 882 | 26 | 76.5 | 71 | 2 | Q71891_9HIV1 | Q71891 | human | immun | 955 | 26 | 76.5 | 71 | 2 | Q9B8T9_9HIV1 | Q9b8t9 | human | immun |
| 883 | 26 | 76.5 | 71 | 2 | Q71939_9HIV1 | Q71939 | human | immun | 956 | 26 | 76.5 | 71 | 2 | Q9B8T9_9HIV1 | Q9b8t9 | human | immun |
| 884 | 26 | 76.5 | 71 | 2 | Q71945_9HIV1 | Q71945 | human | immun | 957 | 26 | 76.5 | 71 | 2 | Q9B8T9_9HIV1 | Q9b8t9 | human | immun |
| 885 | 26 | 76.5 | 71 | 2 | Q71968_9HIV1 | Q71968 | human | immun | 958 | 26 | 76.5 | 71 | 2 | Q9B8T9_9HIV1 | Q9b8t9 | human | immun |
| 886 | 26 | 76.5 | 71 | 2 | Q71974_9HIV1 | Q71974 | human | immun | 959 | 26 | 76.5 | 71 | 2 | Q9B8T9_9HIV1 | Q9b8t9 | human | immun |
| 887 | 26 | 76.5 | 71 | 2 | Q71980_9HIV1 | Q71980 | human | immun | 960 | 26 | 76.5 | 71 | 2 | Q9B8T9_9HIV1 | Q9b8t9 | human | immun |
| 888 | 26 | 76.5 | 71 | 2 | Q71987_9HIV1 | Q71987 | human | immun | 961 | 26 | 76.5 | 71 | 2 | Q9B8T9_9HIV1 | Q9b8t9 | human | immun |
| 889 | 26 | 76.5 | 71 | 2 | Q71993_9HIV1 | Q71993 | human | immun | 962 | 26 | 76.5 | 71 | 2 | Q9B8T9_9HIV1 | Q9b8t9 | human | immun |
| 890 | 26 | 76.5 | 71 | 2 | Q72000_9HIV1 | Q72000 | human | immun | 963 | 26 | 76.5 | 71 | 2 | Q9B8T9_9HIV1 | Q9b8t9 | human | immun |
| 891 | 26 | 76.5 | 71 | 2 | Q72005_9HIV1 | Q72005 | human | immun | 964 | 26 | 76.5 | 71 | 2 | Q9B8T9_9HIV1 | Q9b8t9 | human | immun |
| 892 | 26 | 76.5 | 71 | 2 | Q72009_9HIV1 | Q72009 | human | immun | 965 | 26 | 76.5 | 71 | 2 | Q9B8T9_9HIV1 | Q9b8t9 | human | immun |
| 893 | 26 | 76.5 | 71 | 2 | Q72019_9HIV1 | Q72019 | human | immun | 966 | 26 | 76.5 | 71 | 2 | Q9B8T9_9HIV1 | Q9b8t9 | human | immun |
| 894 | 26 | 76.5 | 71 | 2 | Q8AIK0_9HIV1 | Q8aik0 | human | immun | 967 | 26 | 76.5 | 71 | 2 | Q9B8T9_9HIV1 | Q9b8t9 | human | immun |
| 895 | 26 | 76.5 | 71 | 2 | Q8AIK1_9HIV1 | Q8aik1 | human | immun | 968 | 26 | 76.5 | 71 | 2 | Q9B8T9_9HIV1 | Q9b8t9 | human | immun |
| 896 | 26 | 76.5 | 71 | 2 | Q8AIK2_9HIV1 | Q8aik2 | human | immun | 969 | 26 | 76.5 | 72 | 2 | Q89717_9HIV1 | Q89717 | human | immun |
| 897 | 26 | 76.5 | 71 | 2 | Q8AIK3_9HIV1 | Q8aik3 | human | immun | 970 | 26 | 76.5 | 72 | 2 | Q89718_9HIV1 | Q89718 | human | immun |
| 898 | 26 | 76.5 | 71 | 2 | Q8AIK4_9HIV1 | Q8aik4 | human | immun | 971 | 26 | 76.5 | 72 | 2 | Q89719_9HIV1 | Q89719 | human | immun |
| 899 | 26 | 76.5 | 71 | 2 | Q8AIK5_9HIV1 | Q8aik5 | human | immun | 972 | 26 | 76.5 | 72 | 2 | Q89720_9HIV1 | Q89720 | human | immun |
| 900 | 26 | 76.5 | 71 | 2 | Q8AIK9_9HIV1 | Q8aik9 | human | immun | 973 | 26 | 76.5 | 72 | 2 | Q89721_9HIV1 | Q89721 | human | immun |
| 901 | 26 | 76.5 | 71 | 2 | Q8AIL0_9HIV1 | Q8ail0 | human | immun | 974 | 26 | 76.5 | 72 | 2 | Q89722_9HIV1 | Q89722 | human | immun |
| 902 | 26 | 76.5 | 71 | 2 | Q8AIL1_9HIV1 | Q8ail1 | human | immun | 975 | 26 | 76.5 | 72 | 2 | Q89723_9HIV1 | Q89723 | human | immun |
| 903 | 26 | 76.5 | 71 | 2 | Q8AIL5_9HIV1 | Q8ail5 | human | immun | 976 | 26 | 76.5 | 72 | 2 | Q89725_9HIV1 | Q89725 | human | immun |
| 904 | 26 | 76.5 | 71 | 2 | Q8AIL6_9HIV1 | Q8ail6 | human | immun | 977 | 26 | 76.5 | 72 | 2 | Q89727_9HIV1 | Q89727 | human | immun |
| 905 | 26 | 76.5 | 71 | 2 | Q8ATV4_9HIV1 | Q8atv4 | human | immun | 978 | 26 | 76.5 | 72 | 2 | Q89728_9HIV1 | Q89728 | human | immun |
| 906 | 26 | 76.5 | 71 | 2 | Q8ATV5_9HIV1 | Q8atv5 | human | immun | 979 | 26 | 76.5 | 72 | 2 | Q89913_9HIV1 | Q89913 | human | immun |
| 907 | 26 | 76.5 | 71 | 2 | Q8ATV6_9HIV1 | Q8atv6 | human | immun | 980 | 26 | 76.5 | 72 | 2 | P88697_9HIV1 | P88697 | human | immun |

DR EMBL; CP000004; AAW59682.1; -; Genomic_DNA.
 KW Complete proteome; Plasmid.
 SQ SEQUENCE 197 AA; 20780 MW; A6471ERC023EFF91 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 197;
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
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 DB 136 TSGLGVS 142

RESULT 4
 Q4R029_9BILA PRELIMINARY; PRT; 219 AA.
 AC Q4R029;
 DT 13-SEP-2005 (TReMBLrel. 31, Created)
 DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
 DE Cytochrome oxidase subunit I (Fragment).
 GN Name=COI;
 OS Oligacanthorhynchus tortuosa.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Acanthocephala; Archiacanthocephala;
 OC Oligacanthorhynchida; Oligacanthorhynchidae; Oligacanthorhynchus.
 OX NCBI_TaxID=84287;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RA Garcia-Varela M., Cummings M.P., Laclette J.P.;
 RT "Phylogenetic Relationships of Archiacanthocephala (Acanthocephala)
 Based on Gene Sequences of 16S, 5.8S and 18S rRNA, Internal
 Transcribed Spacers 1 and 2, and COI".
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory
 chain that catalyzes the reduction of oxygen to water. Subunits 1-
 3 form the functional core of the enzyme complex. CO I is the
 catalytic subunit of the enzyme. Electrons originating in
 cytochrome c are transferred via the copper A center of subunit 2
 and heme A of subunit 1 to the bimetallic center formed by heme A3
 and copper B (By similarity).
 CC -!- CATALYTIC ACTIVITY: 4 ferrocycochrome c + O(2) = 4 ferrocycochrome
 c + 2 H(2)O.
 CC -!- PATHWAY: Respiratory chain; terminal step.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 inner membrane (By similarity).
 CC -!- SIMILARITY: Belongs to the heme-copper respiratory oxidase family.

DR EMBL; AF416999; AAY85944.1; -; Genomic_DNA.
 DR InterPro; IPR000883; COX1.
 DR Pfam; PF00115; COX1; 1.
 DR PRINTS; PR01165; CYCOXIDASE1.
 DR PROSITE; PS50855; COX1; 1.
 KW Copper; Electron transport; Heme; Inner membrane; Membrane;
 KW Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
 KW Transport.
 FT NON_TER 1 1
 FT NON_TER 219 219
 SQ SEQUENCE 219 AA; 23629 MW; DF9DA0B5262F833E CRC64;

Query Match 91.2%; Score 31; DB 2; Length 219;
 Best Local Similarity 85.7%; Pred. No. 2.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
 |||||
 DB 155 TAGMGVS 161

RESULT 5
 Q4IDB8_GIBZE PRELIMINARY; PRT; 285 AA.
 ID Q4IDB8_GIBZE PRELIMINARY; PRT; 285 AA.
 AC Q4IDB8;
 DT 13-SEP-2005 (TReMBLrel. 31, Created)

DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
 DE Hypothetical protein.
 GN OFNames=FG04790.1;
 OS Gibberella zeae PH-1.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
 OX NCBI_TaxID=229533;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
 RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
 RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
 RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
 RA Erickson J., Faro S., Ferraira P., FitzGerald M., Gage D., Galagan J.,
 RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
 RA Jaffe D., Johnson R., Jones C., Kamal A., Karatas A.,
 RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
 RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
 RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
 RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
 RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
 RA Rachupka A., Ramasamy U., Raymond C., Rietz R., Rise C., Rogov P.,
 RA Roman J., Schauer S., Schupbach R., Seaman S., Severy P., Smirnov S.,
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
 RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
 RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
 RA Lander E.;
 RT "Fusarium graminearum genome sequence."
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; AACM01000196; EAA75749.1; -; Genomic_DNA.
 DR Hypothetical protein.
 KW Hypothetical protein.
 SQ SEQUENCE 285 AA; 31434 MW; 779697211D84C67C CRC64;

Query Match 91.2%; Score 31; DB 2; Length 285;
 Best Local Similarity 85.7%; Pred. No. 2.7e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
 |||||
 DB 13 TSGMGVS 19

RESULT 6
 Q898J4_CLOTE PRELIMINARY; PRT; 292 AA.
 ID Q898J4_CLOTE PRELIMINARY;
 AC Q898J4;
 DT 01-JUN-2003 (TReMBLrel. 24, Created)
 DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Putative sialidase (EC 3.2.1.18).
 GN OrderedLocusNames=CTC00453;
 OS Clostridium tetani.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1513;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RA MEDLINE=22457253; PubMed=12552129; DOI=10.1073/pnas.0335853100;
 RA Brueggemann H., Baumeister S., Fricke W.F., Wierze A., Liesegang H.,
 RA Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
 RA Gottschalk G.;
 RT "The genome sequence of Clostridium tetani, the causative agent of
 tetanus disease."

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RL Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).
DR EMBL; AE015937; AAC35087.1; -; Genomic_DNA.
DR GO; GO:0004308; F:exo-alpha-sialidase activity; IEA.
DR GO; GO:0016798; F:hydroxylase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
KW Complete proteome; Glycosidase; Hydrolase.
SQ SEQUENCE 292 AA; 33689 MW; EF27726FDCGEADEE CRC64;

Query Match 91.2%; Score 31; DB 2; Length 292;
Best Local Similarity 85.7%; Pred. NO. 2.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7
Db 36 TSLGLGS 42

RESULT 7
Q6EW72 NYMAL PRELIMINARY; PRT; 498 AA.
ID Q6EW72 NYMAL PRELIMINARY; PRT; 498 AA.
AC Q6EW72;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE ATP synthase beta chain.
GN Name=atpB;
OS Nymphaea alba (White water-lily).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; basal Magnoliophyta; Nymphaeales;
OC Nymphaeaceae; Nymphaea.
OX NCBI_TaxID=34301;
RN Nymphaea alba (White water-lily).
RP PubMed=15084583; DOI=10.1093/molbev/msh147;
RA Goremkyin V., Hirsch-Erns K.I., Wolf S., Hellwig F.H.;
RT "The chloroplast genome of Nymphaea alba: whole-genome analyses and
the problem of identifying the most basal angiosperm.";
RL Mol. Biol. Evol. 21:1445-1454(2004).
RN Nymphaea alba (White water-lily).
RP NUCLEOTIDE SEQUENCE.
RA Goremkyin V.;
RA NUCLEOTIDE SEQUENCE.
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Produces ATP from ADP in the presence of a proton
CC gradient across the membrane. The beta chain is the catalytic
CC subunit (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
CC H(+) (Out).
CC -!- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic
CC core - and CF(0) - the membrane proton channel. CF(1) has five
CC subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0)
CC has three main subunits: a, b and c (By similarity).
CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane (By
CC similarity).
CC -!- SIMILARITY: Belongs to the ATPase alpha/beta chains family.
DR EMBL; AJ627251; CAP28600.1; -; Genomic_DNA.
DR SRR; Q6EW72; 19-485.
DR GO; GO:0009507; C:hydrogen-translocating F-type ATPase complex; IEA.
DR GO; GO:0045255; C:hydrogen-translocating F-type ATPase complex; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0045281; C:proton-transporting ATP synthase complex, c. .; IEA.
DR GO; GO:0009579; C:thylakoid; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008553; F:hydrogen-exporting ATPase activity, phospho. .; IEA.
DR GO; GO:0046933; F:hydrogen-transporting ATP synthase activity. .; IEA.
DR GO; GO:0046961; F:hydrogen-transporting ATPase activity, rota. .; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0015986; P:ATP synthesis coupled proton transport; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR GO; GO:0015992; P:proton transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.

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DR InterPro; IPR005722; ATP_synthF1_beta.
DR InterPro; IPR000793; ATPase_a/b_C.
DR InterPro; IPR004100; ATPase_a/b_N.
DR InterPro; IPR000194; ATPase_a/bcentre.
DR Pfam; PF00006; ATP-synt_ab_1.
DR Pfam; PF00306; ATP-synt_ab_C; 1.
DR Pfam; PF02874; ATP-synt_ab_N; 1.
DR SMART; SM00382; AAA; 1.
DR TIGRFAMs; TIGR01039; atpD; 1.
DR PROSITE; PS00152; ATPASE ALPHA BETA; 1.
KW ATP synthesis; ATP-binding; CF(1); Chloroplast;
KW Hydrogen ion transport; Hydrolase; Ion transport; Membrane;
KW Nucleotide-binding; Thylakoid; Transport.
SQ SEQUENCE 498 AA; 53678 MW; AE984F2728341879 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 498;
Best Local Similarity 85.7%; Pred. No. 4.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7
Db 7 TSLGLGS 13

RESULT 8
Q8BVH0 MOUSE PRELIMINARY; PRT; 511 AA.
ID Q8BVH0 MOUSE PRELIMINARY; PRT; 511 AA.
AC Q8BVH0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus adult male olfactory brain cDNA, RIKEN full-length
DE enriched library, clone:643053K21 product:hypothetical Zinc finger,
DE C2H2 type/KRAB box containing protein, full insert sequence.
GN Name=zfp398;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN Mus musculus (Mouse).
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=CS7BL/6J; TISSUE=Olfactory brain;
RA MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RA "High-efficiency full-length cDNA cloning.";
RA Meth. Enzymol. 303:19-44(1999).
RN Mus musculus (Mouse).
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=CS7BL/6J; TISSUE=Olfactory brain;
RA MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Bono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guncich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RA Nature 409:685-690(2001).
RN Nature 409:685-690(2001).
RP NUCLEOTIDE SEQUENCE.

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RC STRAIN-C57BL/6J; TISSUE=Olfactory brain;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara K., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tonaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK078250; BAC37193.1; -; mRNA.
DR HSSP; P08047; 1SP2.
DR Ensembl; ENSMUSG0000062519; Mus musculus.
DR MGI; MGI:1917856; Zfp398.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001309; KRAB.
DR InterPro; IPR003655; KRAB-related.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF01352; KRAB; 1.
DR Pfam; PF00096; zf-C2H2; 7.
DR ProDom; PD000003; Znf_C2H2; 2.
DR SMART; SM00349; KRAB; 1.
DR SMART; SM00355; Znf_C2H2; 8.
DR PROSITE; PS0806; KRAB; 1.
DR PROSITE; PS0806; KRAB RELATED; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 7.
KW Hypothetical protein.
SQ SEQUENCE 511 AA; 56815 MW; CAF60690B0F93F3C CRC64;
Query Match 91.2%; Score 31; DB 2; Length 511;
Best Local Similarity 85.7%; Pred. No. 4.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TSGMGVS 7

Db 486 TSGLGVS 492
|||:||||
RESULT 9
Q9BGH2_PIG PRELIMINARY; PRT; 616 AA.
ID Q9BGH2; AC
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AggreCan C52 domain (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Grimm D.R., Westling-Fredericks J., Colter M.B., Sandy S.D.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF314814; AAK01170.1; -; mRNA.
DR InterPro; IPR001000; Glyco_hydro_10.
DR PROSITE; PS00591; GLYCOSYL_HYDROL_F10; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 616
SQ SEQUENCE 616 AA; 59816 MW; 85C408F3A27A45E0 CRC64;
Query Match 91.2%; Score 31; DB 2; Length 616;
Best Local Similarity 85.7%; Pred. No. 5.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TSGMGVS 7
|||:||||
Db 543 TSGLGVS 549
RESULT 10
Q8BV16_MOUSE PRELIMINARY; PRT; 643 AA.
ID Q8BV16_MOUSE PRELIMINARY;
AC Q8BV16;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length
DE enriched library, clone:B930095J06 product:hypothetical zinc finger,
DE C2H2 type/KRAB box containing protein, full insert sequence.
GN Name=Zfp398;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito K., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staabli F., Suzuki R., Tonita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gutting S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuiki S.,
RA Hayashizaki Y.,
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20530913; PubMed=11078861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamoto H., Hazama M., Nishino T., Harada A.,
RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akai H. S., Takeda Y., Tanaka I.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK081169; BAC38154.1; -, mRNA.
DR HSSP; P08047; 1SP2.
DR Ensembl; ENSMUSG00000062519; Mus musculus.
DR MGI; MGI:1917856; Zfp398.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001909; KRAB.
DR InterPro; IPR003655; KRAB-related.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF01352; KRAB; 1.
DR Pfam; PF00096; zf-C2H2; 7.
DR ProDom; PD000003; Znf_C2H2; 2.
DR SMART; SM00349; KRAB; 1.
DR SMART; SM00355; Znf_C2H2; 8.

DR PROSITE; PS50805; KRAB; 1.
DR PROSITE; PS50806; KRAB-RELATED; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 7.
KW Hypothetical protein.
SQ SEQUENCE 643 AA; 71479 MW; 4B847133DCD2522 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 643;
Best Local Similarity 85.7%; Pred. No. 5.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7
Db 618 TSGLGVS 624
|||:||||
|:|:|

RESULT 11
TRI_SULSO
ID TRI_SULSO STANDARD; PRT; 1068 AA.
AC P95871;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Tricorn protease homolog (EC 3.4.21.-)
GN Name=tri; OrderedLocustNames=SSO2098; ORFNames=C06024, C06_007;
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=37055432; PubMed=8893719;
RA Sensen C.W., Klenk H.-P., Singh R.K., Allard G., Chan C.C.-Y.,
RA Liu Q.Y., Penny S.L., Young F., Schenk M.E., Gaasterland T.,
RA Doolittle W.F., Ragan M.A., Charlebois R.L.;
RT "Organizational characteristics and information content of an archaeal
RT genome: 156 kb of sequence from Sulfolobus solfataricus P2.";
RL Mol. Microbiol. 22:175-191(1996).
[2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=11427726; DOI=10.1073/pnas.141222098;
RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Aweya M.J., Chan-Weiler C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
CC -!- FUNCTION: Degrades oligopeptides in a sequential manner (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the peptidase S41 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; Y08256; CAA69507.1; -, Genomic DNA.
CC EMBL; AE006816; AAK42276.1; -, Genomic DNA.
DR PIR; S73091; S73091.
DR HSSP; P96086; 1K32.
DR MEROPS; S41.005; -.
DR InterPro; IPR011659; PD40.
DR InterPro; IPR012393; Pept_S41_tricorn.
DR InterPro; IPR005151; Peptidase_S41.
DR Pfam; PF07676; PD40; 2.
DR Pfam; PF03572; Peptidase_S41; 1.

DR PROSITE; PS00963; LINK_2; 4.
SQ SEQUENCE 2149 AA; 220968 MW; 11FFBAAB15196EE6 CRC64;
Query Match 91.2%; Score 31; DB 2; Length 2149;
Best Local Similarity 85.7%; Pred. No. 1.9e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
|||:
Db 1977 TSGLGVS 1983

RESULT 13
Q6XL66 BOVIN PRELIMINARY; PRT; 2327 AA.
ID Q6XL66_BOVIN PRELIMINARY; PRT; 2327 AA.
AC Q6XL66;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Aggrecan.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Cavanagh J.A.L., Tammen I., Nicholas F.W., Gill C.A., Raadema H.W.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY226875; AAP44492.1; -; Genomic DNA.
DR EMBL; AY226858; AAP44492.1; JOINED; Genomic DNA.
DR EMBL; AY226860; AAP44492.1; JOINED; Genomic DNA.
DR EMBL; AY226859; AAP44492.1; JOINED; Genomic DNA.
DR EMBL; AY226863; AAP44492.1; JOINED; Genomic DNA.
DR EMBL; AY226865; AAP44492.1; JOINED; Genomic DNA.
DR EMBL; AY226867; AAP44492.1; JOINED; Genomic DNA.
DR EMBL; AY226871; AAP44492.1; JOINED; Genomic DNA.
DR EMBL; AY226873; AAP44492.1; JOINED; Genomic DNA.
DR EMBL; AY226874; AAP44492.1; JOINED; Genomic DNA.
DR EMBL; AY226872; AAP44492.1; JOINED; Genomic DNA.
DR EMBL; AY226868; AAP44492.1; JOINED; Genomic DNA.
DR EMBL; AY226866; AAP44492.1; JOINED; Genomic DNA.
DR EMBL; AY226864; AAP44492.1; JOINED; Genomic DNA.
DR EMBL; AY226862; AAP44492.1; JOINED; Genomic DNA.
DR EMBL; AY226861; AAP44492.1; JOINED; Genomic DNA.
DR SMR; Q6XL66; 2117-2240.
DR GO; GO:0005540; F-hyaluronic acid binding; IEA.
DR GO; GO:0005529; F-sugar binding; IEA.
DR GO; GO:0007155; P-cell adhesion; IEA.
DR InterPro; IPRO002353; AntifreezeII.
DR InterPro; IPRO01000; Glyco_hydro_10.
DR InterPro; IPRO03599; IG-like.
DR InterPro; IPRO07110; IG-like.
DR InterPro; IPRO03596; IG v.
DR InterPro; IPRO01304; Lectin_C.
DR InterPro; IPRO00538; Link.
DR InterPro; IPRO00436; Sushi_SCR_CCP.
DR Pfam; PF00059; Lentin_C; 1.
DR Pfam; PF00084; Sushi; 1.
DR Pfam; PF00193; Xlink; 4.
DR PRINTS; PR00356; ANTIFREEZEII.
DR PRINTS; PR01265; LINKMODULE.
DR SMART; SM00032; CCP; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00445; LINK; 4.
DR PROSITE; PS00615; C-TYPE LECTIN_1; 1.
DR PROSITE; PS00041; C-TYPE LECTIN_2; 1.
DR PROSITE; PS00591; GLYCOSYL_HYDROL_F10; UNKNOWN_1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS01241; LINK_1; 4.
DR PROSITE; PS00963; LINK_2; 4.

QY 1 TSGMGVS 7
|||:
Db 97 TSGLGVS 103

RESULT 12
Q6XL68 BOVIN PRELIMINARY; PRT; 2149 AA.
ID Q6XL68_BOVIN PRELIMINARY; PRT; 2149 AA.
AC Q6XL68;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Aggrecan.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Cavanagh J.A.L., Tammen I., Nicholas F.W., Gill C.A., Raadema H.W.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY226869; AAP44493.1; -; Genomic DNA.
DR EMBL; AY226858; AAP44493.1; JOINED; Genomic DNA.
DR EMBL; AY226859; AAP44493.1; JOINED; Genomic DNA.
DR EMBL; AY226860; AAP44493.1; JOINED; Genomic DNA.
DR EMBL; AY226862; AAP44493.1; JOINED; Genomic DNA.
DR EMBL; AY226864; AAP44493.1; JOINED; Genomic DNA.
DR EMBL; AY226866; AAP44493.1; JOINED; Genomic DNA.
DR EMBL; AY226868; AAP44493.1; JOINED; Genomic DNA.
DR EMBL; AY226867; AAP44493.1; JOINED; Genomic DNA.
DR EMBL; AY226865; AAP44493.1; JOINED; Genomic DNA.
DR EMBL; AY226863; AAP44493.1; JOINED; Genomic DNA.
DR EMBL; AY226861; AAP44493.1; JOINED; Genomic DNA.
DR GO; GO:0005540; F-hyaluronic acid binding; IEA.
DR GO; GO:0007155; P-cell adhesion; IEA.
DR InterPro; IPRO06209; EGF_like.
DR InterPro; IPRO01000; Glyco_hydro_10.
DR InterPro; IPRO03599; IG.
DR InterPro; IPRO07110; IG-like.
DR InterPro; IPRO03596; IG v.
DR InterPro; IPRO00538; Link.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00193; Xlink; 4.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 4.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00445; LINK; 4.
DR PROSITE; PS00591; GLYCOSYL_HYDROL_F10; UNKNOWN_1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS01241; LINK_1; 4.

QY 1 TSGMGVS 7
|||:
Db 97 TSGLGVS 103

Query Match 91.2%; Score 31; DB 1; Length 1068;
Best Local Similarity 85.7%; Pred. No. 9.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
|||:
Db 97 TSGLGVS 103

RESULT 12
Q6XL68 BOVIN PRELIMINARY; PRT; 2149 AA.
ID Q6XL68_BOVIN PRELIMINARY; PRT; 2149 AA.
AC Q6XL68;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Aggrecan.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Cavanagh J.A.L., Tammen I., Nicholas F.W., Gill C.A., Raadema H.W.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY226869; AAP44493.1; -; Genomic DNA.
DR EMBL; AY226858; AAP44493.1; JOINED; Genomic DNA.
DR EMBL; AY226859; AAP44493.1; JOINED; Genomic DNA.
DR EMBL; AY226860; AAP44493.1; JOINED; Genomic DNA.
DR EMBL; AY226862; AAP44493.1; JOINED; Genomic DNA.
DR EMBL; AY226864; AAP44493.1; JOINED; Genomic DNA.
DR EMBL; AY226866; AAP44493.1; JOINED; Genomic DNA.
DR EMBL; AY226868; AAP44493.1; JOINED; Genomic DNA.
DR EMBL; AY226867; AAP44493.1; JOINED; Genomic DNA.
DR EMBL; AY226865; AAP44493.1; JOINED; Genomic DNA.
DR EMBL; AY226863; AAP44493.1; JOINED; Genomic DNA.
DR EMBL; AY226861; AAP44493.1; JOINED; Genomic DNA.
DR GO; GO:0005540; F-hyaluronic acid binding; IEA.
DR GO; GO:0007155; P-cell adhesion; IEA.
DR InterPro; IPRO06209; EGF_like.
DR InterPro; IPRO01000; Glyco_hydro_10.
DR InterPro; IPRO03599; IG.
DR InterPro; IPRO07110; IG-like.
DR InterPro; IPRO03596; IG v.
DR InterPro; IPRO00538; Link.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00193; Xlink; 4.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 4.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00445; LINK; 4.
DR PROSITE; PS00591; GLYCOSYL_HYDROL_F10; UNKNOWN_1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS01241; LINK_1; 4.

QY 1 TSGMGVS 7
|||:
Db 97 TSGLGVS 103

Query Match 91.2%; Score 31; DB 1; Length 1068;
Best Local Similarity 85.7%; Pred. No. 9.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
|||:
Db 97 TSGLGVS 103

Query Match 91.2%; Score 31; DB 2; Length 2149;
Best Local Similarity 85.7%; Pred. No. 1.9e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
|||:
Db 1977 TSGLGVS

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DR PROSITE; PS50923; SUSHI; 1;
SQ SEQUENCE 2327 AA; 242481 MW; 5C048060465806B0 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 2327;
Best Local Similarity 85.7%; Pred. No. 2e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7
Db 1977 TSGLGVS 1983
|||||
|||:|

RESULT 14
PGCA_BOVIN STANDARD; PRT; 2364 AA.
AC P13608; P79117; Q28159;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Aggrecan core protein precursor (Cartilage-specific proteoglycan core
DE protein) (CSPCP).
GN Name=AGC1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hering T.M., Kollar J., Huynh T.D.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE OF 563-1056.
RX MEDLINE=89380219; PubMed=2528543;
RA Antonsson P., Heinegaard D., Oldberg A.;
RT "The keratan sulfate-enriched region of bovine cartilage proteoglycan
RT consists of a consecutively repeated hexapeptide motif.";
RL J. Biol. Chem. 264:16170-16173 (1989).
RN [3]
RP NUCLEOTIDE SEQUENCE OF 1609-2113 AND 2151-2364.
RX MEDLINE=87270630; PubMed=3111460;
RA Oldberg A., Antonsson P., Heinegaard D.;
RT "The partial amino acid sequence of bovine cartilage proteoglycan,
RT deduced from a cDNA clone, contains numerous Ser-Gly sequences
RT arranged in homologous repeats.";
RL Biochem. J. 243:255-259 (1987).
RN [4]
RP NUCLEOTIDE SEQUENCE OF 2114-2150.
RC TISSUE=Cartilage;
RX MEDLINE=93352525; PubMed=8349621;
RA Fuelep C., Walcz E., Vallyon M., Glant T.T.;
RT "Expression of alternatively spliced epidermal growth factor-like
RT domains in aggrecans of different species. Evidence for a novel
RT module.";
RL J. Biol. Chem. 268:17377-17383 (1993).
RN [5]
RP PARTIAL PROTEIN SEQUENCE.
RX MEDLINE=85027710; PubMed=6489519; DOI=10.1016/0014-5793(84)80907-2;
RA Perin J.-P., Bonnet F., Jolles J., Jolles P.;
RT "Sequence data concerning the protein core of the cartilage
RT proteoglycan monomers. Characterization of a sequence allowing the
RT synthesis of an oligonucleotide probe.";
RL FEBS Lett. 176:37-42 (1984).
RN [6]
RP PARTIAL PROTEIN SEQUENCE.
RX MEDLINE=87005253; PubMed=3530809; DOI=10.1016/0014-5793(86)81343-6;
RA Perin J.P., Bonnet F., Jolles P.;
RT "Structural relationship between link proteins and proteoglycan
RT monomers.";
RL FEBS Lett. 206:73-77 (1986).
RN [7]
RP PROTEIN SEQUENCE OF 152-157; 210-230; 482-506; 566-584; 631-641;
660-684; 2161-2167; 2276-2291; 2298-2307 AND 2318-2334.
RX PROSITE; PS00290; IG_MHC; FALSE_NEG.
RX MEDLINE=91217051; PubMed=2022637;
RA Sandy J.D., Boynton R.E., Flannery C.R.;
RT "Analysis of the catabolism of aggrecan in cartilage explants by
RT quantitation of peptides from the three globular domains.";
RL J. Biol. Chem. 266:8198-8205 (1991).
CC -I- FUNCTION; This proteoglycan is a major component of extracellular
CC matrix of cartilaginous tissues. A major function of this protein
CC is to resist compression in cartilage. It binds avidly to
CC hyaluronic acid via an N-terminal globular region. May play a
CC regulatory role in the matrix assembly of the cartilage.
CC -I- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
CC similarity).
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P13608-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P13608-2; Sequence=VSP_003072;
CC -I- DOMAIN: Two globular domains, G1 and G2, comprise the N-terminus
CC of the proteoglycan, while another globular region, G3, makes up
CC the C-terminus. G1 contains link domains and thus consists of
CC three disulfide-bonded loop structures designated as the A, B, B'
CC motifs. G2 is similar to G1. The keratan sulfate (KS) and the
CC chondroitin sulfate (CS) attachment domains lie between G2 and G3.
CC -I- PTM: Contains mostly chondroitin sulfate, but also N-linked and O-
CC linked (about 40) oligosaccharides.
CC -I- PTM: The keratan sulfate contents differ considerably between
CC adult and fetal bovine proteoglycans.
CC -I- SIMILARITY: Belongs to the aggrecan/versican family.
CC -I- SIMILARITY: Contains 1 C-type lectin domain.
CC -I- SIMILARITY: Contains 1 EGF-like domain.
CC -I- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
CC domain.
CC -I- SIMILARITY: Contains 4 Link domains.
CC -I- SIMILARITY: Contains 1 Sushi (CCP/SCR) domain.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
DR EMBL; U76615; AAB38524.1; -; mRNA.
DR EMBL; L07053; -; NOT_ANNOTATED_CDS; mRNA.
DR PIR; A34234; A39808.
DR PIR; T42630; T42630.
DR HSP; P01132; 1GK5.
DR SMR; P13608; 2154-2277.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR000152; Aax_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca_bd.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR000538; Link.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00008; EGF_1.
DR Pfam; PF00059; Lectin_C; 1.
DR Pfam; PF00084; Sushi_1.
DR Pfam; PF00193; Xlink; 4.
DR PRINTS; PR00356; ANTIFREEZEII.
DR PRINTS; PR01265; LINKMODULE.
DR PRODOM; PD000918; Link; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; FALSE_NEG.
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DR PROSITE; PS01241; LINK 1; 4.
DR PROSITE; PS0963; LINK 2; 4.
DR PROSITE; PS0923; SUSHI; 1.
KW Alternative splicing; Calcium; Direct protein sequencing;
KW EGF-like domain; Glycoprotein; Immunoglobulin domain; Lectin;
KW Proteoglycan; Repeat; Signal; Sushi.
FT SIGNAL 1 16 Potential.
FT CHAIN 17 2364 Aggrecan core protein.
FT DOMAIN 25 147 Ig-like V-type.
FT DOMAIN 153 248 Link 1.
FT DOMAIN 254 350 Link 2.
FT DOMAIN 487 582 Link 3.
FT DOMAIN 588 684 Link 4.
FT REPEAT 774 779 1.
FT REPEAT 780 785 2.
FT REPEAT 786 791 3.
FT REPEAT 792 797 4.
FT REPEAT 798 803 5.
FT REPEAT 804 809 6.
FT REPEAT 810 815 7.
FT REPEAT 816 821 8.
FT REPEAT 822 827 9.
FT REPEAT 828 833 10.
FT REPEAT 834 839 11.
FT REPEAT 840 845 12.
FT REPEAT 846 851 13.
FT REPEAT 852 857 14.
FT REPEAT 858 863 15.
FT REPEAT 864 869 16.
FT REPEAT 870 875 17.
FT REPEAT 876 881 18.
FT REPEAT 882 887 19.
FT REPEAT 888 893 20.
FT REPEAT 894 899 21.
FT REPEAT 900 905 22.
FT DOMAIN 2113 2149 EGF-like; calcium-binding (Potential).
FT DOMAIN 2161 2276 EGF-like lectin.
FT DOMAIN 2279 2339 Sushi.
FT REGION 774 905 22 x 6 AA tandem repeats of E-[EKGV]-[PL]-[FSI]-[PAT]-[STPL].
FT REGION 1433 2112 CS-2.
FT REGION 2114 2364 G3.
FT CARBOHYD 126 126 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 239 239 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 333 333 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 387 387 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 611 611 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 667 667 N-linked (GlcNAc. . .) (Potential).
FT DISULFID 51 133 By similarity.
FT DISULFID 175 246 By similarity.
FT DISULFID 199 220 By similarity.
FT DISULFID 273 348 By similarity.
FT DISULFID 297 318 By similarity.
FT DISULFID 509 580 By similarity.
FT DISULFID 533 554 By similarity.
FT DISULFID 607 682 By similarity.
FT DISULFID 631 652 By similarity.
FT DISULFID 2117 2128 By similarity.
FT DISULFID 2182 2274 By similarity.
FT DISULFID 2250 2266 By similarity.
FT DISULFID 2281 2324 By similarity.
FT DISULFID 2310 2337 By similarity.
FT VARSPLIC 2114 2150 Missing (in isoform 2).
FT CONFLICT 573 576 SETY -> QSET (in Ref. 7).
FT SEQUENCE 2364 AA; 246362 MW; 6FF83763420C3D4C CRC64;
Query Match 91.2%; Score 31; DB 1; Length 2364;
Best Local Similarity 85.7%; Pred. No. 2.1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TSGMGVS 7
|||:|

DB 1977 TSLGLVS 1983
RESULT 15
Q6XL67 BOVIN PRELIMINARY; PRT; 2365 AA.
ID Q6XL67; BOVIN
AC Q6XL67;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Aggrecan.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Cavanagh J.A.L., Tammen I., Nicholas F.W., Gill C.A., Raadsma H.W.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY226875; AAP44494.1; -; Genomic DNA.
DR EMBL; AY226858; AAP44494.1; JOINED; Genomic DNA.
DR EMBL; AY226859; AAP44494.1; JOINED; Genomic DNA.
DR EMBL; AY226860; AAP44494.1; JOINED; Genomic DNA.
DR EMBL; AY226862; AAP44494.1; JOINED; Genomic DNA.
DR EMBL; AY226864; AAP44494.1; JOINED; Genomic DNA.
DR EMBL; AY226866; AAP44494.1; JOINED; Genomic DNA.
DR EMBL; AY226868; AAP44494.1; JOINED; Genomic DNA.
DR EMBL; AY226871; AAP44494.1; JOINED; Genomic DNA.
DR EMBL; AY226874; AAP44494.1; JOINED; Genomic DNA.
DR EMBL; AY226873; AAP44494.1; JOINED; Genomic DNA.
DR EMBL; AY226872; AAP44494.1; JOINED; Genomic DNA.
DR EMBL; AY226870; AAP44494.1; JOINED; Genomic DNA.
DR EMBL; AY226867; AAP44494.1; JOINED; Genomic DNA.
DR EMBL; AY226865; AAP44494.1; JOINED; Genomic DNA.
DR EMBL; AY226863; AAP44494.1; JOINED; Genomic DNA.
DR EMBL; AY226861; AAP44494.1; JOINED; Genomic DNA.
DR HSSP; Q9H8F0; 1K9J.
DR SMR; Q6XL67; 1L55-2278.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007155; F:cell adhesion; IEA.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR000152; Asx hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca_bd.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001000; Glyco_hydro_10.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR000538; Link.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00008; EGF_1.
DR Pfam; PF00059; Lectin_C; 1.
DR Pfam; PF00084; Sushi; 1.
DR Pfam; PF00193; Xlink; 4.
DR PRINTS; PR00356; ANTIFREEZEII.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 4.
DR SMART; SM00032; CCP; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00445; LINK; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

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DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00591; GLYCOSYL_HYDROL_F10; UNKNOWN_1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS01241; LINK_1; 4.
DR PROSITE; PS50963; LINK_2; 4.
DR PROSITE; PS50923; SUSHI; 1.
SQ SEQUENCE 2365 AA; 246477 MW; 39D84712B8F9391E CRC64;

Query Match 91.2%; Score 31; DB 2; Length 2365;
Best Local Similarity 85.7%; Pred. No. 2.1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
DB 1977 TSLGVSV 1983
|||||

RESULT 16
Q7Y2T1_9CAUD
ID Q7Y2T1_9CAUD PRELIMINARY; PRT; 2576 AA.
AC QY2T1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Stx2 converting bacteriophage II.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC Lambda-like viruses.
OC NCBI_TaxID=194949;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Stx2 phage-II;
RX MEDLINE=42697399; PubMed=12813092;
RA DOI=10.1128/JB.185.13.3966-3971.2003;
RA Sato T., Shimizu T., Watarai M., Kobayashi M., Kano S., Hamabata T.,
Takeda Y., Yamasaki S.;
RT "Genome analysis of a novel Shiga toxin 1 (Stx1)-converting phage
which is closely related to Stx2-converting phages but not to other
Stx1-converting phages.";
RL J. Bacteriol. 185:3966-3971(2003).
DR EMBL; AP005154; BAC78032.1; -; Genomic_DNA.
DR InterPro; IPR006025; Pept M Zn BS.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 2576 AA; 284255 MW; 23E34828764E016C CRC64;

Query Match 91.2%; Score 31; DB 2; Length 2576;
Best Local Similarity 85.7%; Pred. No. 2.2e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
DB 404 TAGMGVS 410
|||||

RESULT 17
Q8X2Q2_ECO57
ID Q8X2Q2_ECO57 PRELIMINARY; PRT; 2793 AA.
AC Q8X2Q2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein ECs1242.
GN OrderedLocNameNames=ECs1242;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OC NCBI_TaxID=83334;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHCC;

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RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Stx1 phage;
RX MEDLINE=22697399; PubMed=12813092;
RX DOI=10.1128/JB.185.13.3966-3971.2003;
RA Sato T., Shimizu T., Watarai M., Kobayashi M., Kano S., Hamabata T.,
RA Takeda Y., Yamasaki S.;
RT "Genome analysis of a novel Shiga toxin 1 (Stx1)-converting phage
RT which is closely related to Stx2-converting phages but not to other
RT Stx1-converting phages.";
RL J. Bacteriol. 185:3966-3971(2003).
DR EMBL: AP008153; BAC77866.1; -; Genomic_DNA.
DR InterPro: IPR006025; Pept_M_Zn_BS.
DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 2806 AA; 309690 MW; 0335F50D6E4EA9A9 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 2806;
Best Local Similarity 85.7%; Pred. No. 2.4e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
DB 404 TAGMGVS 410

RESULT 20
Q9TIK9_BPV2 PRELIMINARY; PRT; 2806 AA.
AC Q9TIK9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Bacteriophage VT2-Sa.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC Lambda-like viruses.
OX NCBI_TaxID=97081;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=99419919; PubMed=10492170;
RA Miyamoto H., Nakai W., Yajima N., Fujibayashi A., Higuchi T., Sato K.,
RA Matsushiro A.;
RT "Sequence analysis of Stx2-converting phage VT2-Sa shows a great
RT divergence in early regulation and replication regions.";
RL DNA Res. 6:235-240(1999).
DR EMBL: AP000363; BAA84354.1; -; Genomic_DNA.
DR InterPro: IPR006025; Pept_M_Zn_BS.
DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 2806 AA; 309690 MW; 0335F50D6E4EA9A9 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 2806;
Best Local Similarity 85.7%; Pred. No. 2.4e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
DB 404 TAGMGVS 410

RESULT 21
Q9XJMI_BP933 PRELIMINARY; PRT; 2806 AA.
AC Q9XJMI;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein L0134.
GN Name=L0134;
OS Bacteriophage 933W.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC Lambda-like viruses.

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OX NCBI_TaxID=10730;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=99173898; PubMed=10074068;
RA Plunkett G., III, Rose D.J., Durfee T.J., Blattner F.R.;
RT "Sequence of Shiga toxin 2 phage 933W from Escherichia coli O157:H7.
RT Shiga toxin as a phage late-gene product.";
RL J. Bacteriol. 181:1767-1778(1999).
RN NUCLEOTIDE SEQUENCE.
RA Plunkett G., III.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL: AF125520; AAD25477.1; -; Genomic_DNA.
DR InterPro: IPR006025; Pept_M_Zn_BS.
DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 2806 AA; 309701 MW; 5CFAD8824F83B373 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 2806;
Best Local Similarity 85.7%; Pred. No. 2.4e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
DB 404 TAGMGVS 410

RESULT 22
Q9KXA6_ECO57 PRELIMINARY; PRT; 2806 AA.
AC Q9KXA6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein H0150.
GN Name=H0150;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=20198780; PubMed=10734605; DOI=10.1266/ggs.74.227;
RA Makino K., Yokoyama K., Kubota Y., Yutsudo C.H., Kimura S.,
RA Kurokawa K., Ishii K., Hattori M., Tatsuno I., Abe H., Iida T.,
RA Yamamoto K., Ohnishi M., Hayashi T., Yasunaga T., Honda T.,
RA Sakakawa C., Shinagawa H.;
RT "Complete nucleotide sequence of the prophage VT2-Sakai carrying the
RT verotoxin 2 genes of the enterohemorrhagic Escherichia coli O157:H7
RT derived from the Sakai outbreak.";
RL Genes Genet. Syst. 74:227-239(1999).
DR EMBL: AP000422; BAA94178.1; -; Genomic_DNA.
DR InterPro: IPR006025; Pept_M_Zn_BS.
DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 2806 AA; 309632 MW; 53DC583541A60A32 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 2806;
Best Local Similarity 85.7%; Pred. No. 2.4e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
DB 404 TAGMGVS 410

RESULT 23
Q8X470_ECO57 PRELIMINARY; PRT; 2806 AA.
AC Q8X470;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

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DE Hypothetical protein.
GN OrderedLocusNames=21495;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouisis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
DR EMBL; AE005174; AAG55616.1; -; Genomic_DNA.
DR PIR; D85644; D85644.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 2806 AA; 309701 MW; 5CFAD8824F83B373 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 2806;
Best Local Similarity 85.7%; Pred. NO. 2.4e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TSGMGVS 7
   :|||||
Db 404 TAGMGVS 410

RESULT 24
ID Q811U5_MOUSE PRELIMINARY; PRT; 118 AA.
AC Q811U5.
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-human Fc gamma receptor III 3G8 gamma heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RX PubMed=15059139; DOI=10.1111/j.1365-2141.2004.04893.x;
RA Bruenke J., Fischer B., Barbin K., Schreiter K., Wachter Y., Mahr K.,
RA Tigemeyer F., Niederweis M., Peipp M., Zunino S.J., Repp R.,
RA Valerius T., Fey G.H.;
RT "A recombinant bispecific single-chain Fv antibody against HLA class
RT II and Fc gammaRIII (CD16) triggers effective lysis of lymphoma
RT cells.";
RL Br. J. Haematol. 125:167-179(2004).
DR EMBL; AY173025; AAO18227.1; -; mRNA.
DR HSSP; P01820; 1A7N.
DR SMR; Q811U5; 1-118.
DR Ensembl; ENSMUSG000000057010; Mus musculus.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Receptor.
FT NON TER 1
FT NON TER 118
FT SEQUENCE 118 AA; 12979 MW; F57BB07033742E99 CRC64;
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Query Match 88.2%; Score 30; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. NO. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TSGMGV 6
   :|||||
Db 31 TSGMGV 36

RESULT 25
ID Q8UYQ5_PYRAB PRELIMINARY; PRT; 188 AA.
AC Q8UYQ5.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=PYRAB14520; ORFNames=PAB0965;
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GS5 / Orsay;
RX MEDLINE=22511545; PubMed=12622808;
RX DOI=10.1046/j.1365-2958.2003.03381.x;
RA Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O.,
RA Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
RA Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;
RT "An integrated analysis of the genome of the hyperthermophilic
RT archaeon Pyrococcus abyssi.";
RL Mol. Microbiol. 47:1495-1512(2003).
DR EMBL; AJ248287; CAB50357.1; -; Genomic_DNA.
DR PIR; H75057; H75057.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR007501; DUF531.
DR Pfam; PF04407; DUF531; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 188 AA; 20890 MW; C1CF071D9A9D8AB8 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 188;
Best Local Similarity 85.7%; Pred. NO. 3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 TSGMGVS 7
   :|||||
Db 148 TDGNGVS 154

RESULT 26
ID Q82YV2_ENTFA PRELIMINARY; PRT; 253 AA.
AC Q82YV2.
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ATPase, Para family.
GN OrderedLocusNames=Bf3299;
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
RA Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
RA Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
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RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, BAC
RL clone:B1008E06.";
RT Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005829; BAD26267.1; -, Genomic_DNA.
DR Gramene; Q6H4T2; -.
KW Hypothetical protein.
SQ SEQUENCE 417 AA; 45227 MW; 63C6C528B407D56C CRC64;

Query Match      88.2%; Score 30; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSGMGV 6
Db 291 TSGMGV 296

RESULT 30
ID Q57TW1 9TRYP PRELIMINARY; PRT; 434 AA.
AC Q57TW1;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
DE Hypothetical protein.
GN ORFNames=Tb927.8.6520;
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OC NCBI_TaxID=5691;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ghedin E., Blandin G., Bartholomeu D., Caler E., Haas B., Hannick L.,
RA Shalton J., Hou L., Djikver A., Feldblyum T., Hostettler J.,
RA Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J.,
RA Khalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S.,
RA Wanless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC159703; AAX80013.1; -, Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 434 AA; 48547 MW; 69F02D5053C37BF CRC64;

Query Match      88.2%; Score 30; DB 2; Length 434;
Best Local Similarity 85.7%; Pred. No. 6.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7
Db 81 SSGMGVS 87

RESULT 31
ID Q7QUW4 GIALA PRELIMINARY; PRT; 449 AA.
AC Q7QUW4;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GLP 5613816.2467.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OC NCBI_TaxID=184922;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACB01000089; EAA38817.1; -, Genomic DNA.
SQ SEQUENCE 449 AA; 52112 MW; 6A24348FD40F814B CRC64;

Query Match      88.2%; Score 30; DB 2; Length 449;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSGMGV 6
Db 442 TSGMGV 447

RESULT 32
ID Q6AER2 LEIXX PRELIMINARY; PRT; 472 AA.
AC Q6AER2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
DE Hypothetical protein.
GN OrderedLocusNames=Lxx12950;
OS Leifsonia xyli (subsp. xyli).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococineae; Microbacteriaceae; Leifsonia.
OC NCBI_TaxID=59736;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CTCB07;
RX PubMed=15305603;
RA Monteiro-Vitorello C.B., Camargo L.B.A., Van Sluys M.A.,
RA Kitajima J.P., Truffi D., do Amaral A.M., Harakava R.,
RA de Oliveira J.C.F., Wood D., de Oliveira M.C., Miyaki C.Y.,
RA Takita M.A., da Silva A.C.R., Furlan L.R., Carraro D.M., Camarotte G.,
RA Almeida N.F. Jr., Carter H., Coutinho L.L., El-Dorri H.A.,
RA Ferro M.L.T., Gagliardi P.R., Gigliotti E., Goldman M.H.S.,
RA Goldman G.H., Kimura E.T., Ferro E.S., Kuramae E.E., Lemos E.G.M.,
RA Lemos M.V.F., Mauro S.M.Z., Machado M.A., Marino C.L., Menck C.F.,
RA Nunes L.R., Oliveira R.C., Pereira G.G., Siqueira W., de Souza A.A.,
RA Tsai S.M., Zanca A.S., Simpson A.J.G., Brumby S.M., Setubal J.C.;
RT "The genome sequence of the Gram-positive sugarcane pathogen Leifsonia
RT xyli subsp. xyli.";
RL MOL. Plant Microbe Interact. 17:827-836(2004).
DR EMBL; AE016822; AAT89133.1; -, Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 472 AA; 51813 MW; BD1DE271CA4C3787 CRC64;

Query Match      88.2%; Score 30; DB 2; Length 472;
Best Local Similarity 85.7%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7
Db 26 TSGMGAS 32

RESULT 33
ID O67856 AQUAE PRELIMINARY; PRT; 537 AA.
AC O67856;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein aq_2082.
DE OrderedLocusNames=AQ_2082;
GN Aquifex aeolicus.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OC NCBI_TaxID=63363;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;
```

RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujay M., Huber R.,
 RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 RT aeolicus";
 RL Nature 392:353-358(1998).
 DR EMBL; AF000771; AAC07820.1; -; Genomic_DNA.
 DR PIR; D70478; D70478.
 DR InterPro; IPR007816; ResB.
 DR Pfam; PF05140; ResB; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 537 AA; 61601 MW; 8F73489A1A7676C3 CRC64;
 Query Match 88.2%; Score 30; DB 2; Length 537;
 Best Local Similarity 100.0%; Pred. No. 8.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TSGMGV 6
 DB 354 TSGMGV 359
 |||||
 RESULT 34
 QAT137_TETNG
 ID QAT137_TETNG PRELIMINARY; PRT; 580 AA.
 AC QAT137;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome undetermined SCF10731, whole genome shotgun sequence.
 DE (fragment).
 GN ORFNames=GSTENG0009017001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Maucell E., Bounneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
 RA Bionmont C., Skalli Z., Catellano L., Poulain J., De Berardinis V.,
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chappie C., McKernan K.J., McSwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.,
 RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype";
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -!- SIMILARITY: Contains 4 PDZ (DHR) domains.
 DR EMBL; CA9010731; CAF93395.1; -; Genomic_DNA.
 DR InterPro; IPR001478; PDZ.
 DR Pfam; PF00595; PDZ; 4.
 DR SMART; SM00228; PDZ; 4.
 DR PROSITE; PS0106; PDZ; 4.
 FT NON_TER 1 580
 FT NON_TER 580 580
 SQ SEQUENCE 580 AA; 63436 MW; 9D46C5CF0D95FA4D CRC64;
 Query Match 88.2%; Score 30; DB 2; Length 580;

Best Local Similarity 71.4%; Pred. No. 8.8e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TSGMGV 7
 DB 353 TSGMGV 359
 |||||
 RESULT 35
 Q8RTR2_9PROT
 ID Q8RTR2_9PROT PRELIMINARY; PRT; 814 AA.
 AC Q8RTR2;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Glycine cleavage system T protein, putative.
 GN Name=gvT;
 OS uncultured proteobacterium.
 OC Bacteria; Proteobacteria; environmental samples.
 OX NCBI_TaxID=153809;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21822632; PubMed=11832943; DOI=10.1038/415630a;
 RA Beja O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Preston C.M.,
 RA Hamada T., Eisen J.A., Fraser C.M., DeLong E.F.;
 RT "Unsuspected diversity among marine aerobic anoxygenic phototrophs";
 RL Nature 415:630-633(2002).
 DR EMBL; AE008919; AAL76414.1; -; Genomic_DNA.
 DR GO; GO:0005733; Cytoplasm; IEA.
 DR GO; GO:0004047; F:aminomethyltransferase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0006546; P:glycine catabolism; IEA.
 DR InterPro; IPR006076; Fcd oxdred.
 DR InterPro; IPR006222; GCV_T.
 DR InterPro; IPR000205; NAD_BS.
 DR Pfam; PF01266; DAO; 1.
 DR Pfam; PF01571; GCV T; 1.
 SQ SEQUENCE 814 AA; 90233 MW; DBEE615BC2B0D2E4 CRC64;
 Query Match 88.2%; Score 30; DB 2; Length 814;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TSGMGV 6
 DB 576 TSGMGV 581
 |||||
 RESULT 36
 Q6SFA3_9BACT
 ID Q6SFA3_9BACT PRELIMINARY; PRT; 814 AA.
 AC Q6SFA3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Oxidoreductase, FAD-binding.
 GN ORFNames=EBAC000-69B03.68;
 OS uncultured bacterium 581.
 OC Bacteria; environmental samples.
 OX NCBI_TaxID=257401;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA DeLong E.F.;
 RT "Monterey Bay Coastal Ocean Microbial Observatory environmental clone
 RT sequencing";
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., DeLong E.F.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY458648; AAR38319.1; -; Genomic_DNA.
 DR GO; GO:0005737; Cytoplasm; IEA.

DR GO: 0004047; F:aminomethyltransferase activity; IEA.
 DR GO: 0016491; F:oxidoreductase activity; IEA.
 DR GO: 0006118; P:electron transport; IEA.
 DR GO: 0006546; P:glycine catabolism; IEA.
 DR InterPro: IPR006076; F:ad oxid.
 DR InterPro: IPR006222; GCV T.
 DR InterPro: IPR00205; NAD_BS.
 DR Pfam: PF01266; DAO; 1.
 DR Pfam: PF01571; GCV_T; 1.

SQ SEQUENCE 814 AA; 90235 MW; 0D4F9717D6A9F63 CRC64;
 Query Match 88.2%; Score 30; DB 2; Length 814;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSGMGV 6

Db 576 TSGMGV 581

RESULT 37

Q6Z4T5 ORYSA PRELIMINARY; PRT; 1033 AA.
 AC Q6Z4T5;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Putative PolI-like DNA polymerase.
 GN Name=OSJNBa0054L03.39-1; Synonyms=OJ1134_B10.8-1;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 8, BAC
 RT clone:OSJNBa0054L03."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005164; BAD05554.1; -; Genomic DNA.
 DR EMBL; AP003882; BAD05227.1; -; Genomic DNA.
 DR HSSP; P19821; LUXE.
 DR Gramene; Q6Z4T5; -.
 DR GO: 0005622; C:intracellular; IEA.
 DR GO: 0008408; F:3'-5' exonuclease activity; IEA.
 DR GO: 0003677; F:DNA binding; IEA.
 DR GO: 0003887; F:DNA-directed DNA polymerase activity; IEA.
 DR GO: 0006260; P:DNA replication; IEA.
 DR InterPro: IPR002562; 3_5_exonuclease.
 DR InterPro: IPR001098; DNA_pol.
 DR Pfam; PF01612; 3_5_exonuc; 1.
 DR Pfam; PF00476; DNA_pol_A; 1.
 DR PRINTS; PR00868; DNAPOLI.
 DR SMART; SM00482; POLAC; 1.
 DR SEQUENCE 1033 AA; 116237 MW; 187D934EEF6C3FE1 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 1033;
 Best Local Similarity 85.7%; Pred. No. 1.5e+03;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7

Db 55 SSGMGVS 61

RESULT 38

Q6Z4T3 ORYSA PRELIMINARY; PRT; 1035 AA.
 AC Q6Z4T3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Putative PolI-like DNA polymerase.
 GN Name=OSJNBa0054L03.41; Synonyms=OJ1134_B10.10;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 8, BAC
 RT clone:OSJNBa0054L03."
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005164; BAD05556.1; -; Genomic DNA.
 DR EMBL; AP003882; BAD05229.1; -; Genomic DNA.
 DR HSSP; P19821; LUXE.
 DR Gramene; Q6Z4T3; -.
 DR GO: 0005622; C:intracellular; IEA.
 DR GO: 0008408; F:3'-5' exonuclease activity; IEA.
 DR GO: 0003677; F:DNA binding; IEA.
 DR GO: 0003887; F:DNA-directed DNA polymerase activity; IEA.
 DR GO: 0006260; P:DNA replication; IEA.
 DR InterPro: IPR002562; 3_5_exonuclease.
 DR InterPro: IPR001098; DNA_pol.
 DR InterPro: IPR002298; DNA_pol.
 DR Pfam; PF01612; 3_5_exonuc; 1.
 DR Pfam; PF00476; DNA_pol_A; 1.
 DR PRINTS; PR00868; DNAPOLI.
 DR SMART; SM00482; POLAC; 1.
 DR SEQUENCE 1035 AA; 116209 MW; BEBCBA9412AB1F29 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 1035;
 Best Local Similarity 85.7%; Pred. No. 1.5e+03;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7

Db 51 SSGMGVS 57

RESULT 39

Q54XP6 DICDI PRELIMINARY; PRT; 1045 AA.
 AC Q54XP6;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=DD80206214;
 OS Dictyostelium discoideum (slime mold).
 OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA SPAIN=AX4;
 RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
 RA Sugang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
 RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
 RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
 RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,

Query Match 88.2%; Score 30; DB 2; Length 1033;
 Best Local Similarity 85.7%; Pred. No. 1.5e+03;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7

Db 55 SSGMGVS 61

the early vertebrate proto-karyotype.";

RT Nature 431:946-957(2004).

RL [2]

RN NUCLEOTIDE SEQUENCE.

RP Genoscope; Whitehead Institute Centre for Genome Research;

RG Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

RL Submitter (FEB-2004) to the EMBL/GenBank/DBJ databases.

CC -1- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

CC EMBL; CAEE01007518; CAF90393.1; -; Genomic_DNA.

DR NON_TER 1 1

FT NON_TER 1050 1050

FT SEQUENCE 1050 AA; 114803 MW; A400D1E0E728A2E8 CRC64;

SQ

Query Match 88.2%; Score 30; DB 2; Length 1050;

Best Local Similarity 85.7%; Pred. No. 1.6e+03;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps

Qy 1 TSGMGVS 7

Db 531 TSGGVGS 537

|||||

RESULT 41

IF2P SCHPO STANDARD; PRT; 1079 AA.

ID AC Q10251;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Eukaryotic translation initiation factor 5B (eIF-5B) (Translation

DE initiation factor IF-2).

DE ORFNames=SPAC56F8.03;

GN Schizosaccharomyces pombe (Fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

OC NCBI_TaxID=4896;

OX [1]

NUCROTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RP STRAIN=972;

RC MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;

RX Wood V., Gilliam R., Rajandream M.A., Lyne M.H., Lyne R., Stewart A.,

RA Sgouras J.G., Peat N., Hayles J., Baker S.G., Basham D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,

RA Gentles S., Goble A., Hamlin N., Harris D.E., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA James K.D., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Mooney P., Moule S., Mungall K.L., Murphy L.D., Niblett D., Odell C.,

RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitch E.,

RA Rutherford K.M., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Skellton J., Simmonds M.N., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Woodward J.R., Volktaert G., Aert R., Robben J., Grymonprez B.,

RA Waltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

RA Gabel C., Fuchs M., Duesenroeth A., Fritz C., Holzer E., Moesl D.,

RA Hilbert H., Borzym K., Langer I., Beck A., Lehrach R., Reinhardt R.,

RA Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,

RA Daga R.M., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.L.,

RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;

RT "The genome sequence of Schizosaccharomyces pombe.";

CC Nature 415:871-880(2002).

CC -1- FUNCTION: Function in general translation initiation by promoting

CC the binding of the formylmethionine-tRNA to ribosomes. Seems to

CC function along with eIF-2 (By similarity).

CC -1- SIMILARITY: Belongs to the IF-2 family.

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EMBL; Z69728; CAA93574.1; -; Genomic_DNA.
DR PIR; T38913; T38913.
DR HSSP; O26359; IG7S.
DR GeneDB Spombe; SPAC56F8.03; -.
DR InterPro; IPR004161; EFTU_D2.
DR InterPro; IPR000178; IF2.
DR InterPro; IPR000795; ProtSyn_GTP_bd.
DR InterPro; IPR005225; Small_GTP_bd.
DR Pfam; PF00009; GTP_EFTU; 1.
DR Pfam; PF03144; GTP_EFTU_D2; 1.
DR PRINTS; PR00315; ELONGATNFCT.
DR ProDom; PD186100; IF2; 1.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
DR PROSITE; PS01176; IF2; FALSE_NEG.
KW Complete proteome; GTP-binding; Initiation factor; Nucleotide-binding;
KW Protein biosynthesis.
FT NP_BIND 491 498 GTP (By similarity).
SQ SEQUENCE 1079 AA; 119931 MW; 73A01CE9333C1F6AA CRC64;

Query Match 88.2%; Score 30; DB 1; Length 1079;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7
| | | | |

Db 829 TSGIGVS 835

RESULT 42

ID Q9XX01_CABEL PRELIMINARY; PRT; 1088 AA.
AC Q9XX01;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein twk-31.
GN Name=twk-31; ORFNames=Y47D3B.5, Y47D3B.5a;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=Bristol N2; PubMed=9851916;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology."
RL Science 282:2012-2018 (1998).
DR EMBL; AL031635; CAA01041.2; -; Genomic_DNA.
DR PIR; T26953; T26953.
DR HSSP; Q54397; 1BL8.
DR Ensembl; Y47D3B.5; Caenorhabditis elegans.
DR WormBase; WBGene0006683; Y47D3B.5.
DR WormPep; Y47D3B.5a; CE31838.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005267; F:potassium channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR PRINTS; PR01333; 2POREKCHANEL.
KW Complete proteome; Hypothetical protein; Ion transport; Ionic channel;
KW Transmembrane; Transport.
SQ SEQUENCE 1088 AA; 122279 MW; BF8FPA0F9E78C55F7 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 1088;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TSGMGVS 7
| | | | |

Db 956 TSGMGTS 962

RESULT 43

ID Q61BN8_CABER PRELIMINARY; PRT; 1100 AA.
AC Q61BN8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG13286 (Pragmat).
GN Name=CBG13286; briggssae.
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
[1]

RP NUCLEOTIDE SEQUENCE.

RG The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.

DR EMBL; CAA0100063; CAB67712.1; -; Genomic_DNA.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005216; F:ion channel activity; IEA.

DR GO; GO:0005267; F:potassium channel activity; IEA.

DR GO; GO:0006811; P:ion transport; IEA.

DR GO; GO:0006813; P:potassium ion transport; IEA.

DR InterPro; IPR003280; K+channel_2pore.

DR InterPro; IPR001622; K+channel_pore.

DR PRINTS; PR01333; 2POREKCHANEL.

KW Hypothetical protein; Ion transport; Ionic channel; Transmembrane;

KW Transport.

FT NON_TER 1 1
SQ SEQUENCE 1100 AA; 124435 MW; 292B4110B011A843 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 1100;

Best Local Similarity 85.7%; Pred. No. 1.6e+03;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7

Db 942 TSGMGTS 948

RESULT 44

ID Q6EUT8_CABEL PRELIMINARY; PRT; 1136 AA.
AC Q6EUT8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein twk-31.
GN Name=twk-31; ORFNames=Y47D3B.5, Y47D3B.5B;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=Bristol N2;

RX MEDLINE=99069613; PubMed=9851916;

RG The C. elegans sequencing consortium;

RT "Genome sequence of the nematode C. elegans: a platform for

```

RT investigating biology.";
RL Science 282:2012-2018 (1998).
DR EMBL; AL031635; CAH04762.1; -; Genomic DNA.
DR Ensembl; Y47D3B.5; Caenorhabditis elegans.
DR WormBase; WBGene00006683; Y47D3B.5.
DR WormPeP; Y47D3B.5b; CE19178.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005267; F:potassium channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR003280; K:channel_pore.
DR InterPro; IPR001622; K:channel_pore.
DR PRINTS; PR01333; 2PORECHANNEL.
KW Complete proteome; Hypothetical protein; Ion transport; Ionic channel;
KW Transmembrane; Transport.
SQ SEQUENCE 1136 AA; 127586 MW; 3C9B50B1DEBEC1047 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 1136;
Best Local Similarity 85.7%; Pred. No. 1.7e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
   |||||
DB 956 TSGMGTS 962

RESULT 45
Q747Y4 GEOSL
ID Q747Y4 GEOSL PRELIMINARY; PRT; 1175 AA.
AC Q747Y4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=GSU3131;
OS Geobacter sulfurreducens.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Geobacteraceae; Geobacter.
OX NCBI_TaxID=335554;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PCA / ATCC 51573;
RX PubMed=14671304; DOI=10.1126/science.1088727;
RA Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA Daviden T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
RA Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R.,
RA Van Aken S.E., Lovley D.R., Fraser C.M.;
RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
RT environments.";
RL Science 302:1967-1969 (2003).
DR EMBL; AE017180; AAR36522.1; -; Genomic DNA.
DR TIGR; GSU3131; -.
DR InterPro; IPR002173; PFkB.
DR PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 1175 AA; 123298 MW; 3133E9AB71D12267 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 1175;
Best Local Similarity 71.4%; Pred. No. 1.7e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
   |||||
DB 68 TSGMGIA 74

RESULT 46
Q6Y5E0_9VIRU

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ID Q6Y5E0_9VIRU PRELIMINARY; PRT; 1689 AA.
AC Q6Y5E0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein.
OS Crimean-Congo hemorrhagic fever virus.
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Nairovirus.
OX NCBI_TaxID=11593;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14976418; DOI=10.1023/B:VIRU.0000016857.94136.89;
RA Seregin S.V., Samokhvalov E.I., Petrova I.D., Vyshemirskii O.I.,
RA Samokhvalova E.G., Lvov D.K., Gutorov V.V., Tyunnikov G.I.,
RA Shchelkunov S.N., Netesov S.V., Petrov V.S.;
RT "Genetic characterization of the m RNA segment of crimean-congo
RT hemorrhagic fever virus strains isolated in Russia and Tajikistan.";
RL Virus Genes 28:187-193 (2004).
DR EMBL; AY179962; AAO62016.1; -; Genomic RNA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR001865; Ribosomal_S2.
DR InterPro; IPR007087; Znf_C2H2_-.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
KW Envelope protein.
SQ SEQUENCE 1689 AA; 187110 MW; 5DB5F609DCD33B02 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 1689;
Best Local Similarity 71.4%; Pred. No. 2.5e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSGMGVS 7
   |||||
DB 104 TTGMGIS 110

RESULT 47
Q51YX7 MAGGR
ID Q51YX7 MAGGR PRELIMINARY; PRT; 2125 AA.
AC Q51YX7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=MG07408.4;
OS Magnaporthe grisea 70-15.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaportha.
OX NCBI_TaxID=242507;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Ait-zahra M., Allen T., Allen T., Anderson M., Anderson S.,
RA Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
RA Bayul T., Blitshetev B., Bloom T., Blye J., Boguslavskiy L.,
RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Geardin G., Gnerre S.,
RA Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysseles M., Karlsson E.,
RA Kells C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,

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RA Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,
RA Mozes J., Mulrain L., Munson G., Naylor J., Neves C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotohio B.,
RA O'Neill K., Oseman S., Parker S., Perrin D., Phunkhang P., Piquani B.,
RA Purcell S., Rachupka T., Ramaamy U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutman M., Schubach R., Seaman C., Settupalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA Spencer B., Staiker J., Stange-thomann N., Stavropoulos S.,
RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,
RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA Zimmer A., Zody M., Lander E.;
RT "The genome sequence of Magnaporthe grisea";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RP [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RC STRAIN=70-15;
RA Zhu H., Blackmon B.;
DR EMBL; AACU01000890; EAA53131.1; -; Genomic_DNA.
DR InterPro; IPR001440; TPR.
DR InterPro; IPR011990; TPR-like_helical.
DR SMART; SM00028; TPR; 3.
DR PROSITE; PS50005; TPR; 2.
DR PROSITE; PS50293; TPR_REGION; 1.
KW Hypothetical protein; Repeat; TPR repeat.
SQ SEQUENCE 2125 AA; 232813 MW; B1F5A282DA4861C9 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 2125;
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Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db 2115 TSLGLIS 2121

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DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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GN ORFNames=F25C8.3, F25C8.3b;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
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RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z81512; CAE46668.1; -; Genomic DNA.
DR Ensembl; F25C8.3; Caenorhabditis elegans.
KW Hypothetical protein; Repeat; TPR repeat.
SQ SEQUENCE 2125 AA; 232813 MW; B1F5A282DA4861C9 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 2125;
Best Local Similarity 71.4%; Pred. No. 3.1e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7
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Db 2115 TSLGLIS 2121

RESULT 48
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AC Q7JKT8;
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DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein F25C8.3b.
GN ORFNames=F25C8.3, F25C8.3b;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z81512; CAE46668.1; -; Genomic DNA.
DR Ensembl; F25C8.3; Caenorhabditis elegans.

DR WormBase; WBGene00009105; F25C8.3.
DR WormPep; F25C8.3b; CE35507.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 3175 AA; 357150 MW; 2349FAF5914D10AE CRC64;

Query Match 88.2%; Score 30; DB 2; Length 3175;
Best Local Similarity 85.7%; Pred. No. 4.5e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7
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Db 2754 TEGMGVS 2760

RESULT 49
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AC Q9XV66;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein F25C8.3a.
GN ORFNames=F25C8.3, F25C8.3a;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z81512; CAB04172.2; -; Genomic_DNA.
DR PIR; T21328; T21328.
DR Ensembl; F25C8.3; Caenorhabditis elegans.
DR WormBase; WBGene00009105; F25C8.3.
DR WormPep; F25C8.3a; CE31916.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 3184 AA; 358109 MW; F296F176A3AFD120 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 3184;
Best Local Similarity 85.7%; Pred. No. 4.6e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TSGMGVS 7
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Db 2763 TEGMGVS 2769

RESULT 50
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DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE SrfAC surfactin synthetase (Fragment).
GN Name=srfAC;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A1/3;
RX PubMed=15480790; DOI=10.1007/s00438-004-1056-Y;
RA Hofemeister J., Conrad B., Adler B., Hofemeister B., Feesche J.,
RA Kucheryava N., Steinborn G., Franke P., Grammel N., Zwintscher A.,
RA Leenders F., Hitzeroth G., Vater J.;
RT "Genetic analysis of the biosynthesis of non-ribosomal peptide- and
RT polyketide-like antibiotics, iron uptake and biofilm formation by

RT Bacillus subtilis Al/3.";
 RL Mol. Genet. Genomics 272:363-378(2004).
 RN [2]
 RC NUCLEOTIDE SEQUENCE.
 RP STRAIN=Al/3;
 RA Hofemeister J.W., Adler B.C., Conrad B., Hofemeister B.H., Stein T.,
 RA Leenders F., Vater J.;
 RT "Lipopeptide antibiotic, siderophore and polyketide gene activities of
 RT Bacillus subtilis Al/3: Gene tagging and mutation studies.";
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF520864; AAQ08791.1; -; Genomic DNA.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR000873; AMP-bind.
 DR Pfam; PF0501; AMP-binding; 1.
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 FT NON_TER 156
 SQ SEQUENCE 156 AA; 17129 MW; 3EC80F784B3793C7 CRC64;

Query Match 85.3%; Score 29; DB 2; Length 156;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SGMGVS 7
 Db 54 SGMGVS 59

Search completed: February 23, 2006, 09:51:20
 Job time : 89.3077 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 09:29:34 ; Search time 137.846 Seconds
(without alignments)
50.999 Million cell updates/sec

Title: US-10-723-872-24

Perfect score: 95

Sequence: 1 HIYWDKRYNPSLKS 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

A_Geneseq_21.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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|------------|-------|-------------|--------|----|-------------|
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| 2 | 95 | 100.0 | 16 | 2 | AAY23776 |
| 3 | 95 | 100.0 | 16 | 2 | AAY18112 |
| 4 | 95 | 100.0 | 16 | 5 | AAO18532 |
| 5 | 95 | 100.0 | 16 | 6 | ABP58280 |
| 6 | 95 | 100.0 | 16 | 9 | ADZ08829 |
| 7 | 95 | 100.0 | 41 | 3 | AAY91018 |
| 8 | 95 | 100.0 | 120 | 8 | ADQ09629 |
| 9 | 95 | 100.0 | 121 | 2 | AAY23780 |
| 10 | 95 | 100.0 | 121 | 2 | AAY18122 |
| 11 | 95 | 100.0 | 121 | 5 | AAO18528 |
| 12 | 95 | 100.0 | 121 | 8 | AAO18528 |
| 13 | 95 | 100.0 | 122 | 8 | ADG25814 |
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| 15 | 95 | 100.0 | 123 | 6 | ABP58285 |
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| 18 | 95 | 100.0 | 140 | 2 | AAY18121 |
| 19 | 95 | 100.0 | 141 | 2 | AAR70192 |
| 20 | 95 | 100.0 | 141 | 2 | AAR70191 |
| 21 | 95 | 100.0 | 141 | 2 | AAY23770 |
| 22 | 95 | 100.0 | 141 | 2 | AAY23769 |
| 23 | 95 | 100.0 | 141 | 2 | AAY18125 |
| 24 | 95 | 100.0 | 142 | 5 | ABG76934 |

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| 25 | 95 | 100.0 | 142 | 8 | ADR88420 |
| 26 | 95 | 100.0 | 142 | 9 | AdZ08834 |
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| 28 | 95 | 100.0 | 472 | 6 | ABP58289 |
| 29 | 91 | 95.8 | 119 | 7 | ABR62361 |
| 30 | 91 | 95.8 | 123 | 6 | ABP58283 |
| 31 | 91 | 95.8 | 123 | 7 | AAV42963 |
| 32 | 91 | 95.8 | 123 | 7 | AAV42964 |
| 33 | 91 | 95.8 | 142 | 7 | AAV42973 |
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| 36 | 90 | 94.7 | 16 | 2 | AAR54105 |
| 37 | 90 | 94.7 | 22 | 8 | ADP71373 |
| 38 | 90 | 94.7 | 122 | 2 | AAR54101 |
| 39 | 90 | 94.7 | 122 | 2 | AAR54110 |
| 40 | 90 | 94.7 | 148 | 2 | AAW26239 |
| 41 | 90 | 94.7 | 246 | 2 | AAR58612 |
| 42 | 88 | 92.6 | 121 | 9 | AEA37667 |
| 43 | 87 | 91.6 | 118 | 8 | ADF71905 |
| 44 | 87 | 91.6 | 118 | 8 | ADF71910 |
| 45 | 87 | 91.6 | 448 | 8 | ADF71908 |
| 46 | 87 | 91.6 | 448 | 8 | ADF71912 |
| 47 | 85 | 89.5 | 117 | 8 | ADF71914 |
| 48 | 85 | 89.5 | 448 | 8 | ADF71916 |
| 49 | 84.5 | 88.9 | 121 | 5 | ABG67188 |
| 50 | 84 | 88.4 | 120 | 2 | AAR88109 |
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| 53 | 83 | 87.4 | 118 | 7 | ADD05272 |
| 54 | 83 | 87.4 | 118 | 8 | ADM80363 |
| 55 | 83 | 87.4 | 120 | 8 | ADU17896 |
| 56 | 83 | 87.4 | 120 | 8 | ADU17899 |
| 57 | 83 | 87.4 | 120 | 8 | ADU17906 |
| 58 | 83 | 87.4 | 120 | 8 | ADU17897 |
| 59 | 83 | 87.4 | 120 | 8 | ADU17903 |
| 60 | 83 | 87.4 | 120 | 8 | ADU17900 |
| 61 | 83 | 87.4 | 120 | 8 | ADU17902 |
| 62 | 83 | 87.4 | 120 | 8 | ADU17901 |
| 63 | 83 | 87.4 | 120 | 9 | ADV67313 |
| 64 | 83 | 87.4 | 120 | 9 | ADV67324 |
| 65 | 83 | 87.4 | 120 | 9 | ADV67334 |
| 66 | 83 | 87.4 | 120 | 9 | ADV67327 |
| 67 | 83 | 87.4 | 120 | 9 | ADV67317 |
| 68 | 83 | 87.4 | 120 | 9 | ADV67321 |
| 69 | 83 | 87.4 | 120 | 9 | ADV67318 |
| 70 | 83 | 87.4 | 120 | 9 | ADV67323 |
| 71 | 83 | 87.4 | 120 | 9 | ADV67319 |
| 72 | 83 | 87.4 | 120 | 9 | ADV67316 |
| 73 | 83 | 87.4 | 120 | 9 | ADV67322 |
| 74 | 83 | 87.4 | 120 | 9 | ADV67328 |
| 75 | 83 | 87.4 | 120 | 9 | ADV67329 |
| 76 | 83 | 87.4 | 120 | 9 | ADV67331 |
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| 81 | 83 | 87.4 | 121 | 9 | ADV67326 |
| 82 | 83 | 87.4 | 121 | 9 | ADV67325 |
| 83 | 83 | 87.4 | 122 | 9 | ADY96956 |
| 84 | 83 | 87.4 | 122 | 9 | ADY96915 |
| 85 | 83 | 87.4 | 139 | 9 | ADY67307 |
| 86 | 83 | 87.4 | 228 | 8 | ADN41872 |
| 87 | 82 | 86.3 | 126 | 7 | ADP44921 |
| 88 | 82 | 86.3 | 126 | 7 | ADK17395 |
| 89 | 82 | 86.3 | 126 | 8 | ADG42817 |
| 90 | 82 | 86.3 | 139 | 2 | AAR38315 |
| 91 | 82 | 86.3 | 139 | 2 | AAV50688 |
| 92 | 82 | 86.3 | 139 | 6 | ADB17723 |
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| 94 | 82 | 86.3 | 139 | 7 | ADG46843 |
| 95 | 82 | 86.3 | 253 | 7 | ADF44904 |
| 96 | 82 | 86.3 | 253 | 7 | ADF44912 |
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| | | | | | | | | | | | | | | | |
|-----|----|------|-----|---|----------|----------|------------|-----|----|------|-----|---|----------|----------|-----------|
| 98 | 82 | 86.3 | 253 | 7 | ADK17378 | Adk17378 | Anti-huma | 171 | 70 | 73.7 | 120 | 6 | ABO10820 | ABO10820 | Human ger |
| 99 | 82 | 86.3 | 253 | 8 | ADG42808 | Adg42808 | Human CCR | 172 | 70 | 73.7 | 120 | 6 | ABO10813 | ABO10813 | Mouse mon |
| 100 | 82 | 86.3 | 253 | 8 | ADG42800 | Adg42800 | Human CCR | 173 | 70 | 73.7 | 120 | 6 | ADZ47654 | ADZ47654 | Mouse ant |
| 101 | 80 | 84.2 | 118 | 8 | ADG25807 | Adg25807 | Anti-CD30 | 174 | 70 | 73.7 | 122 | 6 | ABO10821 | ABO10821 | Mouse/hum |
| 102 | 80 | 84.2 | 120 | 8 | ADU17907 | Adu17907 | Humanised | 175 | 70 | 73.7 | 122 | 9 | ADZ47748 | ADZ47748 | CDR-graft |
| 103 | 80 | 84.2 | 120 | 8 | ADU17905 | Adu17905 | Humanised | 176 | 70 | 73.7 | 123 | 7 | ADD94127 | ADD94127 | Mouse HUI |
| 104 | 80 | 84.2 | 120 | 8 | ADU17904 | Adu17904 | Humanised | 177 | 69 | 72.6 | 16 | 5 | ABP66465 | ABP66465 | Human RSV |
| 105 | 80 | 84.2 | 259 | 3 | ABO70778 | AbO70778 | Antiviral | 178 | 69 | 72.6 | 16 | 5 | ABP66463 | ABP66463 | Human RSV |
| 106 | 80 | 84.2 | 259 | 4 | ABW70885 | AbW70885 | TMV 54K P | 179 | 69 | 72.6 | 16 | 5 | ABU69326 | ABU69326 | Respirato |
| 107 | 80 | 84.2 | 259 | 8 | ADV20697 | Adv20697 | ScFv 54-1 | 180 | 69 | 72.6 | 16 | 6 | ABU69328 | ABU69328 | Respirato |
| 108 | 79 | 83.2 | 141 | 2 | AAV07486 | AaV07486 | Anti-HIV- | 181 | 69 | 72.6 | 16 | 7 | ADE35823 | ADE35823 | SYNAGIS a |
| 109 | 78 | 82.1 | 103 | 3 | AAQ00042 | AaQ00042 | Human sec | 182 | 69 | 72.6 | 16 | 7 | ADE35821 | ADE35821 | SYNAGIS a |
| 110 | 78 | 82.1 | 124 | 8 | ADP09713 | AdP09713 | Glycosylt | 183 | 69 | 72.6 | 16 | 8 | ADI56985 | ADI56985 | RSV antib |
| 111 | 78 | 82.1 | 143 | 2 | AR54092 | Ar54092 | Sequence | 184 | 69 | 72.6 | 16 | 8 | ADI56983 | ADI56983 | RSV antib |
| 112 | 77 | 81.1 | 16 | 7 | ADJ32099 | AdJ32099 | Human int | 185 | 69 | 72.6 | 16 | 9 | ADW19965 | ADW19965 | RSV anti |
| 113 | 77 | 81.1 | 16 | 9 | ADW77410 | AdW77410 | Human pla | 186 | 69 | 72.6 | 16 | 9 | ADW19963 | ADW19963 | RSV anti |
| 114 | 77 | 81.1 | 99 | 5 | ABG78178 | AbG78178 | Human Fv | 187 | 69 | 72.6 | 16 | 9 | AEB06945 | AEB06945 | RSV-speci |
| 115 | 77 | 81.1 | 99 | 5 | ABG91869 | AbG91869 | Human ant | 188 | 69 | 72.6 | 16 | 9 | AEB06947 | AEB06947 | RSV-speci |
| 116 | 77 | 81.1 | 100 | 5 | ABG78181 | AbG78181 | Human Fv | 189 | 68 | 71.6 | 16 | 4 | AAE10481 | AAE10481 | Humanised |
| 117 | 77 | 81.1 | 100 | 5 | ABG91872 | AbG91872 | Human ant | 190 | 68 | 71.6 | 16 | 4 | AAG63248 | AAG63248 | Complemen |
| 118 | 77 | 81.1 | 100 | 6 | ABO27079 | AbO27079 | Human ger | 191 | 68 | 71.6 | 16 | 5 | ABP66356 | ABP66356 | Human RSV |
| 119 | 77 | 81.1 | 100 | 7 | ADF09906 | AdF09906 | Antibody | 192 | 68 | 71.6 | 16 | 5 | ABG31437 | ABG31437 | Human-mur |
| 120 | 77 | 81.1 | 100 | 7 | ADF10116 | AdF10116 | Antibody | 193 | 68 | 71.6 | 16 | 5 | AAE28011 | AAE28011 | Human mod |
| 121 | 77 | 81.1 | 100 | 7 | ADP10014 | AdP10014 | VEGF anti | 194 | 68 | 71.6 | 16 | 5 | ABU69219 | ABU69219 | Respirato |
| 122 | 77 | 81.1 | 100 | 7 | ADJ80292 | AdJ80292 | VH gene 1 | 195 | 68 | 71.6 | 16 | 6 | ABG75666 | ABG75666 | SYNAGIS h |
| 123 | 77 | 81.1 | 100 | 9 | ADY75297 | AdY75297 | Protein e | 196 | 68 | 71.6 | 16 | 7 | ADE35714 | ADE35714 | SYNAGIS a |
| 124 | 77 | 81.1 | 100 | 9 | AEC20846 | AeC20846 | Human var | 197 | 68 | 71.6 | 16 | 8 | ADI56876 | ADI56876 | RSV antib |
| 125 | 77 | 81.1 | 119 | 2 | AAE62299 | AaE62299 | Human imm | 198 | 68 | 71.6 | 16 | 8 | ADJ37791 | ADJ37791 | SYNAGIS f |
| 126 | 77 | 81.1 | 149 | 2 | AAV34305 | AaV34305 | IGG antib | 199 | 68 | 71.6 | 16 | 8 | ADS94305 | ADS94305 | Antibody |
| 127 | 77 | 81.1 | 159 | 2 | AAV34307 | AaV34307 | IGG antib | 200 | 68 | 71.6 | 16 | 8 | ADT89199 | ADT89199 | Humanised |
| 128 | 77 | 81.1 | 228 | 7 | ADJ32130 | AdJ32130 | Human int | 201 | 68 | 71.6 | 16 | 9 | ADM19856 | ADM19856 | RSV anti |
| 129 | 76 | 80.0 | 129 | 6 | AAE35208 | AaE35208 | Human IGE | 202 | 68 | 71.6 | 16 | 9 | AEB06838 | AEB06838 | RSV-speci |
| 130 | 75 | 78.9 | 16 | 8 | ADL27473 | AdL27473 | CDR from | 203 | 68 | 71.6 | 120 | 2 | AAR92088 | AAR92088 | CDR-graft |
| 131 | 75 | 78.9 | 122 | 9 | ADV14358 | AdV14358 | Hybridoma | 204 | 68 | 71.6 | 120 | 2 | AAE10476 | AAE10476 | Humanised |
| 132 | 75 | 78.9 | 133 | 9 | ADY70950 | AdY70950 | Human mon | 205 | 68 | 71.6 | 120 | 4 | AAE10474 | AAE10474 | Humanised |
| 133 | 75 | 78.9 | 157 | 8 | ADL27471 | AdL27471 | Amino aci | 206 | 68 | 71.6 | 120 | 4 | AAG63259 | AAG63259 | Anti-RSV |
| 134 | 75 | 78.9 | 452 | 9 | ADY70962 | AdY70962 | Human mon | 207 | 68 | 71.6 | 120 | 4 | AAG63263 | AAG63263 | Anti-RSV |
| 135 | 75 | 78.9 | 517 | 6 | ABU08019 | AbU08019 | Monoclonal | 208 | 68 | 71.6 | 120 | 4 | AAG63265 | AAG63265 | Anti-RSV |
| 136 | 75 | 78.9 | 518 | 7 | ADF65782 | AdF65782 | Human ant | 209 | 68 | 71.6 | 120 | 4 | AAG63261 | AAG63261 | Anti-RSV |
| 137 | 75 | 78.9 | 518 | 8 | ADJ92518 | AdJ92518 | Human SOJ | 210 | 68 | 71.6 | 120 | 4 | AAG63267 | AAG63267 | Anti-RSV |
| 138 | 74 | 77.9 | 118 | 7 | ADD05280 | AdD05280 | Female mo | 211 | 68 | 71.6 | 120 | 4 | ABG31432 | ABG31432 | Humanised |
| 139 | 73 | 76.8 | 121 | 2 | ADW25396 | AdW25396 | WO9932630 | 212 | 68 | 71.6 | 120 | 4 | ABG31433 | ABG31433 | Amino aci |
| 140 | 73 | 76.8 | 127 | 6 | ADB97818 | AdB97818 | HEV relat | 213 | 68 | 71.6 | 120 | 5 | ABP66363 | ABP66363 | Human RSV |
| 141 | 73 | 76.8 | 124 | 7 | ABW35207 | AbW35207 | Human IGE | 214 | 68 | 71.6 | 120 | 5 | ABP66432 | ABP66432 | Human RSV |
| 142 | 73 | 76.8 | 131 | 4 | ABE11310 | AbE11310 | Human ant | 215 | 68 | 71.6 | 120 | 5 | ABP66361 | ABP66361 | Human RSV |
| 143 | 73 | 76.8 | 499 | 4 | AAE36203 | AaE36203 | Human imm | 216 | 68 | 71.6 | 120 | 5 | ABP66409 | ABP66409 | Human RSV |
| 144 | 73 | 76.8 | 499 | 8 | ADK70546 | AdK70546 | Respirato | 217 | 68 | 71.6 | 120 | 5 | ABG31432 | ABG31432 | Humanised |
| 145 | 72 | 75.8 | 470 | 3 | AAU77289 | AaU77289 | Protein # | 218 | 68 | 71.6 | 120 | 5 | ABG31433 | ABG31433 | Amino aci |
| 146 | 71 | 74.7 | 16 | 2 | AAE77213 | AaE77213 | Mouse ant | 219 | 68 | 71.6 | 120 | 5 | AAE28016 | AAE28016 | Human mod |
| 147 | 71 | 74.7 | 119 | 8 | ADU18141 | AdU18141 | Humanised | 220 | 68 | 71.6 | 120 | 5 | AAE28087 | AAE28087 | Human mod |
| 148 | 71 | 74.7 | 139 | 2 | AAE67658 | AaE67658 | Anti-huma | 221 | 68 | 71.6 | 120 | 5 | AAE28064 | AAE28064 | Human mod |
| 149 | 71 | 74.7 | 139 | 2 | AAE67655 | AaE67655 | Mouse hea | 222 | 68 | 71.6 | 120 | 5 | AAE28018 | AAE28018 | Human mod |
| 150 | 71 | 74.7 | 139 | 2 | AAE67659 | AaE67659 | Anti-huma | 223 | 68 | 71.6 | 120 | 6 | ABU69272 | ABU69272 | Respirato |
| 151 | 70 | 73.7 | 16 | 5 | ABP66447 | AbP66447 | Human RSV | 224 | 68 | 71.6 | 120 | 6 | ABU69226 | ABU69226 | Respirato |
| 152 | 70 | 73.7 | 16 | 5 | ABP66436 | AbP66436 | Human RSV | 225 | 68 | 71.6 | 120 | 6 | ABU69295 | ABU69295 | Respirato |
| 153 | 70 | 73.7 | 16 | 5 | ABP66445 | AbP66445 | Human RSV | 226 | 68 | 71.6 | 120 | 6 | ABU69224 | ABU69224 | Respirato |
| 154 | 70 | 73.7 | 16 | 6 | ABU69308 | AbU69308 | Respirato | 227 | 68 | 71.6 | 120 | 6 | ABR55858 | ABR55858 | Anti-RSV- |
| 155 | 70 | 73.7 | 16 | 6 | ABU69299 | AbU69299 | Respirato | 228 | 68 | 71.6 | 120 | 7 | ADE35767 | ADE35767 | SYNAGIS a |
| 156 | 70 | 73.7 | 16 | 6 | ABU69310 | AbU69310 | Respirato | 229 | 68 | 71.6 | 120 | 7 | ADE35719 | ADE35719 | SYNAGIS a |
| 157 | 70 | 73.7 | 16 | 7 | ADE35803 | ADE35803 | SYNAGIS a | 230 | 68 | 71.6 | 120 | 7 | ADE35721 | ADE35721 | SYNAGIS a |
| 158 | 70 | 73.7 | 16 | 7 | ADE35794 | ADE35794 | SYNAGIS a | 231 | 68 | 71.6 | 120 | 7 | ADE35790 | ADE35790 | SYNAGIS a |
| 159 | 70 | 73.7 | 16 | 7 | ADE35805 | ADE35805 | SYNAGIS a | 232 | 68 | 71.6 | 120 | 8 | ADI56952 | ADI56952 | RSV antib |
| 160 | 70 | 73.7 | 16 | 7 | ADD94155 | AdD94155 | Mouse HUI | 233 | 68 | 71.6 | 120 | 8 | ADI56929 | ADI56929 | RSV antib |
| 161 | 70 | 73.7 | 16 | 8 | ADI56956 | AdI56956 | RSV antib | 234 | 68 | 71.6 | 120 | 8 | ADI56883 | ADI56883 | RSV antib |
| 162 | 70 | 73.7 | 16 | 8 | ADI56965 | AdI56965 | RSV antib | 235 | 68 | 71.6 | 120 | 8 | ADI56881 | ADI56881 | RSV antib |
| 163 | 70 | 73.7 | 16 | 8 | ADI56967 | AdI56967 | RSV antib | 236 | 68 | 71.6 | 120 | 8 | ADN49709 | ADN49709 | Light cha |
| 164 | 70 | 73.7 | 16 | 9 | ADW19936 | AdW19936 | RSV anti | 237 | 68 | 71.6 | 120 | 8 | ADT89204 | ADT89204 | Humanised |
| 165 | 70 | 73.7 | 16 | 9 | ADW19947 | AdW19947 | RSV anti | 238 | 68 | 71.6 | 120 | 8 | ADT89252 | ADT89252 | Humanised |
| 166 | 70 | 73.7 | 16 | 9 | ADW19945 | AdW19945 | RSV anti | 239 | 68 | 71.6 | 120 | 8 | ADT89275 | ADT89275 | Humanised |
| 167 | 70 | 73.7 | 16 | 9 | AEB06929 | AeB06929 | RSV-speci | 240 | 68 | 71.6 | 120 | 8 | ADU74385 | ADU74385 | SYNAGIS l |
| 168 | 70 | 73.7 | 16 | 9 | AEB06927 | AeB06927 | RSV-speci | 241 | 68 | 71.6 | 120 | 8 | ADU74385 | ADU74385 | SYNAGIS l |
| 169 | 70 | 73.7 | 16 | 9 | AEB06918 | AeB06918 | RSV-speci | 242 | 68 | 71.6 | 120 | 9 | ADW19863 | ADW19863 | RSV anti |
| 170 | 70 | 73.7 | 100 | 9 | ADZ47747 | AdZ47747 | Human ger | 243 | 68 | 71.6 | 120 | 9 | ADW19861 | ADW19861 | RSV anti |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|----------|-----------|-----|----|------|-----|---|----------|-----------|
| 244 | 68 | 71.6 | 120 | 9 | Adw19909 | RSV antiq | 317 | 66 | 69.5 | 16 | 6 | ABU69236 | Respirato |
| 245 | 68 | 71.6 | 120 | 9 | Adw19932 | RSV antiq | 318 | 66 | 69.5 | 16 | 6 | AAE35329 | Respirato |
| 246 | 68 | 71.6 | 120 | 9 | ABE06845 | RSV-speci | 319 | 66 | 69.5 | 16 | 7 | AAE35329 | SYNAGIS a |
| 247 | 68 | 71.6 | 120 | 9 | ABE07115 | RSV-speci | 320 | 66 | 69.5 | 16 | 8 | ADI56893 | RSV antiq |
| 248 | 68 | 71.6 | 120 | 9 | ABE06914 | RSV-speci | 321 | 66 | 69.5 | 16 | 8 | ADT89216 | Humanised |
| 249 | 68 | 71.6 | 120 | 9 | ABE07117 | RSV-speci | 322 | 66 | 69.5 | 16 | 9 | ADW19873 | RSV antiq |
| 250 | 68 | 71.6 | 120 | 9 | ABE06891 | RSV-speci | 323 | 66 | 69.5 | 16 | 9 | ABE06855 | RSV-speci |
| 251 | 68 | 71.6 | 120 | 9 | ABE06843 | RSV-speci | 324 | 66 | 69.5 | 102 | 7 | ADJ32175 | Human int |
| 252 | 68 | 71.6 | 139 | 5 | ABG31445 | Antibody | 325 | 66 | 69.5 | 119 | 6 | AAE35334 | Human RSV |
| 253 | 68 | 71.6 | 141 | 8 | ADU94329 | Antibody | 326 | 66 | 69.5 | 120 | 5 | ABP66421 | Human RSV |
| 254 | 68 | 71.6 | 227 | 6 | ABG75663 | Synagis h | 327 | 66 | 69.5 | 120 | 5 | ABP66402 | Human RSV |
| 255 | 68 | 71.6 | 294 | 9 | ADZ51574 | High-func | 328 | 66 | 69.5 | 120 | 5 | ABP66371 | Human RSV |
| 256 | 68 | 71.6 | 450 | 5 | ABP66590 | Human RSV | 329 | 66 | 69.5 | 120 | 5 | AAE28076 | Human mod |
| 257 | 68 | 71.6 | 450 | 5 | ABP66588 | Human RSV | 330 | 66 | 69.5 | 120 | 5 | AAE28057 | Human mod |
| 258 | 68 | 71.6 | 450 | 5 | ABP66596 | Human RSV | 331 | 66 | 69.5 | 120 | 5 | AAE28026 | Human mod |
| 259 | 68 | 71.6 | 450 | 5 | ABP66586 | Human RSV | 332 | 66 | 69.5 | 120 | 6 | ABU69284 | Respirato |
| 260 | 68 | 71.6 | 450 | 5 | ABP66594 | Human RSV | 333 | 66 | 69.5 | 120 | 6 | ABU69234 | Respirato |
| 261 | 68 | 71.6 | 450 | 5 | ABP66598 | Human RSV | 334 | 66 | 69.5 | 120 | 6 | ABU69265 | Respirato |
| 262 | 68 | 71.6 | 450 | 5 | ABP66564 | Human RSV | 335 | 66 | 69.5 | 120 | 7 | ADJ35779 | SYNAGIS a |
| 263 | 68 | 71.6 | 450 | 5 | ABP66592 | Human RSV | 336 | 66 | 69.5 | 120 | 7 | ADJ35779 | SYNAGIS a |
| 264 | 68 | 71.6 | 450 | 5 | ABP66600 | Human RSV | 337 | 66 | 69.5 | 120 | 7 | ADJ35760 | SYNAGIS a |
| 265 | 68 | 71.6 | 450 | 5 | ABP66562 | Human RSV | 338 | 66 | 69.5 | 120 | 8 | ADI56941 | RSV antiq |
| 266 | 68 | 71.6 | 450 | 6 | ABU69427 | Respirato | 339 | 66 | 69.5 | 120 | 8 | ADI56891 | RSV antiq |
| 267 | 68 | 71.6 | 450 | 6 | ABU69451 | Respirato | 340 | 66 | 69.5 | 120 | 8 | ADI56922 | RSV antiq |
| 268 | 68 | 71.6 | 450 | 6 | ABU69455 | Respirato | 341 | 66 | 69.5 | 120 | 8 | ADJ97212 | Human pro |
| 269 | 68 | 71.6 | 450 | 6 | ABU69459 | Respirato | 342 | 66 | 69.5 | 120 | 8 | ADT89264 | Humanised |
| 270 | 68 | 71.6 | 450 | 6 | ABU69457 | Respirato | 343 | 66 | 69.5 | 120 | 8 | ADT89214 | Humanised |
| 271 | 68 | 71.6 | 450 | 6 | ABU69463 | Respirato | 344 | 66 | 69.5 | 120 | 8 | ADW19871 | RSV antiq |
| 272 | 68 | 71.6 | 450 | 6 | ABU69463 | Respirato | 345 | 66 | 69.5 | 120 | 9 | ADW19921 | RSV antiq |
| 273 | 68 | 71.6 | 450 | 6 | ABU69425 | Respirato | 346 | 66 | 69.5 | 120 | 9 | ADW19902 | RSV antiq |
| 274 | 68 | 71.6 | 450 | 6 | ABU69461 | Respirato | 347 | 66 | 69.5 | 120 | 9 | ADW19902 | RSV-speci |
| 275 | 68 | 71.6 | 450 | 6 | ABU69449 | Respirato | 348 | 66 | 69.5 | 120 | 9 | ABE06853 | RSV-speci |
| 276 | 68 | 71.6 | 450 | 6 | ABG75662 | Synagis h | 349 | 66 | 69.5 | 120 | 9 | ABE06903 | RSV-speci |
| 277 | 68 | 71.6 | 450 | 7 | ABG75662 | Synagis h | 350 | 66 | 69.5 | 120 | 9 | ABE06884 | RSV-speci |
| 278 | 68 | 71.6 | 450 | 7 | ABG75662 | Synagis a | 351 | 66 | 69.5 | 123 | 3 | ABE21367 | Mouse ant |
| 279 | 68 | 71.6 | 450 | 7 | ABE35920 | Synagis a | 352 | 66 | 69.5 | 434 | 7 | AAE35960 | Synagis a |
| 280 | 68 | 71.6 | 450 | 7 | ABE35952 | Synagis a | 353 | 66 | 69.5 | 450 | 4 | AAE10525 | Humanised |
| 281 | 68 | 71.6 | 450 | 7 | ABE35946 | Synagis a | 354 | 66 | 69.5 | 450 | 4 | AAE10517 | Humanised |
| 282 | 68 | 71.6 | 450 | 7 | ABE35958 | Synagis a | 355 | 66 | 69.5 | 450 | 4 | AAE10523 | Humanised |
| 283 | 68 | 71.6 | 450 | 7 | ABE35954 | Synagis a | 356 | 66 | 69.5 | 450 | 5 | ABP66608 | Human RSV |
| 284 | 68 | 71.6 | 450 | 7 | ABE35922 | Synagis a | 357 | 66 | 69.5 | 450 | 5 | ABP66610 | Human RSV |
| 285 | 68 | 71.6 | 450 | 7 | ABE35944 | Synagis a | 358 | 66 | 69.5 | 450 | 5 | ABP66602 | Human RSV |
| 286 | 68 | 71.6 | 450 | 7 | ABE35950 | Synagis a | 359 | 66 | 69.5 | 450 | 5 | ABP66606 | Human RSV |
| 287 | 68 | 71.6 | 450 | 9 | ADW20096 | RSV antiq | 360 | 66 | 69.5 | 450 | 5 | ABP66566 | Human RSV |
| 288 | 68 | 71.6 | 450 | 9 | ADW20100 | RSV antiq | 361 | 66 | 69.5 | 450 | 5 | ABP66580 | Human RSV |
| 289 | 68 | 71.6 | 450 | 9 | ADW20064 | RSV antiq | 362 | 66 | 69.5 | 450 | 5 | ABP66568 | Human RSV |
| 290 | 68 | 71.6 | 450 | 9 | ADW20090 | RSV antiq | 363 | 66 | 69.5 | 450 | 6 | ABU69443 | Respirato |
| 291 | 68 | 71.6 | 450 | 9 | ADW20094 | RSV antiq | 364 | 66 | 69.5 | 450 | 6 | ABU69471 | Respirato |
| 292 | 68 | 71.6 | 450 | 9 | ADW20062 | RSV antiq | 365 | 66 | 69.5 | 450 | 6 | ABU69429 | Respirato |
| 293 | 68 | 71.6 | 450 | 9 | ADW20098 | RSV antiq | 366 | 66 | 69.5 | 450 | 6 | ABU69473 | Respirato |
| 294 | 68 | 71.6 | 450 | 9 | ADW20092 | RSV antiq | 367 | 66 | 69.5 | 450 | 6 | ABU69465 | Respirato |
| 295 | 68 | 71.6 | 450 | 9 | ADW20086 | RSV antiq | 368 | 66 | 69.5 | 450 | 6 | ABU69431 | Respirato |
| 296 | 68 | 71.6 | 450 | 9 | ADW20088 | RSV antiq | 369 | 66 | 69.5 | 450 | 6 | ABU69469 | Respirato |
| 297 | 68 | 71.6 | 450 | 9 | ABE07080 | RSV-speci | 370 | 66 | 69.5 | 450 | 7 | ADJ35926 | Synagis a |
| 298 | 68 | 71.6 | 450 | 9 | ABE07072 | RSV-speci | 371 | 66 | 69.5 | 450 | 7 | ADJ35938 | Synagis a |
| 299 | 68 | 71.6 | 450 | 9 | ABE07082 | RSV-speci | 372 | 66 | 69.5 | 450 | 7 | ADJ35968 | Synagis a |
| 300 | 68 | 71.6 | 450 | 9 | ABE07078 | RSV-speci | 373 | 66 | 69.5 | 450 | 7 | ADJ35966 | Synagis a |
| 301 | 68 | 71.6 | 450 | 9 | ABE07068 | RSV-speci | 374 | 66 | 69.5 | 450 | 7 | ADJ35964 | Synagis a |
| 302 | 68 | 71.6 | 450 | 9 | ABE07076 | RSV-speci | 375 | 66 | 69.5 | 450 | 7 | ADJ35924 | Synagis a |
| 303 | 68 | 71.6 | 450 | 9 | ABE07070 | RSV-speci | 376 | 66 | 69.5 | 450 | 9 | ADW20110 | RSV antiq |
| 304 | 68 | 71.6 | 450 | 9 | ABE07046 | RSV-speci | 377 | 66 | 69.5 | 450 | 9 | ADW20068 | RSV antiq |
| 305 | 68 | 71.6 | 450 | 9 | ABE07044 | RSV-speci | 378 | 66 | 69.5 | 450 | 9 | ADW20080 | RSV antiq |
| 306 | 68 | 71.6 | 450 | 9 | ABE07074 | RSV-speci | 379 | 66 | 69.5 | 450 | 9 | ADW20102 | RSV antiq |
| 307 | 68 | 71.6 | 451 | 5 | ABP66584 | Human RSV | 380 | 66 | 69.5 | 450 | 9 | ADW20106 | RSV antiq |
| 308 | 68 | 71.6 | 451 | 5 | ABP66584 | Human RSV | 381 | 66 | 69.5 | 450 | 9 | ADW20108 | RSV antiq |
| 309 | 68 | 71.6 | 451 | 6 | ADJ35942 | Synagis a | 382 | 66 | 69.5 | 450 | 9 | ADW20066 | RSV antiq |
| 310 | 68 | 71.6 | 451 | 9 | ADW20084 | RSV antiq | 383 | 66 | 69.5 | 450 | 9 | ABE07050 | RSV-speci |
| 311 | 68 | 71.6 | 451 | 9 | ABE07066 | RSV-speci | 384 | 66 | 69.5 | 450 | 9 | ABE07048 | RSV-speci |
| 312 | 66 | 69.5 | 16 | 3 | ABE26971 | Mouse ant | 385 | 66 | 69.5 | 450 | 9 | ABE07062 | RSV-speci |
| 313 | 66 | 69.5 | 16 | 4 | AAE10498 | Humanised | 386 | 66 | 69.5 | 450 | 9 | ABE07084 | RSV-speci |
| 314 | 66 | 69.5 | 16 | 4 | AAE10501 | Humanised | 387 | 66 | 69.5 | 450 | 9 | ABE07090 | RSV-speci |
| 315 | 66 | 69.5 | 16 | 5 | ABP66373 | Human RSV | 388 | 66 | 69.5 | 450 | 9 | ABE07092 | RSV-speci |
| 316 | 66 | 69.5 | 16 | 5 | AAE28028 | Human mod | 389 | 66 | 69.5 | 450 | 9 | ABE07088 | RSV-speci |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|-----------|------------|-----|----|------|-----|---|----------|------------|
| 390 | 65 | 68.4 | 16 | 5 | ABP66399 | Human RSV | 463 | 60 | 63.2 | 127 | 7 | ADF44915 | Single ch |
| 391 | 65 | 68.4 | 16 | 5 | AAE28054 | Human mod | 464 | 60 | 63.2 | 127 | 7 | ADK17389 | Anti-huma |
| 392 | 65 | 68.4 | 16 | 6 | ABU69262 | Respirato | 465 | 60 | 63.2 | 127 | 8 | ADG42811 | scfv heav |
| 393 | 65 | 68.4 | 16 | 7 | ADE35757 | SYNAGIS a | 466 | 60 | 63.2 | 253 | 7 | ADG44898 | Single ch |
| 394 | 65 | 68.4 | 16 | 8 | ADI56919 | RSV antib | 467 | 60 | 63.2 | 253 | 7 | ADF44906 | Single ch |
| 395 | 65 | 68.4 | 16 | 8 | ADT89242 | Humanised | 468 | 60 | 63.2 | 253 | 7 | ADK17380 | Anti-huma |
| 396 | 65 | 68.4 | 16 | 9 | ADM19899 | RSV antiig | 469 | 60 | 63.2 | 253 | 7 | ADK17372 | Anti-huma |
| 397 | 65 | 68.4 | 16 | 9 | ABE06881 | RSV-speci | 470 | 60 | 63.2 | 253 | 8 | ADG42802 | Human CCR |
| 398 | 65 | 68.4 | 120 | 5 | ABP66405 | Human RSV | 471 | 60 | 63.2 | 253 | 8 | ADG42794 | Human CCR |
| 399 | 65 | 68.4 | 120 | 5 | AAE28060 | Human mod | 472 | 60 | 63.2 | 294 | 9 | ADZ51578 | High-func |
| 400 | 65 | 68.4 | 120 | 6 | ABU69268 | Respirato | 473 | 60 | 63.2 | 462 | 3 | AAE29408 | Human mon |
| 401 | 65 | 68.4 | 120 | 7 | ADZ51566 | High-func | 474 | 60 | 63.2 | 481 | 7 | ABR61569 | HIV-1 neu |
| 402 | 65 | 68.4 | 120 | 8 | ADZ515925 | SYNAGIS a | 475 | 59 | 62.1 | 16 | 4 | AAE10499 | Humanised |
| 403 | 65 | 68.4 | 120 | 8 | ADT89248 | Humanised | 476 | 59 | 62.1 | 16 | 5 | ABP66379 | Human RSV |
| 404 | 65 | 68.4 | 120 | 9 | ADM19905 | RSV antiig | 477 | 59 | 62.1 | 16 | 5 | AAE28034 | Human mod |
| 405 | 65 | 68.4 | 120 | 9 | ABE06887 | RSV-speci | 478 | 59 | 62.1 | 16 | 6 | ABU69242 | Respirato |
| 406 | 65 | 68.4 | 294 | 9 | ADZ51566 | High-func | 479 | 59 | 62.1 | 16 | 7 | ADE35737 | SYNAGIS a |
| 407 | 65 | 68.4 | 450 | 4 | AAE10519 | Humanised | 480 | 59 | 62.1 | 16 | 8 | ADI56899 | RSV antib |
| 408 | 65 | 68.4 | 450 | 5 | ABP66582 | Human RSV | 481 | 59 | 62.1 | 16 | 8 | ADT89222 | Humanised |
| 409 | 65 | 68.4 | 450 | 6 | ABU69445 | Respirato | 482 | 59 | 62.1 | 16 | 9 | ADM19879 | RSV antiig |
| 410 | 65 | 68.4 | 450 | 7 | ADZ515940 | SYNAGIS a | 483 | 59 | 62.1 | 16 | 9 | ABE06861 | RSV-speci |
| 411 | 65 | 68.4 | 450 | 9 | ADM20082 | RSV antiig | 484 | 59 | 62.1 | 116 | 9 | ADY21979 | Anti-CD45 |
| 412 | 65 | 68.4 | 450 | 9 | ABE07064 | Human RSV | 485 | 59 | 62.1 | 120 | 5 | ABP66378 | Human RSV |
| 413 | 64 | 67.4 | 16 | 5 | ABP66440 | Human RSV | 486 | 59 | 62.1 | 120 | 5 | ABP66387 | Human RSV |
| 414 | 64 | 67.4 | 16 | 5 | ABU69303 | Respirato | 487 | 59 | 62.1 | 120 | 5 | ABP66382 | Human RSV |
| 415 | 64 | 67.4 | 16 | 6 | ABU69303 | Respirato | 488 | 59 | 62.1 | 120 | 5 | AAE28042 | Human mod |
| 416 | 64 | 67.4 | 16 | 7 | ADZ51598 | SYNAGIS a | 489 | 59 | 62.1 | 120 | 5 | AAE28037 | Human mod |
| 417 | 64 | 67.4 | 16 | 7 | ADD94210 | Mouse HUI | 490 | 59 | 62.1 | 120 | 5 | AAE28033 | Human mod |
| 418 | 64 | 67.4 | 16 | 8 | ADI56960 | RSV antib | 491 | 59 | 62.1 | 120 | 6 | ABU69241 | Respirato |
| 419 | 64 | 67.4 | 16 | 9 | ADM19940 | RSV antiig | 492 | 59 | 62.1 | 120 | 6 | ABU69250 | Respirato |
| 420 | 64 | 67.4 | 16 | 9 | ABE06922 | RSV-speci | 493 | 59 | 62.1 | 120 | 6 | ABU69245 | Respirato |
| 421 | 64 | 67.4 | 121 | 4 | RAG62946 | Amino aci | 494 | 59 | 62.1 | 120 | 7 | ADE35736 | SYNAGIS a |
| 422 | 64 | 67.4 | 293 | 8 | ADT02271 | Human-typ | 495 | 59 | 62.1 | 120 | 7 | ADE35740 | SYNAGIS a |
| 423 | 64 | 67.4 | 293 | 9 | ADZ51596 | High-func | 496 | 59 | 62.1 | 120 | 7 | ADE35745 | SYNAGIS a |
| 424 | 64 | 67.4 | 294 | 9 | ADZ51590 | High-func | 497 | 59 | 62.1 | 120 | 8 | ADI56902 | RSV antib |
| 425 | 64 | 67.4 | 294 | 9 | ADZ51562 | High-func | 498 | 59 | 62.1 | 120 | 8 | ADI56898 | RSV antib |
| 426 | 64 | 67.4 | 294 | 9 | ADZ51580 | High-func | 499 | 59 | 62.1 | 120 | 8 | ADI56907 | RSV antib |
| 427 | 64 | 67.4 | 294 | 9 | ADZ51602 | High-func | 500 | 59 | 62.1 | 120 | 8 | ADT89230 | Humanised |
| 428 | 64 | 67.4 | 294 | 9 | ADZ51598 | High-func | 501 | 59 | 62.1 | 120 | 8 | ADT89225 | Humanised |
| 429 | 64 | 67.4 | 294 | 9 | ADZ51576 | High-func | 502 | 59 | 62.1 | 120 | 8 | ADT89221 | Humanised |
| 430 | 64 | 67.4 | 294 | 9 | ADZ51600 | High-func | 503 | 59 | 62.1 | 120 | 9 | ADM19887 | RSV antiig |
| 431 | 64 | 67.4 | 294 | 9 | ADZ51588 | High-func | 504 | 59 | 62.1 | 120 | 9 | ADM19882 | RSV antiig |
| 432 | 64 | 67.4 | 294 | 9 | ADZ51604 | High-func | 505 | 59 | 62.1 | 120 | 9 | ADM19878 | RSV antiig |
| 433 | 64 | 67.4 | 294 | 9 | ADZ51564 | High-func | 506 | 59 | 62.1 | 120 | 9 | ABE06864 | RSV-speci |
| 434 | 64 | 67.4 | 294 | 9 | ADZ51570 | High-func | 507 | 59 | 62.1 | 120 | 9 | ABE06869 | RSV-speci |
| 435 | 64 | 67.4 | 294 | 9 | ADZ51572 | High-func | 508 | 59 | 62.1 | 120 | 9 | ABE06860 | RSV-speci |
| 436 | 64 | 67.4 | 294 | 9 | ADZ51582 | High-func | 509 | 59 | 62.1 | 133 | 9 | ADY21973 | Anti-CD45 |
| 437 | 63 | 66.3 | 16 | 5 | ABP66460 | Human RSV | 510 | 59 | 62.1 | 143 | 5 | ABB79728 | Anti-Stre |
| 438 | 63 | 66.3 | 16 | 6 | ABU69323 | Respirato | 511 | 59 | 62.1 | 262 | 9 | ADY21977 | Anti-CD45 |
| 439 | 63 | 66.3 | 16 | 7 | ADE35818 | SYNAGIS a | 512 | 59 | 62.1 | 262 | 9 | ADY21981 | Anti-CD45 |
| 440 | 63 | 66.3 | 16 | 8 | ADI56980 | RSV antib | 513 | 59 | 62.1 | 450 | 4 | AAE10521 | Humanised |
| 441 | 63 | 66.3 | 16 | 9 | ADM19960 | RSV antiig | 514 | 59 | 62.1 | 450 | 4 | AAE10515 | Humanised |
| 442 | 63 | 66.3 | 16 | 9 | ABE06942 | RSV-speci | 515 | 59 | 62.1 | 450 | 5 | ABP66572 | Human RSV |
| 443 | 62 | 65.3 | 16 | 4 | AAE10575 | Humanised | 516 | 59 | 62.1 | 450 | 5 | ABP66604 | Human RSV |
| 444 | 62 | 65.3 | 16 | 5 | ABP66468 | Human RSV | 517 | 59 | 62.1 | 450 | 5 | ABP66570 | Human RSV |
| 445 | 62 | 65.3 | 16 | 6 | ABU69331 | Respirato | 518 | 59 | 62.1 | 450 | 6 | ABU69467 | Respirato |
| 446 | 62 | 65.3 | 16 | 7 | ADE35826 | SYNAGIS a | 519 | 59 | 62.1 | 450 | 6 | ABU69435 | Respirato |
| 447 | 62 | 65.3 | 16 | 8 | ADI56988 | RSV antib | 520 | 59 | 62.1 | 450 | 6 | ABU69433 | Respirato |
| 448 | 62 | 65.3 | 16 | 9 | ADM19968 | RSV antiig | 521 | 59 | 62.1 | 450 | 7 | ADE35928 | SYNAGIS a |
| 449 | 62 | 65.3 | 16 | 9 | ABE06950 | RSV-speci | 522 | 59 | 62.1 | 450 | 7 | ADE35930 | SYNAGIS a |
| 450 | 61 | 64.2 | 16 | 5 | ABP66454 | Human RSV | 523 | 59 | 62.1 | 450 | 7 | ADE35962 | SYNAGIS a |
| 451 | 61 | 64.2 | 16 | 6 | ABU69317 | Respirato | 524 | 59 | 62.1 | 450 | 9 | ADM20072 | RSV antiig |
| 452 | 61 | 64.2 | 16 | 7 | ADE35812 | SYNAGIS a | 525 | 59 | 62.1 | 450 | 9 | ADM20104 | RSV antiig |
| 453 | 61 | 64.2 | 16 | 7 | ADD94207 | Mouse HUI | 526 | 59 | 62.1 | 450 | 9 | ADM20070 | RSV antiig |
| 454 | 61 | 64.2 | 16 | 7 | ADD94259 | Mouse HUI | 527 | 59 | 62.1 | 450 | 9 | ABE07086 | RSV-speci |
| 455 | 61 | 64.2 | 16 | 7 | ADD94208 | Mouse HUI | 528 | 59 | 62.1 | 450 | 9 | ABE07054 | RSV-speci |
| 456 | 61 | 64.2 | 16 | 8 | ADI56974 | RSV antib | 529 | 59 | 62.1 | 450 | 9 | ABE07052 | RSV-speci |
| 457 | 61 | 64.2 | 16 | 9 | ADM19954 | RSV antiig | 530 | 59 | 62.1 | 495 | 9 | ADY21985 | Antibody |
| 458 | 61 | 64.2 | 16 | 9 | ABE06936 | RSV-speci | 531 | 59 | 62.1 | 495 | 9 | ADY21983 | Antibody |
| 459 | 61 | 64.2 | 294 | 9 | ADZ51592 | High-func | 532 | 58 | 61.1 | 16 | 4 | AAE10502 | Humanised |
| 460 | 61 | 64.2 | 294 | 9 | ADZ51560 | High-func | 533 | 58 | 61.1 | 16 | 4 | AAE10527 | Humanised |
| 461 | 60 | 63.2 | 16 | 7 | ADD94209 | Mouse HUI | 534 | 58 | 61.1 | 16 | 5 | ABP66395 | Human RSV |
| 462 | 60 | 63.2 | 123 | 9 | ADY96955 | Human imm | 535 | 58 | 61.1 | 16 | 5 | AAE28050 | Human mod |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|-----------|---------------------|-----|----|------|-----|---|----------|---------------------|
| 536 | 58 | 61.1 | 16 | 6 | ABU699258 | Abu69258 Respirato | 609 | 57 | 60.0 | 450 | 7 | ADE35932 | Ade35932 SYNAGIS a |
| 537 | 58 | 61.1 | 16 | 7 | ADRE35753 | Adre35753 SYNAGIS a | 610 | 57 | 60.0 | 450 | 9 | ADW20074 | Adw20074 RSV antiq |
| 538 | 58 | 61.1 | 16 | 8 | ADI56915 | Adi56915 RSV antiq | 611 | 57 | 60.0 | 450 | 9 | ABE07056 | Abe07056 RSV-speci |
| 539 | 58 | 61.1 | 16 | 8 | ADT89238 | Adt89238 Humanised | 612 | 56 | 58.9 | 294 | 9 | ADZ51584 | Adz51584 High-func |
| 540 | 58 | 61.1 | 16 | 9 | ADW19895 | Adw19895 RSV antiq | 613 | 55 | 57.9 | 97 | 2 | AAW80973 | Aaw80973 Heavy cha |
| 541 | 58 | 61.1 | 16 | 9 | AE806877 | Aeb06877 RSV-speci | 614 | 55 | 57.9 | 97 | 6 | ABO04837 | Abo04837 Human epi |
| 542 | 58 | 61.1 | 112 | 8 | ADT89241 | Adt89241 Humanised | 615 | 55 | 57.9 | 97 | 9 | AEA17750 | Aea17750 Hydriona |
| 543 | 58 | 61.1 | 120 | 4 | AAE10508 | Aae10508 Humanised | 616 | 55 | 57.9 | 117 | 2 | AAW62816 | Aaw62816 Amino aci |
| 544 | 58 | 61.1 | 120 | 5 | ABP66394 | Abp66394 Human RSV | 617 | 54 | 56.8 | 96 | 5 | ABG78179 | Abg78179 Human Fv |
| 545 | 58 | 61.1 | 120 | 5 | ABP66398 | Abp66398 Human RSV | 618 | 54 | 56.8 | 96 | 5 | ABG91870 | Abg91870 Human ant |
| 546 | 58 | 61.1 | 120 | 5 | AAE28049 | Aae28049 Human mod | 619 | 54 | 56.8 | 99 | 6 | ABJ18689 | Abj18689 Antibody |
| 547 | 58 | 61.1 | 120 | 5 | AAE28053 | Aae28053 Human mod | 620 | 54 | 56.8 | 100 | 7 | ADF10016 | Adf10016 VEGF anti |
| 548 | 58 | 61.1 | 120 | 6 | ABU69261 | Abu69261 Respirato | 621 | 54 | 56.8 | 100 | 7 | ADF09908 | Adf09908 Antibody |
| 549 | 58 | 61.1 | 120 | 6 | ABU69257 | Abu69257 Respirato | 622 | 54 | 56.8 | 100 | 7 | ADF10118 | Adf10118 Antibody |
| 550 | 58 | 61.1 | 120 | 6 | ADRE35756 | Adre35756 SYNAGIS a | 623 | 54 | 56.8 | 120 | 2 | AAR92086 | Aar92086 Human Cos |
| 551 | 58 | 61.1 | 120 | 7 | ADRE35752 | Adre35752 SYNAGIS a | 624 | 54 | 56.8 | 120 | 5 | AAU83815 | Aau83815 MS-GPC-8- |
| 552 | 58 | 61.1 | 120 | 8 | ADI56918 | Adi56918 RSV antiq | 625 | 54 | 56.8 | 120 | 5 | AAU83805 | Aau83805 MS-GPC-8- |
| 553 | 58 | 61.1 | 120 | 8 | ADI56914 | Adi56914 RSV antiq | 626 | 54 | 56.8 | 120 | 5 | AAU83809 | Aau83809 MS-GPC-8- |
| 554 | 58 | 61.1 | 120 | 8 | ADT89237 | Adt89237 Humanised | 627 | 54 | 56.8 | 120 | 5 | AAU83821 | Aau83821 MS-GPC-8- |
| 555 | 58 | 61.1 | 120 | 9 | ADW19894 | Adw19894 RSV antiq | 628 | 54 | 56.8 | 120 | 5 | AAU83817 | Aau83817 MS-GPC-8- |
| 556 | 58 | 61.1 | 120 | 9 | ADW19898 | Adw19898 RSV antiq | 629 | 54 | 56.8 | 120 | 5 | AAU83819 | Aau83819 MS-GPC-8- |
| 557 | 58 | 61.1 | 120 | 9 | AE806880 | Aeb06880 RSV-speci | 630 | 54 | 56.8 | 120 | 5 | AAU83807 | Aau83807 MS-GPC-10 |
| 558 | 58 | 61.1 | 120 | 9 | AE806876 | Aeb06876 RSV-speci | 631 | 54 | 56.8 | 120 | 5 | AAU83811 | Aau83811 MS-GPC-8- |
| 559 | 58 | 61.1 | 141 | 2 | AAR33325 | Aar33255 Rat immun | 632 | 54 | 56.8 | 120 | 5 | AAU83813 | Aau83813 MS-GPC-8- |
| 560 | 58 | 61.1 | 141 | 2 | AAR53339 | Aar53339 KM50 cell | 633 | 54 | 56.8 | 120 | 5 | AAU83801 | Aau83801 MS-GPC-1 |
| 561 | 58 | 61.1 | 141 | 2 | AAZ28367 | Aay28367 KM50 Rat | 634 | 54 | 56.8 | 120 | 5 | ABBS7583 | Abbs7583 HLA-DR-sp |
| 562 | 58 | 61.1 | 141 | 3 | AAE01626 | Aae01626 Rat activ | 635 | 54 | 56.8 | 120 | 5 | ABBS7577 | Abbs7577 HLA-DR-sp |
| 563 | 58 | 61.1 | 450 | 4 | AAE10513 | Aae10513 Humanised | 636 | 54 | 56.8 | 120 | 5 | ABBS7585 | Abbs7585 HLA-DR-sp |
| 564 | 58 | 61.1 | 450 | 4 | AAE10511 | Aae10511 Humanised | 637 | 54 | 56.8 | 120 | 5 | ABBS7585 | Abbs7585 HLA-DR-sp |
| 565 | 58 | 61.1 | 450 | 5 | ABP66578 | Abp66578 Human RSV | 638 | 54 | 56.8 | 120 | 5 | ABBS7567 | Abbs7567 HLA-DR-sp |
| 566 | 58 | 61.1 | 450 | 5 | ABP66576 | Abp66576 Human RSV | 639 | 54 | 56.8 | 120 | 5 | ABBS7581 | Abbs7581 HLA-DR-sp |
| 567 | 58 | 61.1 | 450 | 6 | ABU69439 | Abu69439 Respirato | 640 | 54 | 56.8 | 120 | 5 | ABBS7587 | Abbs7587 HLA-DR-sp |
| 568 | 58 | 61.1 | 450 | 6 | ABU69441 | Abu69441 Respirato | 641 | 54 | 56.8 | 120 | 5 | ABBS7569 | Abbs7569 HLA-DR-sp |
| 569 | 58 | 61.1 | 450 | 7 | ADRE35934 | Adre35934 SYNAGIS a | 642 | 54 | 56.8 | 120 | 5 | ABBS7551 | Abbs7551 HLA-DR-sp |
| 570 | 58 | 61.1 | 450 | 7 | ADRE35936 | Adre35936 SYNAGIS a | 643 | 54 | 56.8 | 120 | 5 | ABBS7579 | Abbs7579 HLA-DR-sp |
| 571 | 58 | 61.1 | 450 | 9 | ADW20076 | Adw20076 RSV antiq | 644 | 54 | 56.8 | 120 | 5 | ABBS7589 | Abbs7589 HLA-DR-sp |
| 572 | 58 | 61.1 | 450 | 9 | ADW20078 | Adw20078 RSV antiq | 645 | 54 | 56.8 | 120 | 6 | ABJ18674 | Abj18674 Antibody |
| 573 | 58 | 61.1 | 450 | 9 | AE807058 | Aeb07058 RSV-speci | 646 | 54 | 56.8 | 120 | 9 | ADZ70874 | Adz70874 Human Ig |
| 574 | 58 | 61.1 | 450 | 9 | AE807060 | Aeb07060 RSV-speci | 647 | 54 | 56.8 | 120 | 9 | AE828946 | Aeb28946 Human ant |
| 575 | 57 | 60.0 | 16 | 4 | AAE10500 | Aae10500 Humanised | 648 | 54 | 56.8 | 121 | 2 | AAW27552 | Aaw27552 Human Ab |
| 576 | 57 | 60.0 | 16 | 5 | ABP66457 | Abp66457 Human RSV | 649 | 54 | 56.8 | 122 | 5 | ABBS7563 | Abbs7563 HLA-DR-sp |
| 577 | 57 | 60.0 | 16 | 5 | ABP664391 | Aae28046 Human mod | 650 | 54 | 56.8 | 122 | 9 | ADY70835 | Ady70835 MS-GPC-8- |
| 578 | 57 | 60.0 | 16 | 5 | AAE28046 | Aae28046 Human mod | 651 | 54 | 56.8 | 122 | 9 | ADY70837 | Ady70837 MS-GPC-10 |
| 579 | 57 | 60.0 | 16 | 6 | ABU69320 | Abu69320 Respirato | 652 | 54 | 56.8 | 122 | 9 | ADY70837 | Ady70837 MS-GPC-1 |
| 580 | 57 | 60.0 | 16 | 6 | ABU69254 | Abu69254 Respirato | 653 | 54 | 56.8 | 123 | 5 | ABG31431 | Abg31431 Amino aci |
| 581 | 57 | 60.0 | 16 | 7 | ADRE35749 | Adre35749 SYNAGIS a | 654 | 54 | 56.8 | 126 | 5 | ABBS7557 | Abbs7557 HLA-DR-sp |
| 582 | 57 | 60.0 | 16 | 7 | ADRE35815 | Adre35815 SYNAGIS a | 655 | 54 | 56.8 | 128 | 2 | AAR92087 | Aar92087 Human Ces |
| 583 | 57 | 60.0 | 16 | 8 | ADI56911 | Adi56911 RSV antiq | 656 | 54 | 56.8 | 128 | 6 | ADA90119 | Ada90119 Anti-Abet |
| 584 | 57 | 60.0 | 16 | 8 | ADI56977 | Adi56977 RSV antiq | 657 | 54 | 56.8 | 128 | 6 | AAO31084 | Aao31084 Human ant |
| 585 | 57 | 60.0 | 16 | 8 | ADSI9315 | Adsi9315 Heavy cha | 658 | 54 | 56.8 | 130 | 6 | ADA89117 | Ada89117 MS-Pro-12 |
| 586 | 57 | 60.0 | 16 | 8 | ADT89234 | Adt89234 Humanised | 659 | 54 | 56.8 | 130 | 7 | ADG74368 | Adg74368 MSPro hea |
| 587 | 57 | 60.0 | 16 | 9 | ADW19957 | Adw19957 RSV antiq | 660 | 54 | 56.8 | 130 | 9 | ADW38823 | Adw38823 T-cell me |
| 588 | 57 | 60.0 | 16 | 9 | ADW19891 | Adw19891 RSV antiq | 661 | 54 | 56.8 | 130 | 9 | ADZ51568 | Adz51568 High-func |
| 589 | 57 | 60.0 | 16 | 9 | AE806873 | Aeb06873 RSV-speci | 662 | 53 | 55.8 | 96 | 5 | ABG78180 | Abg78180 Human Fv |
| 590 | 57 | 60.0 | 16 | 9 | AE806939 | Aeb06939 RSV-speci | 663 | 53 | 55.8 | 96 | 5 | ABG91871 | Abg91871 Human ant |
| 591 | 57 | 60.0 | 95 | 2 | AAW80977 | Aaw80977 Heavy cha | 664 | 53 | 55.8 | 100 | 6 | ABO27081 | Abo27081 Human ger |
| 592 | 57 | 60.0 | 95 | 6 | ABO04841 | Abo04841 Human epi | 665 | 53 | 55.8 | 100 | 7 | ADJ80294 | Adj80294 VH gene 1 |
| 593 | 57 | 60.0 | 95 | 6 | AEA17754 | Aea17754 Hydriona | 666 | 53 | 55.8 | 100 | 7 | ADY75299 | Ady75299 Protein e |
| 594 | 57 | 60.0 | 119 | 6 | ABR55907 | Abr55907 Human mAb | 667 | 53 | 55.8 | 111 | 3 | AAI64679 | Aay64679 Human 5' |
| 595 | 57 | 60.0 | 120 | 5 | ABP66390 | Abp66390 Human RSV | 668 | 53 | 55.8 | 111 | 8 | ADU72243 | Adu72243 Signal pe |
| 596 | 57 | 60.0 | 120 | 5 | AAE28045 | Aae28045 Human mod | 669 | 53 | 55.8 | 111 | 8 | ADZ73234 | Adz73234 Human inc |
| 597 | 57 | 60.0 | 120 | 6 | ABU69253 | Abu69253 Respirato | 670 | 53 | 55.8 | 120 | 8 | ADU17898 | Adu17898 Humanised |
| 598 | 57 | 60.0 | 120 | 7 | ADRE35748 | Adre35748 SYNAGIS a | 671 | 53 | 55.8 | 123 | 7 | ADD94131 | Add94131 Human VHI |
| 599 | 57 | 60.0 | 120 | 8 | ADI56910 | Adi56910 RSV antiq | 672 | 53 | 55.8 | 130 | 2 | AAW53393 | Aaw53393 Human Ant |
| 600 | 57 | 60.0 | 120 | 8 | ADT89233 | Adt89233 Humanised | 673 | 53 | 55.8 | 130 | 6 | ABU56834 | Abu56834 Human Imm |
| 601 | 57 | 60.0 | 120 | 9 | ADW19890 | Adw19890 RSV antiq | 674 | 53 | 55.8 | 130 | 6 | ABU56794 | Abu56794 Human Imm |
| 602 | 57 | 60.0 | 120 | 9 | AE806872 | Aeb06872 RSV-speci | 675 | 53 | 55.8 | 500 | 7 | ADM05999 | Adm05999 Murine pro |
| 603 | 57 | 60.0 | 126 | 4 | AAE28048 | Aae28048 Amino aci | 676 | 52 | 54.7 | 116 | 8 | ADT89035 | Adt89035 Murine pl |
| 604 | 57 | 60.0 | 128 | 8 | ADSI9313 | Adsi9313 Heavy cha | 677 | 52 | 54.7 | 123 | 7 | ADP03888 | Adp03888 Murine-ex |
| 605 | 57 | 60.0 | 293 | 9 | ADZ51594 | Adz51594 High-func | 678 | 52 | 54.7 | 133 | 2 | AAR42800 | Aar42800 B13/B14 H |
| 606 | 57 | 60.0 | 450 | 4 | AAE10509 | Aae10509 Humanised | 679 | 52 | 54.7 | 139 | 3 | AAI64675 | Aay64675 Human 5' |
| 607 | 57 | 60.0 | 450 | 5 | ABP66574 | Abp66574 Human RSV | 680 | 52 | 54.7 | 139 | 8 | ADU72239 | Adu72239 Signal pe |
| 608 | 57 | 60.0 | 450 | 6 | ABU69437 | Abu69437 Respirato | 681 | 52 | 54.7 | 139 | 9 | ADZ73230 | Adz73230 Human inc |

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|-----|------|------|-----|---|----------|-----------|
| 682 | 52 | 54.7 | 141 | 2 | AAR42797 | Partial B |
| 683 | 51.5 | 54.2 | 111 | 2 | AAR66304 | Human imm |
| 684 | 51 | 53.7 | 16 | 2 | AAW90327 | Human ant |
| 685 | 51 | 53.7 | 16 | 9 | ADZ45479 | Murine fa |
| 686 | 51 | 53.7 | 16 | 9 | ABE70909 | Toll-like |
| 687 | 51 | 53.7 | 19 | 2 | AAW95248 | Anti-prog |
| 688 | 51 | 53.7 | 117 | 5 | ABP52184 | Human mon |
| 689 | 51 | 53.7 | 117 | 5 | AAO19679 | P aerugin |
| 690 | 51 | 53.7 | 117 | 9 | ADZ45477 | Murine fa |
| 691 | 51 | 53.7 | 120 | 2 | AAW90287 | Human ant |
| 692 | 51 | 53.7 | 120 | 7 | ADP03958 | Murine-ex |
| 693 | 51 | 53.7 | 121 | 9 | ABE70907 | Toll-like |
| 694 | 51 | 53.7 | 122 | 4 | AAW65554 | Amino aci |
| 695 | 50 | 52.6 | 16 | 5 | AAU81236 | Human trk |
| 696 | 50 | 52.6 | 16 | 8 | ADO58086 | S9 cell d |
| 697 | 50 | 52.6 | 16 | 9 | ADZ66143 | VH CDR2 f |
| 698 | 50 | 52.6 | 21 | 2 | AAW06708 | Ab6 varia |
| 699 | 50 | 52.6 | 21 | 8 | ADO39705 | Human 12E |
| 700 | 50 | 52.6 | 34 | 8 | ADS84419 | Human ant |
| 701 | 50 | 52.6 | 34 | 8 | ADR68561 | Human EPO |
| 702 | 50 | 52.6 | 76 | 2 | AAW62814 | Amino aci |
| 703 | 50 | 52.6 | 76 | 2 | AAW62815 | Amino aci |
| 704 | 50 | 52.6 | 76 | 2 | AAW80982 | Variable |
| 705 | 50 | 52.6 | 76 | 9 | ABO04836 | Human epi |
| 706 | 50 | 52.6 | 76 | 9 | AEA17739 | Hybridoma |
| 707 | 50 | 52.6 | 96 | 2 | AAW80975 | Heavy cha |
| 708 | 50 | 52.6 | 96 | 6 | ABO04839 | Human epi |
| 709 | 50 | 52.6 | 96 | 9 | AEA17752 | Hybridoma |
| 710 | 50 | 52.6 | 97 | 5 | ABG78229 | Human Fv |
| 711 | 50 | 52.6 | 97 | 5 | ABG78228 | Human Fv |
| 712 | 50 | 52.6 | 97 | 5 | ABG78230 | Human Fv |
| 713 | 50 | 52.6 | 97 | 5 | ABG77152 | Germine |
| 714 | 50 | 52.6 | 97 | 5 | ABG91920 | Human ant |
| 715 | 50 | 52.6 | 97 | 5 | ABG91919 | Human ant |
| 716 | 50 | 52.6 | 97 | 5 | ABG91921 | Human ant |
| 717 | 50 | 52.6 | 97 | 6 | ABJ18691 | Antibody |
| 718 | 50 | 52.6 | 97 | 6 | ABO27119 | Human ger |
| 719 | 50 | 52.6 | 97 | 6 | ABO27109 | Human ger |
| 720 | 50 | 52.6 | 97 | 6 | ABO27120 | Human ger |
| 721 | 50 | 52.6 | 97 | 7 | ADC99840 | Germine |
| 722 | 50 | 52.6 | 97 | 7 | ADC99820 | Germine |
| 723 | 50 | 52.6 | 97 | 7 | ADC99812 | Germine |
| 724 | 50 | 52.6 | 97 | 7 | ADD05416 | Anti-MUC1 |
| 725 | 50 | 52.6 | 97 | 7 | ADD05444 | Anti-MUC1 |
| 726 | 50 | 52.6 | 97 | 7 | ADD05424 | Anti-MUC1 |
| 727 | 50 | 52.6 | 97 | 7 | ADD28098 | Lymphoma |
| 728 | 50 | 52.6 | 97 | 7 | ADF10050 | VEGF anti |
| 729 | 50 | 52.6 | 97 | 7 | ADF09944 | Antibody |
| 730 | 50 | 52.6 | 97 | 7 | ADF10152 | Antibody |
| 731 | 50 | 52.6 | 97 | 7 | ADF09862 | Anti-MUC1 |
| 732 | 50 | 52.6 | 97 | 7 | ADF09882 | Anti-MUC1 |
| 733 | 50 | 52.6 | 97 | 7 | ADF09854 | Anti-MUC1 |
| 734 | 50 | 52.6 | 97 | 7 | ADJ80325 | VH gene 1 |
| 735 | 50 | 52.6 | 97 | 7 | ADP03883 | Murine-ex |
| 736 | 50 | 52.6 | 97 | 8 | ADR28570 | Human ant |
| 737 | 50 | 52.6 | 97 | 9 | ADY75330 | Protein e |
| 738 | 50 | 52.6 | 97 | 9 | ABE13606 | Human var |
| 739 | 50 | 52.6 | 99 | 5 | ABG78216 | Human Fv |
| 740 | 50 | 52.6 | 99 | 5 | ABG91907 | Human ant |
| 741 | 50 | 52.6 | 99 | 6 | ABO27110 | Human ger |
| 742 | 50 | 52.6 | 99 | 7 | ADZ28102 | Lymphoma |
| 743 | 50 | 52.6 | 99 | 7 | ADF09945 | Antibody |
| 744 | 50 | 52.6 | 99 | 7 | ADF10051 | Antibody |
| 745 | 50 | 52.6 | 99 | 7 | ADF10153 | Antibody |
| 746 | 50 | 52.6 | 99 | 7 | AAW42967 | BAA75036- |
| 747 | 50 | 52.6 | 99 | 7 | ADJ80326 | VH gene 1 |
| 748 | 50 | 52.6 | 99 | 9 | ADY75331 | Protein e |
| 749 | 50 | 52.6 | 99 | 9 | ABE13607 | Human var |
| 750 | 50 | 52.6 | 99 | 9 | AEA89839 | Anti-IFN |
| 751 | 50 | 52.6 | 99 | 9 | ABE01022 | Human hea |
| 752 | 50 | 52.6 | 105 | 4 | AAW61408 | Human bra |
| 753 | 50 | 52.6 | 108 | 7 | ADP03930 | Murine-ex |
| 754 | 50 | 52.6 | 108 | 8 | ADP22389 | Human ant |

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|-----|----|------|-----|---|----------|-----------|
| 755 | 50 | 52.6 | 108 | 8 | ADS09395 | Human c-m |
| 756 | 50 | 52.6 | 113 | 5 | ABG77144 | Anti-IGF- |
| 757 | 50 | 52.6 | 113 | 5 | ADR28554 | Human ant |
| 758 | 50 | 52.6 | 114 | 5 | ABG97827 | Human MPL |
| 759 | 50 | 52.6 | 114 | 5 | ABG35304 | Thrombopo |
| 760 | 50 | 52.6 | 116 | 2 | AAR42689 | Vh 71-4 |
| 761 | 50 | 52.6 | 116 | 2 | AAR66346 | Human imm |
| 762 | 50 | 52.6 | 116 | 7 | ADP03957 | Murine-ex |
| 763 | 50 | 52.6 | 116 | 8 | ADS84364 | Human ant |
| 764 | 50 | 52.6 | 116 | 8 | ADR68506 | Anti-EPO- |
| 765 | 50 | 52.6 | 117 | 9 | ABE46911 | Human var |
| 766 | 50 | 52.6 | 118 | 2 | AAR66348 | Human imm |
| 767 | 50 | 52.6 | 118 | 7 | AAW42975 | Germine |
| 768 | 50 | 52.6 | 118 | 9 | ABE11682 | Anti-Pneu |
| 769 | 50 | 52.6 | 119 | 2 | AAW27554 | Human Ab |
| 770 | 50 | 52.6 | 119 | 6 | ABJ18676 | Antibody |
| 771 | 50 | 52.6 | 119 | 7 | ADP03973 | Murine-ex |
| 772 | 50 | 52.6 | 119 | 7 | ADP03890 | Murine-ex |
| 773 | 50 | 52.6 | 119 | 9 | ADY74798 | Human IGG |
| 774 | 50 | 52.6 | 120 | 6 | ABG71454 | Human mon |
| 775 | 50 | 52.6 | 120 | 9 | ADZ70864 | Human Ig |
| 776 | 50 | 52.6 | 120 | 9 | ABE28936 | Human ant |
| 777 | 50 | 52.6 | 121 | 5 | ABB07171 | ebvHigM |
| 778 | 50 | 52.6 | 121 | 7 | ADE28455 | Human ant |
| 779 | 50 | 52.6 | 121 | 7 | ADE28447 | Human ant |
| 780 | 50 | 52.6 | 121 | 7 | ADE28491 | Human ant |
| 781 | 50 | 52.6 | 121 | 7 | ADE28423 | Human ant |
| 782 | 50 | 52.6 | 121 | 7 | ADP03984 | Murine-ex |
| 783 | 50 | 52.6 | 121 | 8 | ADI26658 | Human ant |
| 784 | 50 | 52.6 | 121 | 8 | ADO17219 | Human sof |
| 785 | 50 | 52.6 | 121 | 8 | ADS16559 | Human ant |
| 786 | 50 | 52.6 | 121 | 9 | ADP01828 | SARS coro |
| 787 | 50 | 52.6 | 122 | 7 | ADP03887 | Murine-ex |
| 788 | 50 | 52.6 | 122 | 7 | ADP03887 | Murine-ex |
| 789 | 50 | 52.6 | 122 | 7 | ADP03931 | Murine-ex |
| 790 | 50 | 52.6 | 122 | 7 | ADP03884 | Murine-ex |
| 791 | 50 | 52.6 | 122 | 7 | ADP03885 | Murine-ex |
| 792 | 50 | 52.6 | 122 | 7 | ADP03889 | Murine-ex |
| 793 | 50 | 52.6 | 124 | 9 | ADZ66148 | Variable |
| 794 | 50 | 52.6 | 126 | 5 | ABG92888 | Human imm |
| 795 | 50 | 52.6 | 126 | 6 | ADA90121 | Anti-Abet |
| 796 | 50 | 52.6 | 126 | 6 | AAO31086 | Human ant |
| 797 | 50 | 52.6 | 130 | 5 | AAU81273 | Human trk |
| 798 | 50 | 52.6 | 130 | 8 | ADY72818 | Anti-hepa |
| 799 | 50 | 52.6 | 133 | 5 | ABG97829 | Mouse 12E |
| 800 | 50 | 52.6 | 133 | 5 | ABG35331 | Thrombopo |
| 801 | 50 | 52.6 | 139 | 3 | AAW46476 | Human 5' |
| 802 | 50 | 52.6 | 139 | 8 | ADU72240 | Signal pe |
| 803 | 50 | 52.6 | 139 | 9 | ADZ73231 | Human inc |
| 804 | 50 | 52.6 | 143 | 6 | ABJ36929 | Anti-CD40 |
| 805 | 50 | 52.6 | 152 | 6 | ABO04857 | Human epi |
| 806 | 50 | 52.6 | 152 | 9 | AEA17769 | Hybridoma |
| 807 | 50 | 52.6 | 193 | 5 | ABP43199 | Human ova |
| 808 | 50 | 52.6 | 197 | 2 | AAW34300 | IGM antib |
| 809 | 50 | 52.6 | 240 | 9 | ABE46929 | Human CD1 |
| 810 | 50 | 52.6 | 241 | 8 | ADS84432 | Human ant |
| 811 | 50 | 52.6 | 241 | 8 | ADR68574 | Human ant |
| 812 | 50 | 52.6 | 243 | 2 | AAW06718 | Antibody |
| 813 | 50 | 52.6 | 244 | 2 | ADO39737 | Human c-m |
| 814 | 50 | 52.6 | 244 | 3 | AAW15126 | Anti-muri |
| 815 | 50 | 52.6 | 248 | 9 | ADX01838 | SARS coro |
| 816 | 50 | 52.6 | 248 | 9 | ADX01838 | SARS coro |
| 817 | 50 | 52.6 | 249 | 8 | ADI58076 | Reg IV-sp |
| 818 | 50 | 52.6 | 250 | 8 | ADI58062 | Reg IV-sp |
| 819 | 50 | 52.6 | 256 | 5 | ABG97834 | Single ch |
| 820 | 50 | 52.6 | 256 | 5 | ABG35335 | Thrombopo |
| 821 | 50 | 52.6 | 266 | 5 | ABG97835 | Single ch |
| 822 | 50 | 52.6 | 266 | 5 | ABG35336 | Thrombopo |
| 823 | 50 | 52.6 | 447 | 9 | ABE46954 | CD1a spec |
| 824 | 50 | 52.6 | 466 | 7 | ADE28471 | Human ant |
| 825 | 50 | 52.6 | 466 | 7 | ADE28419 | Human ant |
| 826 | 50 | 52.6 | 466 | 7 | ADE28479 | Human ant |
| 827 | 49 | 51.6 | 16 | 9 | ADX98335 | Human ant |

| | | | | | | | | | | | | |
|-----|----|------|-----|------------|---------------------|-----|----|------|-----|---|----------|--------------------|
| 828 | 49 | 51.6 | 9 | AEB000995 | Aeb00995 Human IPI | 901 | 48 | 50.5 | 99 | 7 | ADC99816 | Adc99816 Germline |
| 829 | 49 | 51.6 | 17 | AAE30602 | Aab30602 Anti-IgE | 902 | 48 | 50.5 | 99 | 7 | ADC99828 | Adc99828 Germline |
| 830 | 49 | 51.6 | 3 | AAW80967 | Aaw80967 Heavy Cha | 903 | 48 | 50.5 | 99 | 7 | ADD05452 | AdD05452 Anti-MUC1 |
| 831 | 49 | 51.6 | 96 | ABG78177 | Abg78177 Human Fv | 904 | 48 | 50.5 | 99 | 7 | ADD05432 | AdD05432 Anti-MUC1 |
| 832 | 49 | 51.6 | 5 | ABG91868 | Abg91868 Human ant | 905 | 48 | 50.5 | 99 | 7 | ADD05420 | AdD05420 Anti-MUC1 |
| 833 | 49 | 51.6 | 96 | ABO04830 | Abo04830 Human epi | 906 | 48 | 50.5 | 99 | 7 | ADD05448 | AdD05448 Anti-MUC1 |
| 834 | 49 | 51.6 | 8 | ADU17935 | Adu17935 Humanised | 907 | 48 | 50.5 | 99 | 7 | ADD28094 | AdD28094 Lymphoma |
| 835 | 49 | 51.6 | 96 | AEA17744 | Aea17744 Hybridoma | 908 | 48 | 50.5 | 99 | 7 | ADF09940 | AdF09940 Antibody |
| 836 | 49 | 51.6 | 97 | ADU04236 | Adu04236 Human imm | 909 | 48 | 50.5 | 99 | 7 | ADF10047 | AdF10047 VEGF anti |
| 837 | 49 | 51.6 | 100 | ABO27080 | Abo27080 Human ger | 910 | 48 | 50.5 | 99 | 7 | ADF09941 | AdF09941 Antibody |
| 838 | 49 | 51.6 | 100 | ADF09907 | Adf09907 Antibody | 911 | 48 | 50.5 | 99 | 7 | ADF10046 | AdF10046 VEGF anti |
| 839 | 49 | 51.6 | 100 | ADF10117 | Adf10117 Antibody | 912 | 48 | 50.5 | 99 | 7 | ADF10148 | AdF10148 Antibody |
| 840 | 49 | 51.6 | 100 | ADF10015 | Adf10015 VEGF anti | 913 | 48 | 50.5 | 99 | 7 | ADF10149 | AdF10149 Antibody |
| 841 | 49 | 51.6 | 100 | ADJ80293 | Adj80293 VH gene 1 | 914 | 48 | 50.5 | 99 | 7 | ADF09858 | AdF09858 Anti-MUC1 |
| 842 | 49 | 51.6 | 100 | ADY75298 | Ady75298 Protein e | 915 | 48 | 50.5 | 99 | 7 | ADF09886 | AdF09886 Anti-MUC1 |
| 843 | 49 | 51.6 | 113 | ADQ09627 | Adq09627 Variable | 916 | 48 | 50.5 | 99 | 7 | ADF09870 | AdF09870 Anti-MUC1 |
| 844 | 49 | 51.6 | 8 | AAW62813 | Aaw62813 Amino aci | 917 | 48 | 50.5 | 99 | 7 | ADF09890 | AdF09890 Anti-MUC1 |
| 845 | 49 | 51.6 | 116 | ADX984420 | Adx984420 Human ant | 918 | 48 | 50.5 | 99 | 7 | ADJ80319 | AdJ80319 VH gene 1 |
| 846 | 49 | 51.6 | 118 | AAAG62938 | Aag62938 Amino aci | 919 | 48 | 50.5 | 99 | 7 | ADJ80322 | AdJ80322 VH gene 1 |
| 847 | 49 | 51.6 | 119 | 2 AAR66318 | Aar66318 Human imm | 920 | 48 | 50.5 | 99 | 7 | ADJ80321 | AdJ80321 VH gene 1 |
| 848 | 49 | 51.6 | 119 | 4 AAG62942 | Aag62942 Amino aci | 921 | 48 | 50.5 | 99 | 7 | ADP03867 | AdP03867 Murine-ex |
| 849 | 49 | 51.6 | 122 | ADY96920 | Ady96920 Human imm | 922 | 48 | 50.5 | 99 | 9 | ADY75324 | AdY75324 Protein e |
| 850 | 49 | 51.6 | 125 | 7 ADP03871 | Adp03871 Murine-ex | 923 | 48 | 50.5 | 99 | 9 | ADY75326 | AdY75326 Protein e |
| 851 | 49 | 51.6 | 125 | 7 ADP03983 | Adp03983 Murine-ex | 924 | 48 | 50.5 | 99 | 9 | ADY75327 | AdY75327 Protein e |
| 852 | 49 | 51.6 | 126 | 3 AAB30584 | Aab30584 A human v | 925 | 48 | 50.5 | 99 | 9 | AEA21518 | Aea21518 Human ant |
| 853 | 49 | 51.6 | 126 | 5 ABP54970 | Abp54970 Anti-idio | 926 | 48 | 50.5 | 99 | 9 | AEI13603 | Aei13603 Human var |
| 854 | 49 | 51.6 | 128 | 2 AAR54798 | Aar54798 SPA-react | 927 | 48 | 50.5 | 99 | 9 | AEI13602 | Aei13602 Human var |
| 855 | 49 | 51.6 | 130 | 3 AEB01018 | Aeb01018 Human IPI | 928 | 48 | 50.5 | 100 | 7 | AEI17740 | Aei17740 Hybridoma |
| 856 | 49 | 51.6 | 139 | 3 AAY82628 | Aay82628 Human PTH | 929 | 48 | 50.5 | 106 | 7 | ADF90887 | AdF90887 Human hep |
| 857 | 49 | 51.6 | 139 | 9 ADX98267 | Adx98267 Human ant | 930 | 48 | 50.5 | 107 | 4 | ABG56007 | AbG56007 Human liv |
| 858 | 49 | 51.6 | 229 | 3 AAB30593 | Aab30593 Variable | 931 | 48 | 50.5 | 110 | 7 | ADP03934 | AdP03934 Murine-ex |
| 859 | 49 | 51.6 | 251 | 5 ABG80712 | Abg80712 Amyloid p | 932 | 48 | 50.5 | 110 | 8 | ADP22366 | AdP22366 Human ant |
| 860 | 49 | 51.6 | 254 | 5 ABG80713 | Abg80713 Amyloid p | 933 | 48 | 50.5 | 110 | 9 | ADW96620 | AdW96620 Human ger |
| 861 | 49 | 51.6 | 263 | 5 ABG80714 | Abg80714 Human IGG | 934 | 48 | 50.5 | 110 | 9 | ADW80192 | AdW80192 Human ant |
| 862 | 49 | 51.6 | 386 | 8 ADM46760 | Adm46760 thermococ | 935 | 48 | 50.5 | 111 | 8 | ADS75570 | AdS75570 Human mon |
| 863 | 49 | 51.6 | 446 | 8 ADX52356 | Adx52356 Human ant | 936 | 48 | 50.5 | 116 | 8 | ADS84408 | AdS84408 Human ant |
| 864 | 48 | 50.5 | 16 | 5 AAU81239 | Aau81239 Human trk | 937 | 48 | 50.5 | 116 | 8 | ADR68550 | AdR68550 Anti-BPO- |
| 865 | 48 | 50.5 | 16 | 8 ADP47152 | Adp47152 Human pho | 938 | 48 | 50.5 | 117 | 2 | AAR38669 | Aar38669 Ab26. 3/2 |
| 866 | 48 | 50.5 | 16 | 9 ADX98331 | Adx98331 Human ant | 939 | 48 | 50.5 | 117 | 2 | AAR40953 | Aar40953 Human ger |
| 867 | 48 | 50.5 | 16 | 9 AEX98333 | Aex98333 Human ant | 940 | 48 | 50.5 | 117 | 2 | AAR66320 | Aar66320 Human imm |
| 868 | 48 | 50.5 | 16 | 9 AEA21460 | Aea21460 Human ant | 941 | 48 | 50.5 | 117 | 7 | ADC99776 | AdC99776 Anti-huma |
| 869 | 48 | 50.5 | 16 | 9 AEA21496 | Aea21496 Human ant | 942 | 48 | 50.5 | 117 | 7 | ADD05380 | AdD05380 Anti-MUC1 |
| 870 | 48 | 50.5 | 76 | 2 AAW62810 | Aaw62810 Amino aci | 943 | 48 | 50.5 | 117 | 7 | ADF09818 | AdF09818 Human imm |
| 871 | 48 | 50.5 | 76 | 2 AAW80979 | Aaw80979 Variable | 944 | 48 | 50.5 | 118 | 2 | AAR66322 | Aar66322 Human imm |
| 872 | 48 | 50.5 | 76 | 6 AAE35891 | Aae35891 Human DP- | 945 | 48 | 50.5 | 118 | 2 | AAW62811 | Aaw62811 Amino aci |
| 873 | 48 | 50.5 | 76 | 6 ABO04824 | Abo04824 Human epi | 946 | 48 | 50.5 | 118 | 2 | ADP03968 | AdP03968 Murine-ex |
| 874 | 48 | 50.5 | 76 | 9 AEA17736 | Aea17736 Hybridoma | 947 | 48 | 50.5 | 119 | 2 | AAR30143 | Aar30143 Mab GAH v |
| 875 | 48 | 50.5 | 97 | 2 AAY05691 | Aay05691 Multiple | 948 | 48 | 50.5 | 119 | 6 | ABP98691 | AbP98691 Human GAH |
| 876 | 48 | 50.5 | 97 | 2 AAW80969 | Aaw80969 Heavy cha | 949 | 48 | 50.5 | 119 | 6 | ABP98683 | AbP98683 Human GAH |
| 877 | 48 | 50.5 | 97 | 3 AAY56648 | Aay56648 Partial p | 950 | 48 | 50.5 | 119 | 7 | ADG43869 | AdG43869 Human pro |
| 878 | 48 | 50.5 | 97 | 6 ABO04832 | Abo04832 Human epi | 951 | 48 | 50.5 | 119 | 7 | ADP03961 | AdP03961 Murine-ex |
| 879 | 48 | 50.5 | 97 | 9 AEA17746 | Aea17746 Hybridoma | 952 | 48 | 50.5 | 119 | 7 | ADP03970 | AdP03970 Murine-ex |
| 880 | 48 | 50.5 | 98 | 2 AAW54002 | Aaw54002 Human ant | 953 | 48 | 50.5 | 119 | 8 | ADI22106 | AdI22106 Anti-plac |
| 881 | 48 | 50.5 | 98 | 2 AAW80963 | Aaw80963 Heavy cha | 954 | 48 | 50.5 | 119 | 8 | ADQ28266 | AdQ28266 Method of |
| 882 | 48 | 50.5 | 98 | 5 ABG78219 | Abg78219 Human Fv | 955 | 48 | 50.5 | 119 | 8 | ADT50353 | AdT50353 Human mon |
| 883 | 48 | 50.5 | 98 | 5 ABG91910 | Abg91910 Human ant | 956 | 48 | 50.5 | 120 | 4 | AAB62775 | Aab62775 Human HIV |
| 884 | 48 | 50.5 | 98 | 6 ABO04826 | Abo04826 Human epi | 957 | 48 | 50.5 | 120 | 7 | ADP03969 | AdP03969 Murine-ex |
| 885 | 48 | 50.5 | 98 | 6 ABR55908 | Abr55908 Human mAb | 958 | 48 | 50.5 | 120 | 7 | ADP03974 | AdP03974 Murine-ex |
| 886 | 48 | 50.5 | 98 | 6 ABO27102 | Abo27102 Human ger | 959 | 48 | 50.5 | 120 | 7 | ADP03873 | AdP03873 Murine-ex |
| 887 | 48 | 50.5 | 98 | 7 ADF10044 | Adf10044 VEGF anti | 960 | 48 | 50.5 | 121 | 7 | ADP03981 | AdP03981 Murine-ex |
| 888 | 48 | 50.5 | 98 | 7 ADF10146 | Adf10146 Antibody | 961 | 48 | 50.5 | 121 | 7 | ADD05412 | AdD05412 Anti-MUC1 |
| 889 | 48 | 50.5 | 98 | 7 ADF09938 | Adf09938 Antibody | 962 | 48 | 50.5 | 121 | 7 | ADJ80377 | AdJ80377 Human ant |
| 890 | 48 | 50.5 | 98 | 7 ADJ80318 | Adj80318 VH gene 1 | 963 | 48 | 50.5 | 121 | 7 | ADP03982 | AdP03982 Murine-ex |
| 891 | 48 | 50.5 | 98 | 9 ADF75323 | Adf75323 Protein e | 964 | 48 | 50.5 | 121 | 7 | ADP03981 | AdP03981 Murine-ex |
| 892 | 48 | 50.5 | 98 | 9 AEB13600 | Aeb13600 Human var | 965 | 48 | 50.5 | 121 | 7 | ADZ70842 | AdZ70842 Human Ig |
| 893 | 48 | 50.5 | 99 | 5 ABG78215 | Abg78215 Human Fv | 966 | 48 | 50.5 | 121 | 9 | AEB28914 | Aeb28914 Human ant |
| 894 | 48 | 50.5 | 99 | 5 ABG91906 | Abg91906 Human ant | 967 | 48 | 50.5 | 121 | 9 | AAB62765 | Aab62765 Human HIV |
| 895 | 48 | 50.5 | 99 | 6 ABO27105 | Abo27105 Human ger | 968 | 48 | 50.5 | 122 | 7 | ADP03977 | AdP03977 Murine-ex |
| 896 | 48 | 50.5 | 99 | 6 ABO27103 | Abo27103 Human ger | 969 | 48 | 50.5 | 122 | 7 | AEA21509 | Aea21509 Human ant |
| 897 | 48 | 50.5 | 99 | 6 ABO27106 | Abo27106 Human ger | 970 | 48 | 50.5 | 122 | 9 | AEA21492 | Aea21492 Human ant |
| 898 | 48 | 50.5 | 99 | 7 ADC99848 | Adc99848 Germline | 971 | 48 | 50.5 | 122 | 9 | AEA21456 | Aea21456 Human ant |
| 899 | 48 | 50.5 | 99 | 7 ADC99844 | Adc99844 Germline | 972 | 48 | 50.5 | 122 | 9 | AAW78433 | Aaw78433 Antibody |
| 900 | 48 | 50.5 | 99 | | | 973 | 48 | 50.5 | 123 | 2 | | |

974 48 50.5 123 5 ABB97976 AbB97976 Heavy cha
 975 48 50.5 123 7 ADG8414 AdG8414 anti-Ob-R
 976 48 50.5 123 7 ADP03870 AdP03870 Murine-ex
 977 48 50.5 123 7 ADP03879 AdP03879 Murine-ex
 978 48 50.5 123 7 ADP03878 AdP03878 Murine-ex
 979 48 50.5 123 7 ADP03869 AdP03869 Murine-ex
 980 48 50.5 123 9 ADX98417 AdX98417 Human ant
 981 48 50.5 124 6 AAE38325 Aae38325 Human ant
 982 48 50.5 124 7 ADP03935 AdP03935 Murine-ex
 983 48 50.5 125 7 ADP03868 AdP03868 Murine-ex
 984 48 50.5 125 7 ADP03876 AdP03876 Murine-ex
 985 48 50.5 125 8 ADS16556 AdS16556 Human ant
 986 48 50.5 127 3 AAG00027 Aag00027 Human sec
 987 48 50.5 127 9 ADX98415 AdX98415 Human ant
 988 48 50.5 129 5 AAU81276 Aau81276 Human trk
 989 48 50.5 139 3 AAY56713 Aay56713 Amino aci
 990 48 50.5 144 9 ADX98263 AdX98263 Human ant
 991 48 50.5 148 9 ADX98259 AdX98259 Human ant
 992 48 50.5 149 9 ADZ57713 Adz57713 Germline
 993 48 50.5 150 2 AAY24373 Aay24373 Human mon
 994 48 50.5 186 8 ADK52388 AdK52388 Human ant
 995 48 50.5 239 8 ADS84461 AdS84461 Human ant
 996 48 50.5 239 8 ADR68603 Adr68603 Human ant
 997 48 50.5 248 7 ADG30499 AdG30499 Human GMC
 998 48 50.5 253 5 ABP45608 Abp45608 Human Bly
 999 48 50.5 253 7 ADG96435 Adg96435 Single ch
 1000 48 50.5 258 7 ADG32317 Adg32317 Chicken s

ALIGNMENTS

RESULT 1
 ID AAR70199 AAR70199 standard; protein; 16 AA.
 AC AAR70199;
 XX
 DT 25-MAR-2003 (revised)
 DT 20-SEP-1995 (first entry)
 XX
 XX MAB 3B9 heavy chain CDR.
 DE
 XX Chimeric antibody; humanized antibody; antibody engineering;
 KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy; CDR;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 XX WO9507301-A1.
 PN
 XX
 PD 16-MAR-1995.
 XX
 XX 07-SEP-1994; 94WO-US010308.
 PF
 XX 07-SEP-1993; 93US-00117366.
 PR 14-OCT-1993; 93US-00136783.
 XX
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 XX Holmes S, Gross MS, Sylvester DR;
 XX
 XX WPI; 1995-123387/16.
 DR
 XX Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from
 PT high affinity mAbs - useful in treatment of IL-4-mediated and IgE-
 PT mediated allergic conditions.
 XX
 XX Disclosure; Page 57; 97pp; English.
 PS
 XX Spleen cells from mice immunized with human IL-4 were used to prepare
 CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only clone

CC 3B9 was positive. cDNA clones of the 3B9 light and heavy chains were
 CC cloned into pGEM7f+ and transformed into E. coli DH5-alpha. A heavy chain
 CC cDNA clone was sequenced (AAQ83491) that encoded the protein given in
 CC AAR70190. 3 CDRs (AAR70198-200) were identified. (Updated on 25-MAR-2003
 CC to correct PN field.)
 XX
 SQ Sequence 16 AA;
 Query Match 100.0%; Score 95; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. NO. 5.6e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 HIYWDDDKRYNP SLKS 16
 |||||
 Db 1 HIYWDDDKRYNP SLKS 16
 |||||
 RESULT 2
 ID AAY23776 AAY23776 standard; peptide; 16 AA.
 XX
 XX AAY23776;
 XX
 DT 13-SEP-1999 (first entry)
 XX
 DE CDR of the heavy chain variable region of antibody 3B9.
 XX
 KW Heavy chain variable region; interleukin-4; IL-4; antibody 3B9;
 KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
 KW Immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 XX US5928904-A.
 PN
 XX 27-JUL-1999.
 PD
 XX 07-JUN-1995; 95US-00483632.
 PF
 XX 07-SEP-1993; 93US-00117366.
 PR 14-OCT-1993; 93US-00136783.
 PR 07-SEP-1994; 94WO-US010308.
 XX
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 XX Holmes SD, Sylvester DR, Gross MS;
 FI
 XX WPI; 1999-429500/36.
 DR N-PSDB; AAX85893.
 XX
 XX New DNA molecules encoding recombinant antibodies useful for treating IL4
 PT -mediated conditions.
 XX
 XX Example 3; Col 47-48; 50pp; English.
 PS
 XX The present sequence represents a complementarity determining region
 CC (CDR) of the heavy chain variable region of murine interleukin-4 (IL-4)
 CC antibody 3B9. The specification describes chimeric and humanised IL-4
 CC monoclonal antibodies. The antibodies of the invention are used in
 CC therapeutic and pharmaceutical compositions for treating IL-4 mediated
 CC and Immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis,
 CC conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock,
 CC rheumatoid arthritis, host-versus-graft disease and renal disease. They
 CC are also useful in the diagnosis of an allergy or condition associated
 CC with excess IL-4 production through the measurement e.g. by ELISA of
 CC circulating endogenous IL-4 levels in humans
 XX
 XX Sequence 16 AA;

```

Query Match      100.0%; Score 95; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HIYWDDDKRYNPSLKS 16
DB      1 HIYWDDDKRYNPSLKS 16

RESULT 3
AA18112
ID      AAY18112 standard; peptide; 16 AA.
AC      AAY18112;
XX
DT      11-AUG-1999 (first entry)
DE      Heavy chain CDR for hIL-4 specific antibody.
XX
KW      Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;
KW      allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
KW      atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
KW      autoimmune disease; graft versus host disease;
KW      complementarity determining region; CDR.
XX
OS      Synthetic.
XX
PN      US5914110-A.
XX
PD      22-JUN-1999.
XX
PF      07-JUN-1995; 95US-00483636.
XX
PR      07-SEP-1993; 93US-00117366.
PR      14-OCT-1993; 93US-00136783.
PR      07-SEP-1994; 94WO-US010308.
XX
PA      (SMIK ) SMITHKLINE BEECHAM PLC.
PA      (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI      Sylvester DR, Holmes SD, Gross MS;
XX
WPI; 1999-370482/31.
DR      N-PSDB; AAX79511.
XX
PT      Recombinant IL4 antibodies useful for treatment of allergic rhinitis,
PT      atopic asthma and anaphylactic shock.
XX
PS      Claim 7; Col 45; 50pp; English.
XX
CC      This sequence represents a heavy chain complementarity determining region
CC      (CDR) from an antibody of the invention. The antibody is a chimeric or
CC      humanised interleukin-4 (IL4) monoclonal antibody for the treatment of
CC      immunoglobulin E (IgE) mediated diseases. The antibodies are useful for
CC      the treatment of allergic disorders such as allergic rhinitis,
CC      conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.
CC      The antibodies are also useful for regulating B and T cell proliferation
CC      and as such are useful in the treatment of autoimmune diseases and graft
CC      versus host disease
XX
SQ      Sequence 16 AA;

Query Match      100.0%; Score 95; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HIYWDDDKRYNPSLKS 16
DB      1 HIYWDDDKRYNPSLKS 16

RESULT 4
AAO18532
ID      AAO18532 standard; peptide; 16 AA.
AC      AAO18532;
XX
DT      11-OCT-2002 (first entry)
DE      Murine Mab 1F7 heavy chain CDR2 region.
XX
KW      Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR;
KW      complementarity determining region; framework-determining region; FR;
KW      heavy chain; light chain; HIV infection.
XX
OS      Mus sp.
XX
PN      WO200255668-A2.
XX
PD      18-JUL-2002.
XX
PF      11-JAN-2002; 2002WO-US000927.
PR      11-JAN-2001; 2001US-00759112.
XX
PA      (IMMP-) IMMIPHERON INC.
XX
PI      Muller S, Kohler H;
XX
WPI; 2002-590668/53.
DR      N-PSDB; AAL48656.
XX
CC      New polynucleotide encoding a complementarity- or framework-determining
CC      region of an anti-idiotypic antibody that binds to human or primate anti-
CC      human immunodeficiency virus (HIV) antibodies, for use in vaccines
CC      against HIV.
XX
PS      Claim 4; Page 21; 27pp; English.
XX
CC      The present invention relates to coding sequences of the murine 1F7 anti-
CC      idiotypic antibody complementarity-determining region (CDR) or framework-
CC      determining region (FR). The antibody binds to human or primate anti-
CC      human immunodeficiency virus (HIV) antibodies and can be used in the
CC      treatment of HIV infection. The present sequence is a region of the 1F7
CC      heavy chain
XX
SQ      Sequence 16 AA;

Query Match      100.0%; Score 95; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HIYWDDDKRYNPSLKS 16
DB      1 HIYWDDDKRYNPSLKS 16

RESULT 5
ABP58280
ID      ABP58280 standard; peptide; 16 AA.
XX
AC      ABP58280;
XX
DT      31-MAR-2003 (first entry)
DE      Murine monoclonal antibody 10D5 heavy chain CDR2.
XX
KW      Monoclonal antibody; 10D5; complementarity determining region; CDR;
KW      mouse; humanised antibody; antibody; Alzheimer's disease;
KW      Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
XX
OS      Mus sp.
XX
PN      WO200288307-A2.
XX
PD      07-NOV-2002.

```

XX 26-APR-2002; 2002WO-US011854.
 XX 30-APR-2001; 2001US-0287653P.
 XX (ELIL) LILLY & CO ELI.
 XX Hinton PR, Vasquez M;
 XX WPI; 2003-183836/18.
 XX New humanized 10D5 antibody, useful for the manufacture of a medicament
 XX for treating Down's syndrome, clinical or pre-clinical Alzheimer's
 XX disease or cerebral amyloid angiopathy.
 XX Claim 2; Page 29; 52pp; English.
 XX The present sequence is that of complementarity determining region (CDR)
 XX 2 of the heavy chain of murine monoclonal antibody 10D5. Novel humanised
 XX antibodies of the invention have CDRs from 10D5 and human framework
 XX sequences. These humanised antibodies have binding affinities (affinity
 XX and epitope location) approximately the same as those of the mouse 10D5
 XX antibody. The invention includes antibodies, single chain antibodies, and
 XX their fragments, as well as nucleotide sequences, vectors, transformed
 XX host cells, and methods of using the humanised antibody to treat,
 XX prevent, alleviate, reverse or otherwise ameliorate symptoms and/or
 XX pathology associated with Down's syndrome, (pre-)clinical Alzheimer's
 XX disease or (pre-)clinical cerebral amyloid angiopathy, and to inhibit
 XX formation or reduce Abeta plaque in the brain
 XX Sequence 16 AA;
 XX Query Match 100.0%; Score 95; DB 6; Length 16;
 XX Best Local Similarity 100.0%; Pred. No. 5.6e-08;
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HIYWDDDKRYNP SLKS 16
 DB 1 HIYWDDDKRYNP SLKS 16
 RESULT 6
 ID AD208829 standard; peptide; 16 AA.
 XX AC AD208829;
 XX 16-JUN-2005 (first entry)
 XX Mammalian amyloid antibody, heavy chain CDR SEQ ID No:54.
 XX amyloid; antibody engineering; antibody production;
 XX amyloid-associated disorder; Alzheimers disease; cancer; allergy;
 XX autoimmune disease; Parkinsons disease;
 XX acquired immune deficiency syndrome; multiple sclerosis; migraine;
 XX dementia; infection; noctropic; neuroprotective; cytostatic;
 XX antiallergic; immunosuppressive; antiparkinsonian; antimigraine;
 XX antimicrobial; anti-HIV; heavy chain; complementarity determining region.
 XX OS Mammalia.
 XX WO2005028511-A2.
 XX 31-MAR-2005.
 XX 26-MAR-2004; 2004WO-US009522.
 XX 28-MAR-2003; 2003US-0458469P.
 XX 28-MAR-2003; 2003US-0458474P.
 XX 28-MAR-2003; 2003US-0458509P.
 XX 28-MAR-2003; 2003US-0458510P.
 XX (CENZ) CENTOCOR INC.
 PA (MERC/) MERCKEN M.
 PA (BENS/) BENSON J M.
 PI Mercken M, Benson JM;
 XX WPI; 2005-242565/25.
 XX New isolated mammalian anti-amyloid antibodies useful for treating
 XX amyloid-associated disorders, such as Alzheimer's disease, cancer,
 XX allergies, autoimmune disease, Parkinson's disease, multiple sclerosis,
 XX migraine and dementia.
 XX Claim 6; SEQ ID NO 54; 306pp; English.
 XX The invention relates to at least one isolated mammalian amyloid antibody
 XX comprising at least one variable region comprising at least one heavy
 XX chain and at least one light chain, of a fully defined sequence of SEQ ID
 XX NOS: 48, 49, 59, 60, 69, 70, 79 and 80, respectively. Also described are:
 XX (i) at least one isolated mammalian amyloid antibody that binds to the
 XX same region of an amyloid polypeptide as an antibody comprising at least
 XX one heavy chain or light chain complementarity determining region (CDR)
 XX having the amino acid sequence of at least one of SEQ ID NO: 73-78, (ii)
 XX at least one isolated mammalian amyloid antibody, comprising at least one
 XX human CDR, where the antibody specifically binds at least one epitope
 XX selected from amino acids 2-7, 3-8, 33-42, or 34-40 of a fully defined
 XX sequence of 42 amino acids (SEQ ID NO: 50), (iii) an isolated nucleic
 XX acid encoding at least one of any of the isolated mammalian amyloid
 XX antibodies mentioned and having at least one human CDR of a fully defined
 XX sequence of SEQ ID NO: 51, 52, 61, 62, 71, 72, 81 and 82, (iv) an
 XX isolated nucleic acid vector comprising an isolated nucleic acid encoding
 XX an amyloid antibody, (v) a prokaryotic or eukaryotic host cell comprising
 XX an isolated nucleic acid encoding an amyloid antibody, (vi) a method of
 XX producing at least one amyloid antibody, (vii) a composition comprising
 XX at least one of any of the isolated mammalian amyloid antibodies
 XX mentioned, and at least one pharmaceutical carrier or diluent, (viii) an
 XX anti-idiotype antibody or fragment that specifically binds at least one
 XX of the amyloid antibodies mentioned, (ix) a method of diagnosing or
 XX treating an amyloid related condition in a cell, tissue, organ or animal,
 XX comprising contacting or administering a composition comprising at least
 XX one of the antibodies mentioned, with, or to, the cell, tissue, organ or
 XX animal, (x) a medical device comprising at least one amyloid antibody
 XX mentioned, where the device is suitable for contacting or administering
 XX at least one amyloid antibody, (xi) an article of manufacture for human
 XX pharmaceutical or diagnostic use, comprising packaging material and a
 XX container comprising a solution or a lyophilized form of at least one of
 XX the amyloid antibodies mentioned, and (xii) a method of producing at
 XX least one of the isolated mammalian amyloid antibodies, comprising
 XX providing a host cell or transgenic animal or transgenic plant or plant
 XX cell capable of expressing the antibody in recoverable amounts. The
 XX methods and compositions of the present invention are useful for
 XX producing therapeutic compositions and devices for treating amyloid-
 XX associated disorders, such as Alzheimer's disease, cancer, allergies,
 XX autoimmune disease, Parkinson's disease, AIDS, multiple sclerosis,
 XX migraine, dementia and infections. This sequence represents a heavy chain
 XX CDR useful in the antibody of the invention.
 XX Sequence 16 AA;
 QY Query Match 100.0%; Score 95; DB 9; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5.6e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HIYWDDDKRYNP SLKS 16
 DB 1 HIYWDDDKRYNP SLKS 16
 RESULT 7
 AAY91018
 ID AAY91018 standard; protein; 41 AA.
 XX AC AAY91018;
 XX

DT 05-SEP-2000 (first entry)
 DE 1F7 antibody variable heavy chain H2 amino acid sequence SEQ ID NO:9.
 KW 1F7 antibody; murine; monoclonal antibody; diagnosis; HIV; infection;
 KW AIDS; anti-HIV; human immunodeficiency virus; detection;
 KW acquired immunodeficiency syndrome.
 OS Mus sp.
 PN US6057421-A.
 XX 02-MAY-2000.
 XX 03-DEC-1997; 97US-00984277.
 XX 30-NOV-1994; 94US-00351193.
 XX (IMMP-) IMMIPHERON INC.
 XX Muller S, Kohler H;
 XX WPI; 2000-338622/29.
 XX Variable heavy and light chain regions of murine monoclonal antibody 1F7,
 PT useful for treating HIV infection and AIDS.
 XX Claim 1; Fig 8; 45pp; English.
 XX The present invention describes the variable heavy and light chain
 CC regions (I) of murine monoclonal antibody (mAb) 1F7. AAY91014 to AAY91016
 CC represent specifically claimed amino acid sequences of the variable light
 CC chain, and AAY91017 to AAY91019 represent specifically claimed amino acid
 CC sequence of the variable heavy chain. The antibodies are used for
 CC treatment of HIV (human immunodeficiency virus) infection and AIDS
 CC (acquired immunodeficiency syndrome). They are also used for detecting
 CC HIV in serum and for stimulating HIV antigen related and committed B
 CC cells to produce broadly reactive and neutralising antibodies by
 CC clonotypic stimulation
 XX
 SQ Sequence 41 AA;
 Query Match 100.0%; Score 95; DB 3; Length 41;
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HIYWDDDKRYNPSLKS 16
 DB 11 HIYWDDDKRYNPSLKS 26
 RESULT 8
 ADQ09629
 ID ADQ09629 standard; protein; 120 AA.
 XX AC
 XX ADQ09629;
 XX 07-OCT-2004 (first entry)
 XX DE Variable heavy chain protein of murine anti-human GPR64-16 antibody ID15.
 XX murine; mouse; antibody; GPR64; cytotoxic; ovarian cancer;
 KW uterine cancer; Ewing's sarcoma; cell death; cytostatic; gene therapy;
 KW immunotherapy; cellular proliferation.
 XX OS Mus sp.
 XX WO2004058171-A2.
 XX 15-JUL-2004.
 XX 19-DEC-2003; 2003WO-US040820.
 XX

PR 20-DEC-2002; 2002US-0435618P.
 XX (PROT-) PROTEIN DESIGN LABS INC.
 XX Law D, Wang Q, Dubridge R, Bhaskar V;
 XX WPI; 2004-525780/50.
 DR N-PSDB; ADQ09619.
 XX New antibody that inhibits binding of a GPR64 polypeptide to an antibody
 PT comprising GPR64-18, GPR64-81, GPR64-93 or GPR64-101, useful in preparing
 PT a composition for diagnosing or treating ovarian cancer.
 XX Example 2; SEQ ID NO 15; 75pp; English.
 XX This invention relates to novel antibodies that bind to the G protein
 CC coupled receptor protein identified as GPR64, namely GPR64-1, GPR64-16,
 CC GPR64-18, GPR64-20 and GPR64-48. Specifically, it refers to the use of
 CC these anti-GPR64 antibodies as selective cytotoxic agents against GPR64
 CC expressing tumour cells such as those associated with ovarian cancer,
 CC uterine cancer and Ewing's sarcoma. The present invention describes
 CC epitope mapping of those antibodies that show high affinity binding to
 CC GPR64 through competitive binding analyses, such that the antibodies can
 CC be assessed for GPR64 dependent cell death in vitro. Accordingly, they
 CC can be used to develop cytostatic compositions for gene therapy or
 CC immunotherapy that inhibit cellular proliferation of an ovarian cancerous
 CC cell and furthermore can diagnose and inhibit growth of tumour cells.
 CC This polypeptide is encoded by a heavy chain variable region DNA sequence
 CC of a murine anti-human GPR64 antibody of the invention.
 XX
 SQ Sequence 120 AA;
 Query Match 100.0%; Score 95; DB 8; Length 120;
 Best Local Similarity 100.0%; Pred. No. 5e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HIYWDDDKRYNPSLKS 16
 DB 52 HIYWDDDKRYNPSLKS 67
 RESULT 9
 AAY23780
 ID AAY23780 standard; protein; 121 AA.
 XX AC
 XX AAY23780;
 XX DT 13-SEP-1999 (first entry)
 XX DE Heavy chain variable region of Ig NEW.
 XX Light chain variable region; interleukin-4; IL-4; antibody 3B9;
 KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
 KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy;
 KW Ig NEW.
 XX OS Synthetic.
 XX US928904-A.
 XX PD 27-JUL-1999.
 XX PF 07-JUN-1995; 95US-00483632.
 XX 07-SEP-1993; 93US-00117366.
 PR 14-OCT-1993; 93US-00136783.
 PR 07-SEP-1994; 94WO-US010308.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX


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XX OS Mus sp.
OS Homo sapiens.
OS Chimeric.

XX Key Location/Qualifiers
XX Region 31..35
XX FT /note= "CDR1"
XX FT Region 52..67
XX FT /note= "CDR2"
XX FT Region 100..112
XX FT /note= "CDR3"
XX WO200298307-A2.
XX 07-NOV-2002.
XX PD
XX PF 26-APR-2002; 2002WO-US011854.
XX PR 30-APR-2001; 2001US-0287653P.
XX PA (ELIL ) LILLY & CO ELI.
XX PI Hinton PR, Vasquez M;
XX PI 2003-183836/18.
XX DR WPI; 2003-183836/18.
XX PT New humanized 10D5 antibody, useful for the manufacture of a medicament
XX PT for treating Down's syndrome, clinical or pre-clinical Alzheimer's
XX PT disease or cerebral amyloid angiopathy.
XX PS Claim 4; Page 9; 52pp; English.
XX CC The present sequence is that of a particularly preferred heavy chain
XX CC variable region of a humanized antibody of the present invention. In this
XX CC sequence, the complementarity determining regions originate from murine
XX CC monoclonal antibody 10D5 and the framework region originates from human
XX CC germline VH segment DP-28 and J segment JH4. Novel humanised antibodies
XX CC of the invention have CDRs from 10D5 and human framework sequences. These
XX CC humanised antibodies have binding affinities (affinity and epitope
XX CC location) approximately the same as those of the mouse 10D5 antibody. The
XX CC invention includes antibodies, single chain antibodies, and their
XX CC fragments, as well as nucleotide sequences, vectors, transformed host
XX CC cells, and methods of using the humanised antibody to treat, prevent,
XX CC alleviate, reverse or otherwise ameliorate symptoms and/or pathology
XX CC associated with Down's syndrome, (pre-)clinical Alzheimer's disease or
XX CC (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or
XX CC reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
XX CC OS field)
XX SQ Sequence 123 AA;

Query Match 100.0%; Score 95; DB 6; Length 123;
Best Local Similarity 100.0%; Pred. No. 5.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HIYWDDDKRYNPSLKS 16
Db |||||
52 HIYWDDDKRYNPSLKS 67

RESULT 15
AAR70190
ID AAR70190 standard; protein; 140 AA.
XX AC
XX AAR70190;
XX XX
XX 25-MAR-2003 (revised)
XX DT 20-SEP-1995 (first entry)
XX XX
XX DE Mouse MAb 3B9 heavy chain.
XX XX
XX Chimeric antibody; humanized antibody; antibody engineering;

monoclonal antibody; MAb; interleukin-4; IL-4; allergy.

KW Mus sp.
XX Key Location/Qualifiers
XX Peptide 1..19
XX FT /label= Sig_peptide
XX FT Region 50..56
XX FT /label= CDR
XX FT /note= "complementarity determining region"
XX FT Region 71..86
XX FT /label= CDR
XX FT /note= "complementarity determining region"
XX FT Region 119..129
XX FT /label= CDR
XX FT /note= "complementarity determining region"
XX WO9507301-A1.
XX PN 16-MAR-1995.
XX PD
XX PF 07-SEP-1994; 94WO-US010308.
XX PR 07-SEP-1993; 93US-00117366.
XX PR 14-OCT-1993; 93US-00136783.
XX XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX PI Holmes S, Gross MS, Sylvester DR;
XX XX
XX DR WPI; 1995-123387/16.
XX DR N-PSDB; AAQ83491.
XX PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from
XX PT high affinity mAbs - useful in treatment of IL-4-mediated and IgE-
XX PT mediated allergic conditions.
XX PS Disclosure; Fig 2; 97pp; English.
XX CC Spleen cells from mice immunized with human IL-4 were used to prepare
XX CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only clone
XX CC 3B9 was positive. cDNA clones of the 3B9 light and heavy chains were
XX CC cloned into pGEM7f+ and transformed into E. coli DH5-alpha. The clones
XX CC were sequenced (AAQ83490-91), and used for antibody engineering. (Updated
XX CC on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 140 AA;

Query Match 100.0%; Score 95; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 5.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HIYWDDDKRYNPSLKS 16
Db |||||
71 HIYWDDDKRYNPSLKS 86

RESULT 16
AAY23768
ID AAY23768 standard; protein; 140 AA.
XX AC
XX AAY23768;
XX DT 13-SEP-1999 (first entry)
XX XX
XX DE Heavy chain variable region of murine IL-4 antibody 3B9.
XX XX
XX Heavy chain variable region; interleukin-4; IL-4; antibody 3B9;
XX KW Chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
XX KW Immunoglobulin E-mediated allergic reaction; allergic rhinitis;
XX KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
XX KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.

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XX OS Mus sp.
XX US5928904-A.
XX PN
XX PD 27-JUL-1999.
XX PF 07-JUN-1995; 95US-00483632.
XX PR 07-SEP-1993; 93US-00117366.
XX PR 14-OCT-1993; 93US-00136783.
XX PR 07-SEP-1994; 94WO-US010308.
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX PI Holmes SD, Sylvestre DR, Gross MS;
XX WPI; 1999-429500/36.
XX DR N-PSDB; AAX85885.
XX PT New DNA molecules encoding recombinant antibodies useful for treating IL4
XX PT -mediated conditions.
XX PS Example 3; Fig 2; 50pp; English.
XX CC The present sequence represents the heavy chain variable region of murine
XX CC interleukin-4 (IL-4) antibody 3B9. The sequences are used in the
XX CC production chimeric and humanised IL-4 monoclonal antibodies. The
XX CC antibodies of the invention are used in therapeutic and pharmaceutical
XX CC compositions for treating IL-4 mediated and immunoglobulin E-mediated
XX CC allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic
XX CC dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host
XX CC -versus-graft disease and renal disease. They are also useful in the
XX CC diagnosis of an allergy or condition associated with excess IL-4
XX CC production through the measurement e.g. by ELISA of circulating
XX CC endogenous IL-4 levels in humans
XX SQ Sequence 140 AA;

Query Match 100.0%; Score 95; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 5.8e-07; Mismatches 0; Gaps 0;
Matches 16; Conservative 0; Indels 0;

QY 1 HIYDDDDKRYNPSLKS 16
| | | | | | | | | | | | | | | |
Db 71 HIYDDDDKRYNPSLKS 86

RESULT 17
AAY18121
ID AAY18121 standard; protein; 140 AA.
XX AC AAY18121;
XX DT 11-AUG-1999 (first entry)
XX DE Heavy chain sequence for murine 3B9 antibody.
XX KW Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;
XX KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
XX KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
XX KW autoimmune disease; graft versus host disease.
XX OS Mus sp.
XX PN US5914110-A.
XX PD 22-JUN-1999.
XX PF 07-JUN-1995; 95US-00483636.
XX PR 07-SEP-1993; 93US-00117366.

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PR 14-OCT-1993; 93US-00136783.
PR 07-SEP-1994; 94WO-US010308.
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX PI Sylvestre DR, Holmes SD, Gross MS;
XX WPI; 1999-370482/31.
XX DR N-PSDB; AAX79520.
XX PT Recombinant IL4 antibodies useful for treatment of allergic rhinitis,
XX PT atopic asthma and anaphylactic shock.
XX PS Claim 24; Fig 2; 50pp; English.
XX CC This sequence represents the heavy chain of the murine 3B9 antibody of
XX CC the invention. The antibody is a chimeric or humanised interleukin-4
XX CC (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE)
XX CC mediated diseases. The antibodies are useful for the treatment of
XX CC allergic disorders such as allergic rhinitis, conjunctivitis, atopic
XX CC dermatitis, atopic asthma and anaphylactic shock. The antibodies are also
XX CC useful for regulating B and T cell proliferation and as such are useful
XX CC in the treatment of autoimmune diseases and graft versus host disease
XX SQ Sequence 140 AA;

Query Match 100.0%; Score 95; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 5.8e-07; Mismatches 0; Gaps 0;
Matches 16; Conservative 0; Indels 0;

QY 1 HIYDDDDKRYNPSLKS 16
| | | | | | | | | | | | | | | |
Db 71 HIYDDDDKRYNPSLKS 86

RESULT 18
AAR70192
ID AAR70192 standard; protein; 141 AA.
XX AC AAR70192;
XX DT 25-MAR-2003 (revised)
XX DT 20-SEP-1995 (first entry)
XX DE Humanized antibody 3B9 heavy chain.
XX KW Humanized antibody; antibody engineering; monoclonal antibody; Mab;
XX KW interleukin-4; IL-4; allergy.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Peptide 1..19 /label= Sig_peptide
XX FT Region 51..57 /label= CDR
XX FT /note= "complementarity determining region"
XX FT Region 72..87 /label= CDR
XX FT /label= "complementarity determining region"
XX FT Region 120..130 /label= CDR
XX FT /note= "complementarity determining region"
XX PN WO9507301-A1.
XX PD 16-MAR-1995.
XX PF 07-SEP-1994; 94WO-US010308.
XX PR 07-SEP-1993; 93US-00117366.
XX PR 14-OCT-1993; 93US-00136783.

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XX The present sequence represents the heavy chain variable region of a
 CC humanised murine interleukin-4 (IL-4) antibody 3B9. The specification
 CC describes chimeric and humanised IL-4 monoclonal antibodies. The
 CC antibodies of the invention are used in therapeutic and pharmaceutical
 CC compositions for treating IL-4 mediated and immunoglobulin E-mediated
 CC allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic
 CC dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host
 CC -versus-graft disease and renal disease. They are also useful in the
 CC diagnosis of an allergy or condition associated with excess IL-4
 CC production through the measurement e.g. by ELISA of circulating
 CC endogenous IL-4 levels in humans
 XX Sequence 141 AA;
 SQ

Query Match 100.0%; Score 95; DB 2; Length 141;
 Best Local Similarity 100.0%; Pred. No. 5.9e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HIYDDDKRYNPSLKS 16
 Db |||||
 72 HIYDDDKRYNPSLKS 87

RESULT 21
 AAY23769
 ID AAY23769 standard; protein; 141 AA.
 XX
 AC AAY23769;
 XX
 DT 17-OCT-2003 (revised)
 DT 13-SEP-1999 (first entry)
 XX
 DE Heavy chain variable region of murine/human chimeric antibody 3B9.
 XX
 KW Heavy chain variable region; interleukin-4; IL-4; antibody 3B9;
 KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
 KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX
 PN US5928904-A.
 XX
 PD 27-JUL-1999.
 XX
 PF 07-JUN-1995; 95US-00483632.
 XX
 PR 07-SEP-1993; 93US-00117366.
 PR 14-OCT-1993; 93US-00136783.
 PR 07-SEP-1994; 94WO-US010308.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Holmes SD, Sylvester DR, Gross MS;
 XX
 DR WPI; 1999-429500/36.
 DR N-PSDB; AAX85886.
 XX
 PT New DNA molecules encoding recombinant antibodies useful for treating IL4
 PT -mediated conditions.
 XX
 PS Example 3; Fig 3; 50pp; English.
 XX
 CC The present sequence represents the heavy chain variable region of
 CC murine/human interleukin-4 (IL-4) chimeric antibody 3B9. The
 CC specification describes chimeric and humanised IL-4 monoclonal
 CC antibodies. The antibodies of the invention are used in therapeutic and
 CC pharmaceutical compositions for treating IL-4 mediated and immunoglobulin

CC E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis,
 CC atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid
 CC arthritis, host-versus-graft disease and renal disease. They are also
 CC useful in the diagnosis of an allergy or condition associated with excess
 CC IL-4 production through the measurement e.g. by ELISA of circulating
 CC endogenous IL-4 levels in humans. (Updated on 17-OCT-2003 to standardise
 CC OS field)
 XX Sequence 141 AA;
 SQ

Query Match 100.0%; Score 95; DB 2; Length 141;
 Best Local Similarity 100.0%; Pred. No. 5.9e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HIYDDDKRYNPSLKS 16
 Db |||||
 72 HIYDDDKRYNPSLKS 87

RESULT 22
 AAY18125
 ID AAY18125 standard; protein; 141 AA.
 XX
 AC AAY18125;
 XX
 DT 11-AUG-1999 (first entry)
 XX
 DE Chimeric 3B9 monoclonal antibody heavy chain.
 XX
 KW Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;
 KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
 KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
 KW autoimmune disease; graft versus host disease.
 XX
 OS Synthetic.
 XX
 PN US5914110-A.
 XX
 PD 22-JUN-1999.
 XX
 PF 07-JUN-1995; 95US-00483636.
 XX
 PR 07-SEP-1993; 93US-00117366.
 PR 14-OCT-1993; 93US-00136783.
 PR 07-SEP-1994; 94WO-US010308.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 PI Sylvester DR, Holmes SD, Gross MS;
 XX
 DR WPI; 1999-370482/31.
 DR N-PSDB; AAX79542.
 XX
 PT Recombinant IL4 antibodies useful for treatment of allergic rhinitis,
 PT atopic asthma and anaphylactic shock.
 XX
 PS Example 5; Fig 3; 50pp; English.
 XX
 CC This sequence represents the light chain of the chimeric 3B9 antibody of
 CC the invention. The antibody is a chimeric or humanised interleukin-4
 CC (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE)
 CC mediated diseases. The antibodies are useful for the treatment of
 CC allergic disorders such as allergic rhinitis, conjunctivitis, atopic
 CC dermatitis, atopic asthma and anaphylactic shock. The antibodies are also
 CC useful for regulating B and T cell proliferation and as such are useful
 CC in the treatment of autoimmune diseases and graft versus host disease
 XX
 SQ Sequence 141 AA;
 SQ

Query Match 100.0%; Score 95; DB 2; Length 141;
 Best Local Similarity 100.0%; Pred. No. 5.9e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 HIYWDDDKRYNPSLKS 16
Db      72 HIYWDDDKRYNPSLKS 87

RESULT 23
ADY18117
ID      AA18117 standard; protein; 141 AA.
XX
XX      AC      AAY18117;
XX
XX      DT      11-AUG-1999 (first entry)
XX
XX      DE      Heavy chain sequence for humanised 3B9 antibody.
XX
XX      KW      Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;
XX      KW      allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
XX      KW      atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
XX      KW      autoimmune disease; graft versus host disease.
XX
XX      OS      Synthetic.
XX
XX      PN      US5914110-A.
XX
XX      PD      22-JUN-1999.
XX
XX      PF      07-JUN-1995; 95US-00483636.
XX
XX      PR      07-SEP-1993; 93US-00117366.
XX      PR      14-OCT-1993; 93US-00136783.
XX      PR      07-SEP-1994; 94WO-US010308.
XX
XX      PA      (SMIK ) SMITHKLINE BEECHAM PLC.
XX      PA      (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX      PI      Sylvester DR, Holmes SD, Gross MS;
XX
XX      WPI; 1999-370482/31.
XX      DR      N-PSDB; AAX79516.
XX
XX      PT      Recombinant IL4 antibodies useful for treatment of allergic rhinitis,
XX      PT      atopic asthma and anaphylactic shock.
XX
XX      PS      Claim 15; Fig 4; 50pp; English.
XX
XX      CC      This sequence represents the heavy chain of the humanised 3B9 antibody of
XX      CC      the invention. The antibody is a chimeric or humanised interleukin-4
XX      CC      (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE)
XX      CC      mediated diseases. The antibodies are useful for the treatment of
XX      CC      allergic disorders such as allergic rhinitis, conjunctivitis, atopic
XX      CC      dermatitis, atopic asthma and anaphylactic shock. The antibodies are also
XX      CC      useful for regulating B and T cell proliferation and as such are useful
XX      CC      in the treatment of autoimmune diseases and graft versus host disease
XX
XX      SQ      Sequence 141 AA;
XX
XX      Query Match      100.0%; Score 95; DB 2; Length 141;
XX      Best Local Similarity 100.0%; Pred. No. 5.9e-07;
XX      Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HIYWDDDKRYNPSLKS 16
Db      72 HIYWDDDKRYNPSLKS 87

RESULT 24
ABG76934
ID      ABG76934 standard; protein; 142 AA.
XX
XX      AC      ABG76934;
XX
XX      DT      05-NOV-2002 (first entry)
XX
XX      DE      Mouse 10D5 VH protein.
XX
XX      KW      Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;
XX      KW      variable region complementarity determining region; 3D6; 10D5;
XX      KW      variable framework region; amyloidogenic disease; Alzheimer's disease;
XX      KW      amyloid deposit; variable light chain; VL; variable heavy chain; VH;
XX      KW      nototropic; neuroprotective; inhibitor of beta amyloid accumulation;
XX      KW      Abeta.
XX
XX      OS      Mus musculus.
XX
XX      PN      WO200246237-A2.
XX
XX      PD      13-JUN-2002.
XX
XX      PF      06-DEC-2001; 2001WO-US046587.
XX
XX      PR      06-DEC-2000; 2000US-0251892P.
XX
XX      PA      (NEUR-) NEURALAB LTD.
XX      PA      (AMHP ) WYETH.
XX
XX      PI      Basi G, Saldanha J, Yednock T;
XX
XX      WPI; 2002-519658/55.
XX      DR      N-PSDB; ABS59429.
XX
XX      PT      Novel light/heavy chain of humanized immunoglobulin for treating
XX      PT      amyloidogenic disease, has 3D6/10D5 variable region complementarity
XX      PT      determining regions and variable framework region from human acceptor
XX      PT      immunoglobulin.
XX
XX      PS      Claim 142; Fig 10; 171pp; English.
XX
XX      CC      The present invention relates to new humanized immunoglobulin (Ig) light
XX      CC      chain (LC) or heavy chain (HC) comprising variable region complementarity
XX      CC      determining regions from 3D6/10D5 Ig LC or HC variable region sequence,
XX      CC      and variable framework region from human acceptor Ig LC or HC sequence.
XX      CC      The invention is useful for preventing or treating an amyloidogenic
XX      CC      disease or Alzheimer's disease in a patient. The invention is also useful
XX      CC      for in vivo imaging amyloid deposits in a patient. The present amino acid
XX      CC      sequence represents a mouse 3D6/10D5 variable light (VL) chain or
XX      CC      variable heavy (VH) chain protein of the invention
XX
XX      SQ      Sequence 142 AA;
XX
XX      Query Match      100.0%; Score 95; DB 5; Length 142;
XX      Best Local Similarity 100.0%; Pred. No. 5.9e-07;
XX      Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HIYWDDDKRYNPSLKS 16
Db      71 HIYWDDDKRYNPSLKS 86

RESULT 25
ADR88420
ID      ADR88420 standard; protein; 142 AA.
XX
XX      AC      ADR88420;
XX
XX      DT      16-DEC-2004 (first entry)
XX
XX      DE      Murine 10D5 immunoglobulin heavy chain variable region SEQ ID NO:16.
XX
XX      KW      3D6; heavy chain variable region; immunoglobulin;
XX      KW      complementarity determining region; CDR; 10D5; variable framework region;
XX      KW      neuroprotective; nototropic; gene therapy; amyloidogenic disease;
XX      KW      Alzheimer's disease.
XX
XX      OS      Mus musculus.
XX
XX      DT      05-NOV-2002 (first entry)

```


FH Key Location/Qualifiers
 FT Peptide 1. .19
 FT /label= signal peptide
 FT Protein 20. .142
 FT /label= mature protein
 XX WO2004080419-A2.
 PN 23-SEP-2004.
 XX
 XX 12-MAR-2004; 2004WO-US007503.
 XX
 XX 12-MAR-2003; 2003US-00388389.
 XX
 XX (NEUR-) NEURALAB LTD.
 XX (AMHP) WYETH.
 XX
 XX Basi G, Saldanha JW, Yednock T;
 PI WPI; 2004-668880/65.
 XX N-PSDB; ADR88419.
 DR
 XX New humanized antibodies that recognize beta amyloid peptides, useful for
 PT preventing or treating amyloidogenic diseases, such as Alzheimer's
 PT disease.
 PT
 XX Claim 85; SEQ ID NO 16; 176pp; English.
 PS
 XX The invention relates to a novel humanised immunoglobulin light or heavy
 CC chain. The humanised immunoglobulin light or heavy chain comprises:
 CC variable region complementarity determining regions (CDR's) from the 3D6
 CC immunoglobulin light chain variable region sequence of 132 amino acids
 CC fully defined in the specification (ADR88406), or heavy chain variable
 CC region sequence of 138 amino acids fully defined in the specification
 CC (ADR88408); or from the 10D5 immunoglobulin light chain variable region
 CC sequence of 131 amino acids given in the specification (ADR88418) or
 CC heavy chain variable region sequence of 142 amino acids fully defined in
 CC the specification (ADR88420); and a variable framework region from a
 CC human acceptor immunoglobulin light or heavy chain sequence, provided
 CC that at least one framework residue is substituted with the corresponding
 CC amino acid residue from the mouse 3D6 or 10D5 light or heavy chain
 CC variable region sequence, where the framework residue is a residue that
 CC non-covalently binds antigen directly, a residue adjacent to a CDR, a CDR
 CC -interacting residue or a residue participating in the VL-VH interface.
 CC An antibody of the invention has neuroprotective and neurotropic activity,
 CC and may have a use in gene therapy. The composition and methods are
 CC useful for preventing or treating an amyloidogenic disease, such as
 CC Alzheimer's disease. The variable region sequence is useful in producing
 CC a three-dimensional image of a 3D6 or 10D5 immunoglobulin, immunoglobulin
 CC chain, or its domain. The present sequence represents the murine 10D5
 CC immunoglobulin heavy chain variable region.
 XX
 XX Sequence 142 AA;
 SQ
 Query Match 100.0%; Score 95; DB 8; Length 142;
 Best Local Similarity 100.0%; Pred. No. 5.9e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HIYDDDKRYNPSLKS 16
 DB 71 HIYDDDKRYNPSLKS 86
 RESULT 26
 ADZ08834
 ID ADZ08834 standard; peptide; 142 AA.
 XX
 AC ADZ08834;
 XX
 DT 16-JUN-2005 (first entry)
 XX
 DE Mammalian amyloid antibody, heavy chain variable region SEQ ID No:59.
 XX

KW amyloid; antibody engineering; antibody production;
 KW amyloid-associated disorder; Alzheimers disease; cancer; allergy;
 KW autoimmune disease; Parkinsons disease;
 KW acquired immune deficiency syndrome; multiple sclerosis; migraine;
 KW dementia; infection; neurotropic; neuroprotective; cytostatic;
 KW antiallergic; immunosuppressive; antiparkinsonian; antimigraine;
 KW antimicrobial; anti-HIV; heavy chain variable region.
 XX
 OS Mammalia.
 XX
 XX WO2005028511-A2.
 PN
 XX 31-MAR-2005.
 PD
 XX 26-MAR-2004; 2004WO-US009522.
 PF
 XX 28-MAR-2003; 2003US-0458469P.
 PR 28-MAR-2003; 2003US-0458474P.
 PR 28-MAR-2003; 2003US-0458509P.
 PR 28-MAR-2003; 2003US-0458510P.
 XX
 XX (CENZ) CENTOCOR INC.
 PA (MERC/) MERCKEN M.
 PA (BENS/) BENSON J M.
 XX
 PI Mercken M, Benson JW;
 PI
 XX WPI: 2005-242565/25.
 DR N-PSDB; ADZ08836.
 DR
 XX New isolated mammalian anti-amyloid antibodies useful for treating
 CC amyloid-associated disorders, such as Alzheimer's disease, cancer,
 PT allergies, autoimmune disease, Parkinson's disease, multiple sclerosis,
 PT migraine and dementia.
 PT
 XX Claim 5; SEQ ID NO 59; 306pp; English.
 PS
 XX The invention relates to at least one isolated mammalian amyloid antibody
 CC comprising at least one variable region comprising at least one heavy
 CC chain and at least one light chain, of a fully defined sequence of SEQ ID
 CC NOS: 48, 49, 59, 60, 69, 70, 79 and 80, respectively. Also described are:
 CC (i) at least one isolated mammalian amyloid antibody that binds to the
 CC same region of an amyloid polypeptide as an antibody comprising at least
 CC one heavy chain or light chain complementarity determining region (CDR)
 CC having the amino acid sequence of at least one of SEQ ID NO: 73-78, (ii)
 CC at least one isolated mammalian amyloid antibody, comprising at least one
 CC human CDR, where the antibody specifically binds at least one epitope
 CC selected from amino acids 2-7, 3-8, 33-42, or 34-40 of a fully defined
 CC sequence of 42 amino acids (SEQ ID NO: 50), (iii) an isolated nucleic
 CC acid encoding at least one of any of the isolated mammalian amyloid
 CC antibodies mentioned and having at least one human CDR of a fully defined
 CC sequence of SEQ ID NO: 51, 52, 61, 62, 71, 72, 81 and 82, (iv) an
 CC isolated nucleic acid vector comprising an isolated nucleic acid encoding
 CC an amyloid antibody, (v) a prokaryotic or eukaryotic host cell comprising
 CC an isolated nucleic acid encoding an amyloid antibody, (vi) a method of
 CC producing at least one amyloid antibody, (vii) a composition comprising
 CC at least one of any of the isolated mammalian amyloid antibodies
 CC mentioned, and at least one pharmaceutical carrier or diluent, (viii) an
 CC anti-idiotypic antibody or fragment that specifically binds at least one
 CC of the amyloid antibodies mentioned, (ix) a method of diagnosing or
 CC treating an amyloid related condition in a cell, tissue, organ or animal,
 CC comprising contacting or administering a composition comprising at least
 CC one of the antibodies mentioned, with or to, the cell, tissue, organ or
 CC animal, (x) a medical device comprising at least one amyloid antibody
 CC mentioned, where the device is suitable for contacting or administering
 CC at least one amyloid antibody, (xi) an article of manufacture for human
 CC pharmaceutical or diagnostic use, comprising packaging material and a
 CC container comprising a solution or a lyophilized form of at least one of
 CC the amyloid antibodies mentioned, and (xii) a method of producing at
 CC least one of the isolated mammalian amyloid antibodies, comprising
 CC providing a host cell or transgenic animal or transgenic plant or plant
 CC cell capable of expressing the antibody in recoverable amounts. The
 CC methods and compositions of the present invention are useful for

CC producing therapeutic compositions and devices for treating amyloid-associated disorders, such as Alzheimer's disease, cancer, allergies, CC autoimmune disease, Parkinson's disease, AIDS, multiple sclerosis, CC migraine, dementia and infections. This sequence represents a heavy chain CC variable region useful in the antibody of the invention.

XX Sequence 142 AA;

SQ Query Match 100.0%; Score 95; DB 9; Length 142;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HIYWDDDKRYNPSLKS 16
Db 71 HIYWDDDKRYNPSLKS 86
|||||

RESULT 27
ABP58287
ID ABP58287 standard; protein; 453 AA.
XX AC ABP58287;
XX AC
XX 23-OCT-2003 (revised)
DT 31-MAR-2003 (first entry)
XX AC
XX Humanised 10D5 antibody heavy chain.

XX Monoclonal antibody; 10D5; complementarity determining region; CDR;
KW mouse; human; humanised antibody; antibody; Alzheimer's disease;
KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
XX

OS Mus sp.
OS Homo sapiens.
OS Chimeric.

FH Key Location/Qualifiers
FT Region 1..123
FT /note= "light chain variable region"
FT Region 31..35
FT /note= "CDR1"
FT Region 52..67
FT /note= "CDR2"
FT Region 100..112
FT /note= "CDR3"

XX WO200288307-A2.

XX 07-NOV-2002.

XX 26-APR-2002; 2002WO-US011854.

XX 30-APR-2001; 2001US-0287653P.

XX (ELIL) LILLY & CO ELI.

XX Hinton PR, Vasquez M;

XX WPI; 2003-183836/18.

XX New humanized 10D5 antibody, useful for the manufacture of a medicament
FT for treating Down's syndrome, clinical or pre-clinical Alzheimer's
FT disease or cerebral amyloid angiopathy.

XX Claim 5; Page 10-12; 52pp; English.

XX The present sequence is the protein sequence of the heavy chain of a
CC humanised antibody of the present invention. In the variable portion, the
CC complementarity determining regions (CDRs) originate from murine
CC monoclonal antibody 10D5 and the framework region originates from human
CC germline VH segment DP-28 and J segment JH4. Novel humanised antibodies
CC of the invention have CDRs from 10D5 and human framework sequences. These
CC humanised antibodies have binding affinities (affinity and epitope

CC location) approximately the same as those of the mouse 10D5 antibody. The
CC invention includes antibodies, single chain antibodies, and their
CC fragments, as well as nucleotide sequences, vectors, transformed host
CC cells, and methods of using the humanised antibody to treat, prevent,
CC alleviate, reverse or otherwise ameliorate symptoms and/or pathology
CC associated with Down's syndrome, (pre-)clinical Alzheimer's disease or
CC (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or
CC reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
CC OS field)

SQ Sequence 453 AA;

Query Match 100.0%; Score 95; DB 6; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HIYWDDDKRYNPSLKS 16
Db 52 HIYWDDDKRYNPSLKS 67
|||||

RESULT 28
ABP58289
ID ABP58289 standard; protein; 472 AA.
XX AC ABP58289;

XX 23-OCT-2003 (revised)
DT 31-MAR-2003 (first entry)
XX AC
XX Humanised 10D5 antibody heavy chain.

XX Monoclonal antibody; 10D5; complementarity determining region; CDR;
KW mouse; human; humanised antibody; antibody; Alzheimer's disease;
KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.

OS Mus sp.
OS Homo sapiens.
OS Chimeric.

FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Signal_peptide
FT Peptide 20..472
FT /label= Mature_protein
FT /note= "the mature light chain is claimed in Claim 5"
FT Region 20..142
FT /note= "light chain variable region, claimed in Claim 4"
FT Region 50..56
FT /note= "CDR1"
FT Region 71..86
FT /note= "CDR2"
FT Region 119..131
FT /note= "CDR3"

XX WO200288307-A2.

XX 07-NOV-2002.

XX 26-APR-2002; 2002WO-US011854.

XX 30-APR-2001; 2001US-0287653P.

XX (ELIL) LILLY & CO ELI.

XX Hinton PR, Vasquez M;

XX WPI; 2003-183836/18.

XX N-PSDB; ABZ24639, ABZ24641.

XX New humanized 10D5 antibody, useful for the manufacture of a medicament
FT for treating Down's syndrome, clinical or pre-clinical Alzheimer's
FT disease or cerebral amyloid angiopathy.

XX Disclosure; Page 13-15; 52pp; English.
PS The present sequence is the protein sequence of the heavy chain of a
XX humanised antibody of the present invention. In the variable portion, the
CC complementarity determining regions (CDRs) originate from murine
CC monoclonal antibody 10D5 and the framework region originates from human
CC germline VH segment DP-28 and J segment JH4. Novel humanised antibodies
CC of the invention have CDRs from 10D5 and human framework sequences. These
CC humanised antibodies have binding affinities (affinity and epitope
CC location) approximately the same as those of the mouse 10D5 antibody. The
CC invention includes antibodies, single chain antibodies, and their
CC fragments, as well as nucleotide sequences, vectors, transformed host
CC cells, and methods of using the humanised antibody to treat, prevent,
CC alleviate, reverse or otherwise ameliorate symptoms and/or pathology
CC associated with Down's syndrome, (pre-)clinical Alzheimer's disease or
CC (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or
CC reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
XX OS field)
XX
SQ Sequence 472 AA;

Query Match 100.0%; Score 95; DB 6; Length 472;
Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HIYWDDDKRYNP SLKS 16
|||||

DB 71 HIYWDDDKRYNP SLKS 86

RESULT 29

ABR62961
ID ABR62961 standard; protein; 119 AA.

AC ABR62961;

DT 04-DEC-2003 (first entry)

DE Monoclonal antibody M130 heavy chain variable region.

XX M130; monoclonal antibody; antibody; Staphylococcus aureus;
KW peptidoglycan; infection; antibacterial.

XX Mus sp.

XX WO2003059259-A2.

XX 24-JUL-2003.

XX 23-DEC-2002; 2002WO-US041032.

XX 21-DEC-2001; 2001US-0341806P.

PR 21-DEC-2001; 2001US-0343444P.

XX (BIOS-) BIOSYNEXUS INC.

XX Schuman RF, Kokai-Kun JF, Foster S, Stinson JR, Fischer GW;

XX WPI; 2003-587257/55.

DR N-PSDB; ACF79291.

XX New medicament comprising at least one MAb that binds to peptidoglycan
FT (PepG) of gram-positive bacteria, useful for treating staphylococcal
FT infections, including nosocomial infections.

XX Claim 11; Fig 2A; 102pp; English.

XX The present sequence is the protein sequence for the heavy chain variable
CC region (VH) of M130, a murine monoclonal antibody (MAb) that binds to
CC Staphylococcus aureus but not to Staphylococcus haemolyticus or
CC Staphylococcus epidermidis. M130 is produced by hybridoma 11-232.3 IE9
CC (ATCC PTA-3659), which was obtained by immunising mice with UV-

CC inactivated whole S. aureus and subcloning by limiting dilution. It is an
CC example of Mabs of the invention that bind to the peptidoglycan of Gram-
CC positive bacteria, and which are useful for treating staphylococcus
CC infections. The antibodies also bind to whole bacteria and enhance
CC phagocytosis and killing of the bacteria in vitro and block nasal
CC colonisation by Gram-positive bacteria in vivo. The variable regions of
CC M130 have been cloned and human/mouse chimeric antibodies were produced
CC that have the M130 variable regions and human constant regions. These
CC chimeric antibodies, referred to as A130, retain the ability to bind to
CC S. aureus peptidoglycan, and are expected to have a reduced human anti-
CC mouse antibody response in humans
XX
SQ Sequence 119 AA;

Query Match 95.8%; Score 91; DB 7; Length 119;

Best Local Similarity 93.8%; Pred. No. 2.1e-06;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HIYWDDDKRYNP SLKS 16
|||||

DB 52 HIFWDDDKRYNP SLKS 67

RESULT 30

ABP58283

ID ABP58283 standard; protein; 123 AA.

XX ABP58283;

XX 23-OCT-2003 (revised)

DT 31-MAR-2003 (first entry)

XX Humanised 10D5 antibody heavy chain variable region.

XX Monoclonal antibody; 10D5; complementarity determining region; CDR;
KW mouse; human; humanised antibody; antibody; Alzheimer's disease;
KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nontropic.

XX Mus sp.

XX Homo sapiens.

XX Chimeric.

XX Key Location/Qualifiers

FT Misc-difference 1 /label= Gln, Glu

FT Misc-difference 2 /label= Val, Ala

FT Region 31..35 /note= "CDR1"

FT Region 52..67 /note= "CDR2"

FT Misc-difference 64 /label= Ser, Thr

FT Misc-difference 77 /label= Lys, Arg

FT Misc-difference 78 /label= Ser, Thr

FT Misc-difference 83 /label= Thr, Ser

FT Misc-difference 84 /label= Met, Ile, Leu

FT Misc-difference 86 /label= Asn, Ser, Thr

FT Misc-difference 87 /label= Met, Val, Leu

FT Region 100..112 /note= "CDR3"

FT Misc-difference 118 /label= Leu, Ser

XX WO200288307-A2.

XX 07-NOV-2002.

XX 26-APR-2002; 2002WO-US011854.
 PF 30-APR-2001; 2001US-0287653P.
 PR (ELIT) LILLY & CO ELI.
 XX Hinton PR, Vasquez M;
 PI WPI; 2003-183836/18.
 DR New humanized 10D5 antibody, useful for the manufacture of a medicament
 XX for treating Down's syndrome, clinical or pre-clinical Alzheimer's
 PT disease or cerebral amyloid angiopathy.
 PT Claim 3; Page 8; 52pp; English.
 PS The present sequence is that of a preferred heavy chain variable region
 XX of a humanised antibody of the present invention. In this sequence, the
 CC complementarity determining regions (CDRs) originate from murine
 CC monoclonal antibody 10D5 and the framework region originates from human
 CC germline VH segment DP-28 and J segment JH4. Novel humanised antibodies
 CC of the invention have CDRs from 10D5 and human framework sequences. These
 CC humanised antibodies have binding affinities (affinity and epitope
 CC location) approximately the same as those of the mouse 10D5 antibody. The
 CC invention includes antibodies, single chain antibodies, and their
 CC fragments, as well as nucleotide sequences, vectors, transformed host
 CC cells, and methods of using the humanised antibody to treat, prevent,
 CC alleviate, reverse or otherwise ameliorate symptoms and/or pathology
 CC associated with Down's syndrome, (pre-)clinical Alzheimer's disease or
 CC (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or
 CC reduce beta plaque in the brain. (Updated on 23-OCT-2003 to standardise
 CC OS field)
 XX Sequence 123 AA;
 SQ

Query Match 95.8%; Score 91; DB 6; Length 123;
 Best Local Similarity 93.8%; Pred. No. 2.2e-06;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 HIYWDDDKRYNPXLS 16
 |||||:|||||
 DB 52 HIYWDDDKRYNPXLS 67

RESULT 31
 AAY42963
 ID AAY42963 standard; protein; 123 AA.
 XX
 AC AAY42963;
 XX 12-FEB-2004 (first entry)
 XX Mouse 12B4 antibody Vh mature peptide sequence.
 XX Immunoglobulin; Ig; neuroprotective; nontropic; gene therapy; vaccine;
 KW amyloidogenic disease; antibody.
 XX Mus sp.
 XX WO2003077858-A2.
 PN 25-SEP-2003.
 XX 12-MAR-2003; 2003WO-US007715.
 XX 12-MAR-2002; 2002US-0363751P.
 XX (NEUR-) NEURALAB LTD.
 PA (AMHP) WYETH.
 XX Basi G, Saldanha J;
 PI WPI; 2003-779077/73.
 DR New humanized immunoglobulin light or heavy chains comprising variable
 XX region complementary determining regions and variable framework regions,
 PT useful for preventing or treating e.g., Alzheimer's disease.
 PT Claim 49; Fig 2A-B; 122pp; English.

DR WPI; 2003-779077/73.
 XX New humanized immunoglobulin light or heavy chains comprising variable
 PT region complementary determining regions and variable framework regions,
 PT useful for preventing or treating e.g., Alzheimer's disease.
 XX Example 5; Fig 2A-B; 122pp; English.
 PS The invention relates to humanized immunoglobulin (Ig) light or heavy
 CC chains comprising variable region complementary determining regions
 CC (CDRs) from the 12B4 Ig variable region sequence and variable framework
 CC regions from a human acceptor Ig light chain or heavy chain sequence. The
 CC humanized Ig light or heavy chain or its nucleic acid molecule is useful
 CC for preventing or treating an amyloidogenic disease in humans, associated
 CC with amyloid deposits of Abeta in the brain, e.g., Alzheimer's disease,
 CC Down's syndrome or mild cognitive impairment, all characterized by
 CC cognitive impairment. The variable region sequence is useful in producing
 CC a three-dimensional image of a 12B4 Ig, 12B4 Ig chain or its domain. A
 CC humanized antibody is useful for reducing plaque or neuritic burden in a
 CC subject. The present sequence represents a mouse 12B4 antibody variable
 CC heavy chain mature peptide sequence
 XX Sequence 123 AA;
 SQ

Query Match 95.8%; Score 91; DB 7; Length 123;
 Best Local Similarity 93.8%; Pred. No. 2.2e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HIYWDDDKRYNPXLS 16
 |||||:|||||
 DB 52 HIYWDDDKRYNPXLS 67

RESULT 32
 AAY42964
 ID AAY42964 standard; protein; 123 AA.
 XX
 AC AAY42964;
 XX 12-FEB-2004 (first entry)
 XX Humanised 12B4VHv1 mature peptide.
 XX Immunoglobulin; Ig; neuroprotective; nontropic; gene therapy; vaccine;
 KW amyloidogenic disease; antibody; 12B4v1.
 XX Synthetic.
 OS WO2003077858-A2.
 PN 25-SEP-2003.
 XX 12-MAR-2003; 2003WO-US007715.
 XX 12-MAR-2002; 2002US-0363751P.
 XX (NEUR-) NEURALAB LTD.
 PA (AMHP) WYETH.
 XX Basi G, Saldanha J;
 PI WPI; 2003-779077/73.
 DR New humanized immunoglobulin light or heavy chains comprising variable
 XX region complementary determining regions and variable framework regions,
 PT useful for preventing or treating e.g., Alzheimer's disease.
 PT Claim 49; Fig 2A-B; 122pp; English.
 XX The invention relates to humanized immunoglobulin (Ig) light or heavy
 CC chains comprising variable region complementary determining regions
 CC (CDRs) from the 12B4 Ig variable region sequence and variable framework
 CC regions from a human acceptor Ig light chain or heavy chain sequence. The

CC humanized Ig light or heavy chain or its nucleic acid molecule is useful
CC for preventing or treating an amyloidogenic disease in humans, associated
CC with amyloid deposits of Abeta in the brain, e.g., Alzheimer's disease,
CC Down's syndrome or mild cognitive impairment, all characterized by
CC cognitive impairment. The variable region sequence is useful in producing
CC a three-dimensional image of a 12B4 Ig, 12B4 Ig chain or its domain. A
CC humanized antibody is useful for reducing plaque or neuritic burden in a
CC subject. The present sequence represents the humanised 12B4VHv1 mature
CC peptide sequence
XX
SQ Sequence 123 AA;

Query Match 95.8%; Score 91; DB 7; Length 123;
Best Local Similarity 93.8%; Pred. No. 2.2e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HIYDDDKRYNPSLKS 16
|||:|||||
DB 52 HIYDDEKRYNPSLKS 67

RESULT 33
AA42973
ID AAY42973 standard; protein; 142 AA.

XX AAY42973;
AC
DT 12-FEB-2004 (first entry)
XX
DE Humanised 12B4VHv1 sequence.
XX
KW Immunoglobulin; Ig; neuroprotective; nootropic; gene therapy; vaccine;
KW amyloidogenic disease; antibody; 12B4V1.
XX
OS Synthetic.

PN WO2003077858-A2.
XX
PD 25-SEP-2003.
XX
PF 12-MAR-2003; 2003WO-US007715.
XX
PR 12-MAR-2002; 2002US-0363751P.
XX
PA (NEUR-) NEURALAB LTD.
PA (AMHP) WYETH.
XX
PI Basi G, Saldanha J;
XX
DR WPI; 2003-779077/73.
DR N-PSDB; ACF58541.
XX
PT New humanized immunoglobulin light or heavy chains comprising variable
PT region complementary determining regions and variable framework regions,
PT useful for preventing or treating e.g., Alzheimer's disease.
XX
PS Example; Fig 4A-D; 122pp; English.

XX The invention relates to humanized immunoglobulin (Ig) light or heavy
XX chains comprising variable region complementary determining regions
XX (CDRs) from the 12B4 Ig variable region sequence and variable framework
XX regions from a human acceptor Ig light chain or heavy chain sequence. The
XX humanized Ig light or heavy chain or its nucleic acid molecule is useful
XX for preventing or treating an amyloidogenic disease in humans, associated
XX with amyloid deposits of Abeta in the brain, e.g., Alzheimer's disease,
XX Down's syndrome or mild cognitive impairment, all characterized by
XX cognitive impairment. The variable region sequence is useful in producing
XX a three-dimensional image of a 12B4 Ig, 12B4 Ig chain or its domain. A
XX humanized antibody is useful for reducing plaque or neuritic burden in a
XX subject. The present sequence represents the humanised 12B4VHv1 sequence
XX
SQ Sequence 142 AA;

Query Match 95.8%; Score 91; DB 7; Length 142;
Best Local Similarity 93.8%; Pred. No. 2.6e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HIYDDDKRYNPSLKS 16
|||:|||||
DB 71 HIYDDEKRYNPSLKS 86

RESULT 34
AA42957
ID AAY42957 standard; protein; 142 AA.

XX AAY42957;
AC
DT 12-FEB-2004 (first entry)
XX
DE Mouse 12B4 antibody VH region.
XX
KW Immunoglobulin; Ig; neuroprotective; nootropic; gene therapy; vaccine;
KW amyloidogenic disease; antibody.
XX
OS Mus sp.

XX Key Location/Qualifiers
FT Peptide 1..20
FT Protein 21..142
FT /note= "leader peptide"
FT /note= "mature protein"
FT Region 51..56
FT /note= "CDR 1"
FT Region 71..86
FT /note= "CDR 2"
FT Region 119..131
FT /note= "CDR 3"

XX WO2003077858-A2.

XX 25-SEP-2003.

XX 12-MAR-2003; 2003WO-US007715.

XX 12-MAR-2002; 2002US-0363751P.

XX (NEUR-) NEURALAB LTD.
XX (AMHP) WYETH.

XX Basi G, Saldanha J;

XX WPI; 2003-779077/73.
XX N-PSDB; ACF58516.

XX New humanized immunoglobulin light or heavy chains comprising variable
XX region complementary determining regions and variable framework regions,
XX useful for preventing or treating e.g., Alzheimer's disease.

XX Claim 2; Page 63; 122pp; English.

XX The invention relates to humanized immunoglobulin (Ig) light or heavy
XX chains comprising variable region complementary determining regions
XX (CDRs) from the 12B4 Ig variable region sequence and variable framework
XX regions from a human acceptor Ig light chain or heavy chain sequence. The
XX humanized Ig light or heavy chain or its nucleic acid molecule is useful
XX for preventing or treating an amyloidogenic disease in humans, associated
XX with amyloid deposits of Abeta in the brain, e.g., Alzheimer's disease,
XX Down's syndrome or mild cognitive impairment, all characterized by
XX cognitive impairment. The variable region sequence is useful in producing
XX a three-dimensional image of a 12B4 Ig, 12B4 Ig chain or its domain. A
XX humanized antibody is useful for reducing plaque or neuritic burden in a
XX subject. The present sequence represents a mouse 12B4 antibody variable
XX heavy chain sequence
XX
SQ Sequence 142 AA;

```

Query Match      95.8%; Score 91; DB 7; Length 142;
Best Local Similarity 93.8%; Pred. No. 2.6e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HIYWDDDKRYNP SLKS 16
Db      71 HIYWDEDKRYNP SLKS 86

RESULT 35
AAY42972
ID AAY42972 standard; protein; 142 AA.
XX
AC AAY42972;
XX
DT 12-FEB-2004 (first entry)
XX
DE Chimeric 12B4VH region sequence.
XX
KW Immunoglobulin; Ig; neuroprotective; nootropic; gene therapy; vaccine;
KW amyloidogenic disease; antibody; 12B4; chimeric.
XX
OS Chimeric - Mus sp.
XX
PN WO2003077858-A2.
XX
PD 25-SEP-2003.
XX
PF 12-MAR-2003; 2003WO-US007715.
XX
PR 12-MAR-2002; 2002US-0363751P.
XX
PA (NEUR-) NEURALAB LTD.
PA (AMHP) WYETH.
XX
PI Basi G, Saldanha J;
XX
WPI; 2003-779077/73.
DR N-PSDB; ACF58540.
XX

New humanized immunoglobulin light or heavy chains comprising variable
region complementary determining regions and variable framework regions,
PT useful for preventing or treating e.g., Alzheimer's disease.
XX
PS Example; Fig 4A-D; 122pp; English.
XX
CC The invention relates to humanized immunoglobulin (Ig) light or heavy
CC chains comprising variable region complementary determining regions
CC (CDRs) from the 12B4 Ig variable region sequence and variable framework
CC regions from a human acceptor Ig light chain or heavy chain sequence. The
CC humanized Ig light or heavy chain or its nucleic acid molecule is useful
CC for preventing or treating an amyloidogenic disease in humans, associated
CC with amyloid deposits of Abeta in the brain, e.g., Alzheimer's disease,
CC Down's syndrome or mild cognitive impairment, all characterized by
CC cognitive impairment. The variable region sequence is useful in producing
CC a three-dimensional image of a 12B4 Ig, 12B4 Ig chain or its domain. A
CC humanized antibody is useful for reducing plaque or neuritic burden in a
CC subject. The present sequence represents a chimeric 12B4VH region
CC sequence
XX
SQ Sequence 142 AA;

Query Match      95.8%; Score 91; DB 7; Length 142;
Best Local Similarity 93.8%; Pred. No. 2.6e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HIYWDDDKRYNP SLKS 16
Db      71 HIYWDEDKRYNP SLKS 86

RESULT 36

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AAR54105
ID AAR54105 standard; protein; 16 AA.
XX
AC AAR54105;
XX
DT 08-FEB-1995 (first entry)
XX
DE Humanised anti-HIV MAB fragment #3.
XX
KW Human; mouse; murine; heavy; light; chain; monoclonal; antibody;
KW complementarity determining region; CDR; IgG; kappa; IIIB; IIIMN;
KW polymerase chain reaction; primer; amplify; PCR.
XX
OS Synthetic.
XX
PN JP06141885-A.
XX
PD 24-MAY-1994.
XX
PF 05-NOV-1992; 92JP-00322476.
XX
PR 05-NOV-1992; 92JP-00322476.
XX
PA (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
DR WPI; 1994-205040/25.
XX
PT Recombinant anti-HIV monoclonal antibody - capable of neutralising
PT strains which can not be neutralised by anti-IIIB and IIIMN antibodies.
XX
PS Disclosure; Page 14; 23pp; Japanese.
XX
CC The sequences given in AAR54103-11 are fragments of the heavy and light
CC chains of the humanised monoclonal antibody (MAB) of the invention. The
CC antibody has the ability to neutralise human immunodeficiency virus. The
CC antibody is classified as IgG kappa and has the sequence RIGPGR or RVGPGR
CC in the principal neutralising domain. The antibody may be used to
CC neutralise the clinically separate strains which cannot be neutralised by
CC the neutralising antibodies against IIIB and IIIMN strains
XX
SQ Sequence 16 AA;

Query Match      94.7%; Score 90; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.5e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 HIYWDDDKRYNP SLKS 16
Db      1 HIYWDDDKRYNP SLKS 16

RESULT 37
ADP71373
ID ADP71373 standard; peptide; 22 AA.
XX
AC ADP71373;
XX
DT 26-AUG-2004 (first entry)
XX
DE CDR sequence 2 for the heavy chain of 105AD7 anti-idiotypic antibody.
XX
KW naked binding material; short consensus complement receptor; SCR1; SCR2;
KW cancer; Cytostatic; CD55.
XX
OS Unidentified.
XX
PN WO2004048413-A2.
XX
PD 10-JUN-2004.
XX
PF 26-NOV-2003; 2003WO-GB005163.
XX
PR 27-NOV-2002; 2002GB-00027644.

```

XX (CANC-) CANCER RES TECHNOLOGY LTD.
 XX Durrant GL;
 XX WPI; 2004-441153/41.
 XX Naked binding material useful for treating cancer, and for neutralizing
 PT CD55 binds to both short consensus complement receptor SCR1 and SCR2
 PT and/or active agent as combined preparation.
 XX Disclosure; SEQ ID NO 5; 53pp; English.
 XX The present invention relates to a naked binding material which binds to
 CC both short consensus complement receptor (SCR1) and SCR2 and/or an active
 CC agent as a combined preparation for simultaneous, separate or sequential
 CC use in the treatment of cancer. The material and the nucleic acid
 CC encoding the material are useful in the preparation of a medicament for
 CC the neutralization of CD55, for the enhancement of complement deposition
 CC on a tissue, and for treating cancer, which involve administering the
 CC material to the subject, which is mammal. The cancer is one or more of
 CC colorectal, breast, ovarian, cervical, gastric, lung, liver, skin and
 CC myeloid (e.g., bone marrow) cancer. The material is useful for
 CC identifying an agent capable of inhibiting CD55, which involve bringing
 CC into contact a candidate agent with at least a portion of SCR1 and SCR2
 CC of CD55 in the presence of the material which in the absence of the
 CC candidate agent is capable of binding both SCR1 and SCR2 of CD55, and
 CC determining the extent to which the candidate agent inhibits binding of
 CC the material to SCR1 and SCR2 of CD55. The method further involves
 CC selecting a candidate agent, which bind both SCR1 and SCR2 of CD55,
 CC and/or determining the amount of complement deposition on a cell sample
 CC in the presence and absence of the candidate agent. The agent identified
 CC by the assay method is useful in the manufacture of a medicament for the
 CC treatment of cancer. The present sequence represents a CDR sequence for
 CC the heavy chain of 105AD7 anti-idiotypic antibody.
 XX SQ Sequence 22 AA;
 Query Match 94.7%; Score 90; DB 8; Length 22;
 Best Local Similarity 93.8%; Pred. No. 4.9e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HIYWDDDKRYNPSLKS 16
 Db 4 HIYWDDDKRYNPSLKS 19
 RESULT 38
 AAR54101
 ID AAR54101 standard; protein; 122 AA.
 AC AAR54101;
 XX 16-OCT-2003 (revised)
 DT 08-FEB-1995 (first entry)
 XX Humanised MAB H-chain.
 DE Human; mouse; murine; heavy; light; chain; monoclonal; antibody;
 XX complementarity determining region; CDR; IgG; kappa; IIIB; IIIMN.
 KW Mus musculus.
 XX Homo sapiens.
 OS Chimeric.
 XX Key Location/Qualifiers
 FH Region 31..37
 FT /label= CDR1
 FT Region 52..67
 FT /label= CDR2
 FT 100..111
 FT /label= CDR3
 XX

PN JP06141885-A.
 XX 24-MAY-1994.
 XX 05-NOV-1992; 92JP-00322476.
 PF 05-NOV-1992; 92JP-00322476.
 PR (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 XX WPI; 1994-205040/25.
 DR N-PSDB; AAQ68709.
 XX Recombinant anti-HIV monoclonal antibody - capable of neutralising
 PT strains which can not be neutralised by anti-IIIB and IIIMN antibodies.
 XX Disclosure; Page 13; 23pp; Japanese.
 PS The sequences given in AAR54101-02 represent the heavy and light chains
 CC respectively of the humanised monoclonal antibody (MAB) of the invention.
 CC The antibody has the ability to neutralise human immunodeficiency virus.
 CC The antibody is classified as IgG kappa and has the sequence RIGPGR or
 CC RVGPER in the principal neutralising domain. The antibody may be used to
 CC neutralise the clinically separate strains which cannot be neutralised by
 CC the neutralising antibodies against IIIB and IIIMN strains. (Updated on
 CC 16-OCT-2003 to standardise OS field)
 XX SQ Sequence 122 AA;
 Query Match 94.7%; Score 90; DB 2; Length 122;
 Best Local Similarity 93.8%; Pred. No. 3.1e-06;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 HIYWDDDKRYNPSLKS 16
 Db 52 HIYWDDDKRYNPSLKS 67
 RESULT 39
 AAR54110
 ID AAR54110 standard; protein; 122 AA.
 XX AC AAR54110;
 XX 08-FEB-1995 (first entry)
 DT Humanised anti-HIV MAB fragment #8.
 DE Human; mouse; murine; heavy; light; chain; monoclonal; antibody;
 KW complementarity determining region; CDR; IgG; kappa; IIIB; IIIMN;
 XX polymerase chain reaction; primer; amplify; PCR.
 OS Synthetic.
 XX JP06141885-A.
 XX 24-MAY-1994.
 PF 05-NOV-1992; 92JP-00322476.
 XX 05-NOV-1992; 92JP-00322476.
 PR (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 XX WPI; 1994-205040/25.
 DR Recombinant anti-HIV monoclonal antibody - capable of neutralising
 PT strains which can not be neutralised by anti-IIIB and IIIMN antibodies.
 XX Disclosure; Page 14; 23pp; Japanese.
 PS The sequences given in AAR54103-11 are fragments of the heavy and light
 CC chains of the humanised monoclonal antibody (MAB) of the invention. The

CC antibody has the ability to neutralise human immunodeficiency virus. The
 CC antibody is classified as IgG kappa and has the sequence RIGPGR or RVGPGR
 CC in the principal neutralising domain. The antibody may be used to
 CC neutralise the clinically separate strains which cannot be neutralised by
 CC the neutralising antibodies against IIB and IIIN strains
 XX
 SQ Sequence 122 AA;

Query Match 94.7%; Score 90; DB 2; Length 122;
 Best Local Similarity 93.8%; Pred. No. 3.1e-06;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HIYWDDDKRYNPSLKS 16
 |||||:|||||
 Db 52 HIYWDDDKRYNPSLKS 67

RESULT 40
 AAW26239
 ID AAW26239 standard; protein; 148 AA.

XX
 AC AAW26239;
 XX
 DT 02-APR-1998 (first entry)
 XX

DE Monoclonal antibody 105AD7 heavy chain variable region.

XX Monoclonal antibody 105AD7; complementarity determining region; CDR;
 KW human; immune response; treatment; cancer.
 KW

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Region 48..54
 FT /note= "complementarity determining region 1"
 FT Misc-difference 53 /note= "encoded by GTG"
 FT /note= "encoded by GGC"
 FT Misc-difference 54 /note= "encoded by GGC"
 FT Region 69..84
 FT /note= "complementarity determining region 2"
 FT Region 117..132
 FT /note= "complementarity determining region 3"
 XX

XX WO9732021-A1.

XX 04-SEP-1997.

XX 28-FEB-1997; 97WO-GB000591.

XX 28-FEB-1996; 96GB-00004177.

XX 29-FEB-1996; 96GB-00004321.

XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

XX Spendlove I, Robins RA, Durrant LG;

XX WPI; 1997-448689/41.

XX N-PSDB; AAT80181.

XX Nucleic acid encoding peptide derived from antibody 105AD7 - used to
 PT induce an immune response for treatment and prevention of cancer.

XX Claim 1; Fig 1A; 32pp; English.

XX This is the variable region of the monoclonal antibody 105AD7 heavy
 CC chain. 105AD7 is a human monoclonal anti-idiotypic antibody that mimics T
 CC cell epitopes on the tumour associated antigen gp72 and has been used for
 CC therapeutic vaccination. A peptide derived from this antibody contains
 CC the 105AD7 heavy chain variable region and a 105AD7 kappa chain. The
 CC complementarity determining regions (CDR) of this peptide and its
 CC fragments can stimulate immune responses. The peptide can be used for
 CC screening for its functional equivalents and mimetics. The peptides, and

CC the fragments, equivalents and mimetics are used to stimulate an immune
 CC response to a tumour antigen, for the treatment or prevention of tumours.
 CC Transfected host cells are used to produce this peptide and the vectors
 CC can be used to generate the peptide in vivo for stimulation of an immune
 CC response. The peptide contains promiscuous helper epitopes which
 CC stimulate a response against tumour antigens other than gp72. These
 CC epitopes may help a cytotoxic T lymphocyte response to any co-injected
 CC antigen
 XX
 SQ Sequence 148 AA;

Query Match 94.7%; Score 90; DB 2; Length 148;
 Best Local Similarity 93.8%; Pred. No. 3.8e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HIYWDDDKRYNPSLKS 16
 |||||:|||||
 Db 69 HIYWDDDKRYNPSLKS 84

RESULT 41
 AAR58612
 ID AAR58612 standard; protein; 246 AA.

XX
 AC AAR58612;
 XX

DT 25-MAR-2003 (revised)
 DT 28-APR-1995 (first entry)
 XX
 XX IL-6 binding inhibitor.
 DE

XX Human interleukin-6 binding inhibitor; IL-6; rheumatoid arthritis;
 KW septic shock; multiple myeloma; ss.
 KW

XX Homo sapiens.

XX EP617126-A2.

XX 28-SEP-1994.

XX 16-FEB-1994; 94EP-00102346.

XX 17-FEB-1993; 93JP-00028173.

XX (AJIN) AJINOMOTO KK.

XX Shimamura T, Nakazawa H, Hamuro J;

XX WPI; 1994-295777/37.

XX N-PSDB; AAQ70612.

XX Polypeptide inhibiting binding of human interleukin-6 (IL-6) to its
 PT receptor - useful for treating auto:immune disease induced or aggravated
 PT by IL-6.

XX Claim 5; Page 18; 26pp; English.

XX AAQ70612 codes for human interleukin-6 binding inhibitor, the polypeptide
 CC described in AAR58612. This polypeptide inhibits the binding of human IL-6
 CC to its receptor, and can therefore be useful in the treatment of a
 CC variety of autoimmune diseases; specifically in the treatment of a
 CC rheumatoid arthritis, septic shock due to bacterial infection and
 CC multiple myeloma. (Updated on 25-MAR-2003 to correct PN field.)
 XX

SQ Sequence 246 AA;

Query Match 94.7%; Score 90; DB 2; Length 246;
 Best Local Similarity 93.8%; Pred. No. 6.6e-06;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HIYWDDDKRYNPSLKS 16
 |||||:|||||
 Db 174 HIYWDDDKRYNPSLKS 189

RESULT 42

AEA37667
ID AEA37667 standard; protein; 121 AA.

XX AEA37667;

XX 28-JUL-2005 (first entry)

XX Mouse CD44 antibody V segment.

XX antibody engineering; CD44; leukemia; hematological disease; neoplasm;
KW cytotatic.

XX Mus musculus.

XX CN1552735-A.

XX 08-DEC-2004.

XX 18-DEC-2003; 2003CN-01107583.

XX 18-DEC-2003; 2003CN-01107583.

XX (HEMA-) HEMATOLOGY INST CHINESE MEDICINE ACAD.

XX Han Z, Song G;

XX WPI; 2005-173920/19.

XX N-PSDB; AEA37666.

XX Engineering antibody against CD44 for inducing leukemia cell
PT differentiation and necrosis.

XX Claim 2; SEQ ID NO 2; 19pp; Chinese.

XX The invention relates to an engineered CD44 antibody for inducing the
CC differentiation and wither of leukemia cells, the gene in the heavy chain
CC and light chain variable region of monoclonal antibody H144 of CD44, the
CC polypeptide coded by said gene, the carrier containing said gene, and the
CC application of said gene and polypeptide in preparing medicines for
CC diagnosing and treating leukemia and disclosed. The present sequence
CC represents the amino acid sequence of the mouse CD44 antibody V segment.

XX Sequence 121 AA;

Query Match 92.6%; Score 88; DB 9; Length 121;

Best Local Similarity 93.8%; Pred. No. 6.4e-06;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HIYDDDKRYNPSLKS 16

DB 52 HIYDDGKRYNPSLKS 67

RESULT 43

ADF71905

ID ADF71905 standard; protein; 118 AA.

XX ADF71905;

XX 26-FEB-2004 (first entry)

XX Hu3G8VH-1 amino acid sequence SEQ ID NO:104.

XX anti-CD16A antibody; mouse; 3G8 antibody; humanised anti-CD16A antibody;
KW immune response; haemostatic; antirheumatic; antiarthritic;
KW dermatological; immunosuppressive; antiinflammatory; antianaemic;
KW vasotropic; nephrotropic; neuroprotective; antipsoriatic; uropathic;
KW ophthalmological; antiasthmatic; inflammatory response;
KW autoimmune disease; idiopathic thrombocytopenic purpura;
KW rheumatoid arthritis; systemic lupus erythematosus;

KW autoimmune haemolytic anaemia; scleroderma;
KW autoantibody triggered urticaria; pemphigus; vasculitis syndrome;
KW systemic vasculitis; Goodpasture's syndrome; multiple sclerosis;
KW psoriatic arthritis; ankylosing spondylitis; Sjogren's syndrome;
KW Reiter's syndrome; Kawasaki's disease; polymyositis; dermatomyositis;
KW allergic asthma.

XX Synthetic.

OS Mus sp.

OS Homo sapiens.

PN WO2003101485-A1.

XX 11-DEC-2003.

XX 29-MAY-2003; 2003WO-US017111.

XX 30-MAY-2002; 2002US-0384689P.

PR 10-JAN-2003; 2003US-0439320P.

XX (MACR-) MACROGENICS INC.

XX Johnson LS, Huang L, Li H, Tuailon N;

XX WPI; 2004-042985/04.

XX Novel anti-CD16A antibody comprising complementarity determining regions
PT derived from mouse 3G8 antibody and humanized anti-CD16A antibody that
PT lacks effector function, useful for treating deleterious immune response.

PS Claim 12; SEQ ID NO 104; 103pp; English.

XX The present invention describes an anti-CD16A antibody (I) comprising a
CC VH domain comprising complementarity determining regions (CDRs) derived
CC from the mouse 3G8 antibody heavy chain and a VL domain comprising CDRs
CC derived from the mouse 3G8 antibody light chain or a humanised anti-CD16A
CC antibody (II) that lacks effector function and comprises all six CDRs of
CC mouse antibody 3G8. Also described is a method (M1) for reducing a
CC deleterious immune response in a mammal in need of such reduction, which
CC involves administering to the mammal a CD16A binding protein comprising
CC an Fc region derived from a human IgG heavy chain, where the Fc region
CC lacks effector function or is modified to reduce binding to an Fc
CC effector ligand. (I) and (II) have haemostatic, antirheumatic,
CC antiarthritic, dermatological, immunosuppressive, antiinflammatory,
CC antianaemic, vasotropic, nephrotropic, neuroprotective, antipsoriatic,
CC uropathic, ophthalmological and antiasthmatic activities. (I) or (II) is
CC useful for reducing a deleterious immune response in a mammal which
CC involves administering to the mammal (I) or (II). The deleterious immune
CC response is an inflammatory response caused by autoimmune disease such as
CC idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA),
CC systemic lupus erythematosus (SLE), autoimmune haemolytic anaemia (AHA),
CC scleroderma, autoantibody triggered urticaria, pemphigus, vasculitis
CC syndrome, systemic vasculitis, Goodpasture's syndrome, multiple sclerosis
CC (MS), psoriatic arthritis, ankylosing spondylitis, Sjogren's syndrome,
CC Reiter's syndrome, Kawasaki's disease, polymyositis and dermatomyositis
CC and also for treating diseases susceptible to treatment with intravenous
CC immunoglobulin (IVIg) therapy e.g., allergic asthma. The present sequence
CC is used in the exemplification of the present invention.

XX Sequence 118 AA;

Query Match 91.6%; Score 87; DB 8; Length 118;

Best Local Similarity 87.5%; Pred. No. 9e-06;

Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HIYDDDKRYNPSLKS 16

DB 52 HIYDDDKRYNPSLKS 67

RESULT 44

ADF71910

ID ADF71910 standard; protein; 118 AA.

XX AC ADF71910;
XX DT 26-FEB-2004 (first entry)
XX DE Hu3G8VH-5 amino acid sequence SEQ ID NO:109.
XX
KW anti-CD16A antibody; mouse; 3G8 antibody; humanised anti-CD16A antibody;
KW immune response; haemostatic; antirheumatic; antiarthritic;
KW dermatological; immunosuppressive; antiinflammatory; antianaemic;
KW vasotropic; nephrotropic; neuroprotective; antipsoriatic; uropathic;
KW ophthalmological; antiasthmatic; inflammatory response;
KW autoimmune disease; idiopathic thrombocytopenic purpura;
KW rheumatoid arthritis; systemic lupus erythematosus;
KW autoimmune haemolytic anaemia; scleroderma;
KW autoantibody triggered urticaria; pemphigus; vasculitis syndrome;
KW systemic vasculitis; Goodpasture's syndrome; multiple sclerosis;
KW psoriatic arthritis; ankylosing spondylitis; Sjogren's syndrome;
KW Reiter's syndrome; Kowasaki's disease; polymyositis; dermatomyositis;
KW allergic asthma.
XX
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX WO2003101485-A1.
XX 11-DEC-2003.
XX 29-MAY-2003; 2003WO-US017111.
XX 30-MAY-2002; 2002US-0384689P.
XX 10-JAN-2003; 2003US-0439320P.
XX (MACR-) MACROGENICS INC.
XX Johnson LS, Huang L, Li H, Tuailon N;
XX WPI; 2004-042985/04.
XX Novel anti-CD16A antibody comprising complementarity determining regions
XX derived from mouse 3G8 antibody and humanized anti-CD16A antibody that
XX lacks effector function, useful for treating deleterious immune response.
XX
XX Claim 12; SEQ ID NO 109; 103pp; English.
XX
XX The present invention describes an anti-CD16A antibody (I) comprising a
XX VH domain comprising complementarity determining regions (CDRs) derived
XX from the mouse 3G8 antibody heavy chain and a VL domain comprising CDRs
XX derived from the mouse 3G8 antibody light chain or a humanised anti-CD16A
XX antibody (II) that lacks effector function and comprises all six CDRs of
XX mouse antibody 3G8. Also described is a method (M1) for reducing a
XX deleterious immune response in a mammal in need of such reduction, which
XX involves administering to the mammal a CD16A binding protein comprising
XX an Fc region derived from a human IgG heavy chain, where the Fc region
XX lacks effector function or is modified to reduce binding to an Fc
XX effector ligand. (I) and (II) have haemostatic, antirheumatic,
XX antiarthritic, dermatological, immunosuppressive, antiinflammatory,
XX antianaemic, vasotropic, nephrotropic, neuroprotective, antipsoriatic,
XX uropathic, ophthalmological and antiasthmatic activities. (I) or (II) is
XX useful for reducing a deleterious immune response in a mammal which
XX involves administering to the mammal (I) or (II). The deleterious immune
XX response is an inflammatory response caused by autoimmune disease such as
XX idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA),
XX systemic lupus erythematosus (SLE), autoimmune haemolytic anaemia (AHA),
XX scleroderma, autoantibody triggered urticaria, pemphigus, vasculitis
XX syndrome, systemic vasculitis, Goodpasture's syndrome, multiple sclerosis
XX (MS), psoriatic arthritis, ankylosing spondylitis, Sjogren's syndrome,
XX Reiter's syndrome, Kowasaki's disease, polymyositis and dermatomyositis,
XX and also for treating diseases susceptible to treatment with intravenous
XX immunoglobulin (IVIg) therapy e.g., allergic asthma. The present sequence
XX is used in the exemplification of the present invention.

SQ Sequence 118 AA;
Query Match 91.6%; Score 87; DB 8; Length 118;
Best Local Similarity 87.5%; Pred. No. 9e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 HIYDDDKRYNPSLKS 16
DB 52 HIWDDDKRYNPAKS 67
||:|||||:|||||
RESULT 45
ADF71908
ID ADF71908 standard; protein; 448 AA.
XX AC ADF71908;
XX 26-FEB-2004 (first entry)
XX Hu3G8VH-1G1 amino acid sequence SEQ ID NO:107.
XX
KW anti-CD16A antibody; mouse; 3G8 antibody; humanised anti-CD16A antibody;
KW immune response; haemostatic; antirheumatic; antiarthritic;
KW dermatological; immunosuppressive; antiinflammatory; antianaemic;
KW vasotropic; nephrotropic; neuroprotective; antipsoriatic; uropathic;
KW ophthalmological; antiasthmatic; inflammatory response;
KW autoimmune disease; idiopathic thrombocytopenic purpura;
KW rheumatoid arthritis; systemic lupus erythematosus;
KW autoimmune haemolytic anaemia; scleroderma;
KW autoantibody triggered urticaria; pemphigus; vasculitis syndrome;
KW systemic vasculitis; Goodpasture's syndrome; multiple sclerosis;
KW psoriatic arthritis; ankylosing spondylitis; Sjogren's syndrome;
KW Reiter's syndrome; Kowasaki's disease; polymyositis; dermatomyositis;
KW allergic asthma.
XX
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX WO2003101485-A1.
XX 11-DEC-2003.
XX 29-MAY-2003; 2003WO-US017111.
XX 30-MAY-2002; 2002US-0384689P.
XX 10-JAN-2003; 2003US-0439320P.
XX (MACR-) MACROGENICS INC.
XX Johnson LS, Huang L, Li H, Tuailon N;
XX WPI; 2004-042985/04.
XX Novel anti-CD16A antibody comprising complementarity determining regions
XX derived from mouse 3G8 antibody and humanized anti-CD16A antibody that
XX lacks effector function, useful for treating deleterious immune response.
XX
XX Claim 12; SEQ ID NO 109; 103pp; English.
XX
XX The present invention describes an anti-CD16A antibody (I) comprising a
XX VH domain comprising complementarity determining regions (CDRs) derived
XX from the mouse 3G8 antibody heavy chain and a VL domain comprising CDRs
XX derived from the mouse 3G8 antibody light chain or a humanised anti-CD16A
XX antibody (II) that lacks effector function and comprises all six CDRs of
XX mouse antibody 3G8. Also described is a method (M1) for reducing a
XX deleterious immune response in a mammal in need of such reduction, which
XX involves administering to the mammal a CD16A binding protein comprising
XX an Fc region derived from a human IgG heavy chain, where the Fc region
XX lacks effector function or is modified to reduce binding to an Fc
XX effector ligand. (I) and (II) have haemostatic, antirheumatic,
XX antiarthritic, dermatological, immunosuppressive, antiinflammatory,
XX antianaemic, vasotropic, nephrotropic, neuroprotective, antipsoriatic,
XX uropathic, ophthalmological and antiasthmatic activities. (I) or (II) is
XX useful for reducing a deleterious immune response in a mammal which
XX involves administering to the mammal (I) or (II). The deleterious immune
XX response is an inflammatory response caused by autoimmune disease such as
XX idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA),
XX systemic lupus erythematosus (SLE), autoimmune haemolytic anaemia (AHA),
XX scleroderma, autoantibody triggered urticaria, pemphigus, vasculitis
XX syndrome, systemic vasculitis, Goodpasture's syndrome, multiple sclerosis
XX (MS), psoriatic arthritis, ankylosing spondylitis, Sjogren's syndrome,
XX Reiter's syndrome, Kowasaki's disease, polymyositis and dermatomyositis,
XX and also for treating diseases susceptible to treatment with intravenous
XX immunoglobulin (IVIg) therapy e.g., allergic asthma. The present sequence
XX is used in the exemplification of the present invention.

CC uropathic, ophthalmological and antiasthmatic activities. (I) or (II) is
 CC useful for reducing a deleterious immune response in a mammal which
 CC involves administering to the mammal (I) or (II). The deleterious immune
 CC response is an inflammatory response caused by autoimmune disease such as
 CC idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA),
 CC systemic lupus erythematosus (SLE), autoimmune haemolytic anaemia (AHA),
 CC scleroderma, autoantibody triggered urticaria, pemphigus, vasculitis
 CC syndrome, systemic vasculitis, Goodpasture's syndrome, multiple sclerosis
 CC (MS), psoriatic arthritis, ankylosing spondylitis, Sjogren's syndrome,
 CC Reiter's syndrome, Kawasaki's disease, polymyositis and dermatomyositis
 CC and also for treating diseases susceptible to treatment with intravenous
 CC immunoglobulin (IVIG) therapy e.g., allergic asthma. The present sequence
 CC is used in the exemplification of the present invention.

XX Sequence 448 AA;

Query Match 91.6%; Score 87; DB 8; Length 448;
 Best Local Similarity 87.5%; Pred. No. 3.8e-05;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HIYWDDDKRYNPSLKS 16
 ||:|||||:|||||
 Db 52 HIWDDDKRYNPAKLS 67

RESULT 46
 ADP71912
 ID ADP71912 standard; protein; 448 AA.

XX AC ADP71912;

XX DT 26-FEB-2004 (first entry)

XX DE Hu3G8VH-5G1Ag amino acid sequence SEQ ID NO:111.

XX anti-CD16A antibody; mouse; 3G8 antibody; humanised anti-CD16A antibody;
 KW immune response; haemostatic; antirheumatic; antiarthritic;
 KW dermatological; immunosuppressive; antiinflammatory; antianaemic;
 KW vasotropic; nephrotropic; neuroprotective; antipsoriatic; uropathic;
 KW ophthalmological; antiasthmatic; inflammatory response;
 KW autoimmune disease; idiopathic thrombocytopenic purpura;
 KW rheumatoid arthritis; systemic lupus erythematosus;
 KW autoimmune haemolytic anaemia; scleroderma;
 KW autoantibody triggered urticaria; pemphigus; vasculitis syndrome;
 KW systemic vasculitis; Goodpasture's syndrome; multiple sclerosis;
 KW psoriatic arthritis; ankylosing spondylitis; Sjogren's syndrome;
 KW Reiter's syndrome; Kawasaki's disease; polymyositis; dermatomyositis;
 KW allergic asthma.

XX OS Synthetic.

XX OS Mus sp.

XX OS Homo sapiens.

XX FN WO2003101485-A1.

XX PD 11-DEC-2003.

XX PF 29-MAY-2003; 2003WO-US017111.

XX PR 30-MAY-2002; 2002US-0384689P.

XX PR 10-JAN-2003; 2003US-0439320P.

XX PA (MACR-) MACROGENICS INC.

XX PI Johnson LS, Huang L, Li H, Tuallon N;

XX DR WPI; 2004-042985/04.

XX Novel anti-CD16A antibody comprising complementarity determining regions
 PT derived from mouse 3G8 antibody and humanized anti-CD16A antibody that
 PT lacks effector function, useful for treating deleterious immune response.

XX PS Disclosure; SEQ ID NO 111; 103pp; English.

XX

CC The present invention describes an anti-CD16A antibody (I) comprising a
 CC VH domain comprising complementarity determining regions (CDRs) derived
 CC from the mouse 3G8 antibody heavy chain and a VL domain comprising CDRs
 CC derived from the mouse 3G8 antibody light chain or a humanised anti-CD16A
 CC antibody (II) that lacks effector function and comprises all six CDRs of
 CC mouse antibody 3G8. Also described is a method (MI) for reducing a
 CC deleterious immune response in a mammal in need of such reduction, which
 CC involves administering to the mammal a CD16A binding protein comprising
 CC an FC region derived from a human IGG heavy chain, where the FC region
 CC lacks effector function or is modified to reduce binding to an FC
 CC effector ligand. (I) and (II) have haemostatic, antirheumatic,
 CC antiarthritic, dermatological, immunosuppressive, antiinflammatory,
 CC antianaemic, vasotropic, nephrotropic, neuroprotective, antipsoriatic,
 CC uropathic, ophthalmological and antiasthmatic activities. (I) or (II) is
 CC useful for reducing a deleterious immune response in a mammal which
 CC involves administering to the mammal (I) or (II). The deleterious immune
 CC response is an inflammatory response caused by autoimmune disease such as
 CC idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA),
 CC systemic lupus erythematosus (SLE), autoimmune haemolytic anaemia (AHA),
 CC scleroderma, autoantibody triggered urticaria, pemphigus, vasculitis
 CC syndrome, systemic vasculitis, Goodpasture's syndrome, multiple sclerosis
 CC (MS), psoriatic arthritis, ankylosing spondylitis, Sjogren's syndrome,
 CC Reiter's syndrome, Kawasaki's disease, polymyositis and dermatomyositis
 CC and also for treating diseases susceptible to treatment with intravenous
 CC immunoglobulin (IVIG) therapy e.g., allergic asthma. The present sequence
 CC is used in the exemplification of the present invention.

XX Sequence 448 AA;

Query Match 91.6%; Score 87; DB 8; Length 448;
 Best Local Similarity 87.5%; Pred. No. 3.8e-05;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HIYWDDDKRYNPSLKS 16
 ||:|||||:|||||
 Db 52 HIWDDDKRYNPAKLS 67

RESULT 47

ADP71914
 ID ADP71914 standard; protein; 117 AA.

XX AC ADP71914;

XX DT 26-FEB-2004 (first entry)

XX DE Hu3G8VH-22 amino acid sequence SEQ ID NO:113.

XX anti-CD16A antibody; mouse; 3G8 antibody; humanised anti-CD16A antibody;
 KW immune response; haemostatic; antirheumatic; antiarthritic;
 KW dermatological; immunosuppressive; antiinflammatory; antianaemic;
 KW vasotropic; nephrotropic; neuroprotective; antipsoriatic; uropathic;
 KW ophthalmological; antiasthmatic; inflammatory response;
 KW autoimmune disease; idiopathic thrombocytopenic purpura;
 KW rheumatoid arthritis; systemic lupus erythematosus;
 KW autoimmune haemolytic anaemia; scleroderma;
 KW autoantibody triggered urticaria; pemphigus; vasculitis syndrome;
 KW systemic vasculitis; Goodpasture's syndrome; multiple sclerosis;
 KW psoriatic arthritis; ankylosing spondylitis; Sjogren's syndrome;
 KW Reiter's syndrome; Kawasaki's disease; polymyositis; dermatomyositis;
 KW allergic asthma.

XX OS Synthetic.

XX OS Mus sp.

XX OS Homo sapiens.

XX PN WO2003101485-A1.

XX PD 11-DEC-2003.

XX PF 29-MAY-2003; 2003WO-US017111.

PR 30-MAY-2002; 2002US-0384689P.
 PR 10-JAN-2003; 2003US-0439320P.
 XX (MACR-) MACROGENICS INC.
 XX Johnson LS, Huang L, Li H, Tuaillon N;
 XX WPI; 2004-042985/04.
 XX Novel anti-CD16A antibody comprising complementarity determining regions
 PT derived from mouse 3G8 antibody and humanized anti-CD16A antibody that
 PT lacks effector function, useful for treating deleterious immune response.
 XX
 XX Claim 9; SEQ ID NO 113; 103pp; English.
 PS
 CC The present invention describes an anti-CD16A antibody (I) comprising a
 CC VH domain comprising complementarity determining regions (CDRs) derived
 CC from the mouse 3G8 antibody heavy chain and a VL domain comprising CDRs
 CC derived from the mouse 3G8 antibody light chain or a humanised anti-CD16A
 CC antibody (II) that lacks effector function and comprises all six CDRs of
 CC mouse antibody 3G8. Also described is a method (M1) for reducing a
 CC deleterious immune response in a mammal in need of such reduction, which
 CC involves administering to the mammal a CD16A binding protein comprising
 CC an Fc region derived from a human IgG heavy chain, where the Fc region
 CC lacks effector function or is modified to reduce binding to an Fc
 CC effector ligand. (I) and (II) have haemostatic, antirheumatic,
 CC antiarthritic, dermatological, immunosuppressive, antiinflammatory,
 CC antianaemic, vasotropic, nephrotropic, neuroprotective, antipsoriatic,
 CC uropathic, ophthalmological and antiasthmatic activities. (I) or (II) is
 CC useful for reducing a deleterious immune response in a mammal which
 CC involves administering to the mammal (I) or (II). The deleterious immune
 CC response is an inflammatory response caused by autoimmune disease such as
 CC idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA),
 CC scleroderma, autoimmune triggered urticaria, pemphigus, vasculitis
 CC (MS), psoriatic arthritis, Goodpasture's syndrome, multiple sclerosis
 CC Reiter's syndrome, Kawasaki's disease, polymyositis and dermatomyositis
 CC and also for treating diseases susceptible to treatment with intravenous
 CC immunoglobulin (IVIg) therapy e.g., allergic asthma. The present sequence
 CC is used in the exemplification of the present invention.
 XX
 SQ Sequence 117 AA;
 Query Match 89.5%; Score 85; DB 8; Length 117;
 Best Local Similarity 87.5%; Pred. No. 1.8e-05;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HIYWDDDKRYNPSLKS 16
 Db ||:|||||:|||||
 52 HIWDDDKRYSPSLKS 67
 RESULT 48
 ADF71916
 ID ADF71916 standard; protein; 448 AA.
 XX ADF71916;
 AC
 XX
 XX 26-FEB-2004 (first entry)
 DT
 XX Hu3G8VH-22GIAG amino acid sequence SEQ ID NO:115.
 DE
 XX anti-CD16A antibody; mouse; 3G8 antibody; humanised anti-CD16A antibody;
 XX immune response; haemostatic; antirheumatic; antiarthritic;
 XX dermatological; immunosuppressive; antiinflammatory; antianaemic;
 XX vasotropic; nephrotropic; neuroprotective; antipsoriatic; uropathic;
 XX ophthalmological; antiasthmatic; inflammatory response;
 XX autoimmune disease; idiopathic thrombocytopenic purpura;
 XX rheumatoid arthritis; systemic lupus erythematosus;
 XX autoimmune haemolytic anaemia; scleroderma;
 XX autoantibody triggered urticaria; pemphigus; vasculitis syndrome;
 XX systemic vasculitis; Goodpasture's syndrome; multiple sclerosis;

KW psoriatic arthritis; ankylosing spondylitis; Sjogren's syndrome;
 KW Reiter's syndrome; Kawasaki's disease; polymyositis; dermatomyositis;
 KW allergic asthma.
 OS Synthetic.
 OS Mus sp.
 OS Homo sapiens.
 XX
 PN WO2003101485-A1.
 XX
 XX 11-DEC-2003.
 PD
 XX
 XX 29-MAY-2003; 2003WO-US017111.
 PF
 XX
 XX 30-MAY-2002; 2002US-0384689P.
 PR
 XX 10-JAN-2003; 2003US-0439320P.
 XX
 XX (MACR-) MACROGENICS INC.
 XX
 XX Johnson LS, Huang L, Li H, Tuaillon N;
 XX WPI; 2004-042985/04.
 DR
 XX Novel anti-CD16A antibody comprising complementarity determining regions
 PT derived from mouse 3G8 antibody and humanized anti-CD16A antibody that
 PT lacks effector function, useful for treating deleterious immune response.
 XX
 XX Disclosure; SEQ ID NO 115; 103pp; English.
 PS
 CC The present invention describes an anti-CD16A antibody (I) comprising a
 CC VH domain comprising complementarity determining regions (CDRs) derived
 CC from the mouse 3G8 antibody heavy chain and a VL domain comprising CDRs
 CC derived from the mouse 3G8 antibody light chain or a humanised anti-CD16A
 CC antibody (II) that lacks effector function and comprises all six CDRs of
 CC mouse antibody 3G8. Also described is a method (M1) for reducing a
 CC deleterious immune response in a mammal in need of such reduction, which
 CC involves administering to the mammal a CD16A binding protein comprising
 CC an Fc region derived from a human IgG heavy chain, where the Fc region
 CC lacks effector function or is modified to reduce binding to an Fc
 CC effector ligand. (I) and (II) have haemostatic, antirheumatic,
 CC antiarthritic, dermatological, immunosuppressive, antiinflammatory,
 CC antianaemic, vasotropic, nephrotropic, neuroprotective, antipsoriatic,
 CC uropathic, ophthalmological and antiasthmatic activities. (I) or (II) is
 CC useful for reducing a deleterious immune response in a mammal which
 CC involves administering to the mammal (I) or (II). The deleterious immune
 CC response is an inflammatory response caused by autoimmune disease such as
 CC idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA),
 CC scleroderma, autoimmune triggered urticaria, pemphigus, vasculitis
 CC (MS), psoriatic arthritis, Goodpasture's syndrome, multiple sclerosis
 CC Reiter's syndrome, Kawasaki's disease, polymyositis and dermatomyositis
 CC and also for treating diseases susceptible to treatment with intravenous
 CC immunoglobulin (IVIg) therapy e.g., allergic asthma. The present sequence
 CC is used in the exemplification of the present invention.
 XX
 SQ Sequence 448 AA;
 Query Match 89.5%; Score 85; DB 8; Length 448;
 Best Local Similarity 87.5%; Pred. No. 7.9e-05;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HIYWDDDKRYNPSLKS 16
 Db ||:|||||:|||||
 52 HIWDDDKRYSPSLKS 67
 RESULT 49
 ABG67188
 ID ABG67188 standard; protein; 121 AA.
 XX
 XX ABG67188;
 AC
 XX

DT 24-SEP-2002 (first entry)
 XX Human IgG1 antibody heavy chain variable region 15H4VH.
 XX
 KW Hepatitis C virus vaccine; HCV; hypervariable region 1; HVR1;
 KW envelope protein E2; antibody; helper T-lymphocyte; IgG1;
 KW cytotoxic T-lymphocyte; HCV infection; virucide; heavy chain.
 XX
 OS Homo sapiens.
 XX
 PN WO200245743-A2.
 XX
 PD 13-JUN-2002.
 XX
 PF 07-DEC-2001; 2001WO-GB005421.
 XX
 PR 09-DEC-2000; 2000GB-00030102.
 PR 18-DEC-2000; 2000GB-00030789.
 XX
 PA (ALLA/) ALLAIN J.
 XX
 PI Allain J, Li C, Piccolella E;
 XX
 DR WPI; 2002-508540/54.
 XX
 XX Hepatitis C virus (HCV) vaccines able to raise antibodies, helper T
 PT lymphocytes and/or cytotoxic T lymphocytes able to bind to the
 PT hypervariable 1 region of the infecting HCV strain.
 XX
 PS Example 4; Fig 2; 52pp; English.
 XX
 CC The present invention relates to a hepatitis C virus (HCV) vaccine
 CC comprising different groups of peptides each group being capable of
 CC raising, in an infected individual, an antibody able to bind to the
 CC hypervariable 1 (HVR1) region of the envelope protein E2 of the infecting
 CC HCV strain. The different groups of peptides are administered
 CC sequentially to raise antibodies, helper T-lymphocytes, and cytotoxic T-
 CC lymphocytes which are cross-reactive to the HVR1 region of the infecting
 CC HCV. The vaccines are useful for preventing and treating chronic HCV
 CC infections. ABG67186-ABG67189 represent variable regions of human IgG1
 CC antibody heavy chain
 XX
 SQ Sequence 121 AA;
 Query Match 88.9%; Score 84.5; DB 5; Length 121;
 Best Local Similarity 94.1%; Pred. No. 2.3e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 HIY-WDDDKRYNPSLKS 16
 ||| |||||
 DB 52 HIYPWDDDKRYNPSLKS 68
 RESULT 50
 AAR88109
 ID AAR88109 standard; peptide; 120 AA.
 XX
 AC AAR88109;
 XX
 DT 25-JUL-1996 (first entry)
 XX
 DE Murine anti-Protein C MAB HPC-4 VH gamma mature peptide.
 XX
 KW Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;
 KW zymogen; cleavage; mouse; humanised antibody; variable region;
 KW light chain; inhibition; anticoagulant; coagulation; tumour.
 XX
 OS Mus musculus.
 XX
 PN WO9534652-A1.
 XX
 PD 21-DEC-1995.
 XX

PF 09-JUN-1995; 95WO-US007372.
 XX
 PR 10-JUN-1994; 94US-00259321.
 XX
 PA (OKLA-) OKLAHOMA MED RES FOUND.
 XX
 PI Rezaie A, Eamon CT;
 XX
 DR WPI; 1996-049681/05.
 DR N-PSDB; AAT09300.
 XX
 PT Calcium-binding monoclonal antibody immunoreactive with Protein C -
 PT inhibits Protein C anticoagulant activation by thrombin-thrombomodulin,
 PT e.g. for treating tumours.
 XX
 PS Claim 2; Page 29; 41pp; English.
 XX
 CC This is the amino acid sequence of the mature peptide from the murine
 CC anti-protein C monoclonal antibody HPC-4 heavy chain variable region. HPC
 CC -4 recognises the activation peptide region (AAR88106) of the heavy chain
 CC of protein C, a vitamin K-dependent plasma protein zymogen. Protein C is
 CC converted to activated protein C (APC) by cleavage between the Arg-Leu
 CC amino acid contained within the activation peptide sequence. HPC-4
 CC prevents protein C activation to APC by binding to this region. The DNA
 CC sequences encoding the variable regions of the heavy and light chains of
 CC the antibody (AAT09299-302) were used to construct humanised antibodies
 CC using the PCR primers AAT09303-9. The humanised antibodies are useful as
 CC inhibitors of coagulation and can be used for the treatment of tumours by
 CC inhibiting the anticoagulant activity of APC by preventing conversion of
 CC protein C to APC
 XX
 SQ Sequence 120 AA;
 Query Match 88.4%; Score 84; DB 2; Length 120;
 Best Local Similarity 87.5%; Pred. No. 2.7e-05;
 Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 HIYWDDDKRYNPSLKS 16
 ||| |||||
 DB 52 HIWDDDKRYNPSLKS 67

Search completed: February 23, 2006, 09:40:49
 Job time : 146.846 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 09:41:24 ; Search time 22.6462 Seconds
(without alignments)
67.979 Million cell updates/sec

Title: US-10-723-872-24

Perfect score: 95

Sequence: 1 HIYWDDKRYNPSLKS 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

PIR_80.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 95 | 100.0 | 122 | 2 | S11740 |
| 2 | 84 | 88.4 | 107 | 2 | A49442 |
| 3 | 83 | 87.4 | 113 | 2 | S26455 |
| 4 | 82 | 86.3 | 41 | 2 | S26936 |
| 5 | 82 | 86.3 | 118 | 2 | S18556 |
| 6 | 82 | 86.3 | 138 | 2 | S31513 |
| 7 | 77 | 81.1 | 119 | 2 | S18555 |
| 8 | 76 | 80.0 | 121 | 1 | G1HJHE |
| 9 | 74 | 77.9 | 124 | 2 | A49002 |
| 10 | 74 | 77.9 | 143 | 2 | P01174 |
| 11 | 72 | 75.8 | 374 | 2 | S69339 |
| 12 | 66 | 69.5 | 103 | 2 | B25913 |
| 13 | 66 | 69.5 | 116 | 2 | S26328 |
| 14 | 65 | 68.4 | 125 | 1 | MHJWC |
| 15 | 57 | 60.0 | 121 | 2 | S09959 |
| 16 | 55 | 57.9 | 120 | 1 | G1HJCO |
| 17 | 54 | 56.8 | 96 | 2 | S26923 |
| 18 | 54 | 56.8 | 121 | 2 | A36005 |
| 19 | 53 | 55.8 | 56 | 2 | S46471 |
| 20 | 53 | 55.8 | 78 | 2 | S46411 |
| 21 | 53 | 55.8 | 96 | 2 | S26924 |
| 22 | 52 | 54.7 | 115 | 2 | S78053 |
| 23 | 50 | 52.6 | 97 | 2 | S26906 |
| 24 | 50 | 52.6 | 97 | 2 | S12412 |
| 25 | 50 | 52.6 | 99 | 2 | S44125 |
| 26 | 50 | 52.6 | 105 | 2 | S44135 |
| 27 | 50 | 52.6 | 115 | 2 | S57464 |
| 28 | 50 | 52.6 | 116 | 2 | B26340 |
| 29 | 50 | 52.6 | 118 | 2 | A26340 |

| | | | | | | |
|-----|------|------|------|---|--------|--------------------|
| 30 | 50 | 52.6 | 130 | 2 | S31690 | Ig heavy chain V r |
| 31 | 50 | 52.6 | 140 | 2 | I37782 | Ig variable region |
| 32 | 49 | 51.6 | 96 | 2 | S26922 | Ig heavy chain V r |
| 33 | 49 | 51.6 | 97 | 2 | PH0876 | Ig heavy chain V r |
| 34 | 49 | 51.6 | 147 | 1 | G2HUCS | Ig heavy chain pre |
| 35 | 48 | 50.5 | 98 | 2 | S12414 | Ig heavy chain V r |
| 36 | 48 | 50.5 | 98 | 2 | S26903 | Ig heavy chain V r |
| 37 | 48 | 50.5 | 99 | 2 | S26801 | Ig heavy chain V r |
| 38 | 48 | 50.5 | 99 | 2 | S26802 | Ig heavy chain V r |
| 39 | 48 | 50.5 | 99 | 2 | S26803 | Ig heavy chain V r |
| 40 | 48 | 50.5 | 116 | 2 | S37456 | Ig mu chain - huma |
| 41 | 48 | 50.5 | 117 | 2 | E34964 | Ig heavy chain pre |
| 42 | 47 | 49.5 | 122 | 2 | S69912 | Ig V-D-J region (N |
| 43 | 47 | 49.5 | 128 | 2 | S31514 | Ig heavy chain - h |
| 44 | 47 | 49.5 | 137 | 2 | S31585 | Ig heavy chain V r |
| 45 | 47 | 49.5 | 144 | 2 | S54228 | Ig mu heavy chain |
| 46 | 47 | 49.5 | 146 | 2 | S09711 | Ig heavy chain V r |
| 47 | 46 | 48.4 | 99 | 2 | S26807 | Ig heavy chain V r |
| 48 | 46 | 48.4 | 99 | 2 | S26800 | Ig heavy chain V r |
| 49 | 46 | 48.4 | 99 | 2 | S12418 | Ig heavy chain V r |
| 50 | 46 | 48.4 | 100 | 2 | S78056 | Ig heavy chain V r |
| 51 | 46 | 48.4 | 110 | 2 | S44110 | Ig heavy chain V-D |
| 52 | 46 | 48.4 | 120 | 2 | PT0370 | Ig mu chain precu |
| 53 | 46 | 48.4 | 121 | 2 | S44113 | Ig heavy chain V r |
| 54 | 46 | 48.4 | 124 | 2 | S31684 | Ig heavy chain V r |
| 55 | 46 | 48.4 | 135 | 2 | S31604 | Ig heavy chain V r |
| 56 | 46 | 48.4 | 147 | 2 | S13519 | Ig heavy chain V r |
| 57 | 46 | 48.4 | 598 | 2 | A82839 | hypothetical prote |
| 58 | 45.5 | 47.9 | 332 | 2 | F84888 | probable RAD51C-li |
| 59 | 45 | 47.4 | 104 | 2 | S26467 | Ig heavy chain V r |
| 60 | 45 | 47.4 | 116 | 1 | HVMS1B | Ig heavy chain V r |
| 61 | 45 | 47.4 | 116 | 1 | HVMS31 | Ig heavy chain pre |
| 62 | 45 | 47.4 | 119 | 2 | C25114 | Ig heavy chain V r |
| 63 | 45 | 47.4 | 120 | 2 | A25114 | Ig heavy chain V r |
| 64 | 45 | 47.4 | 134 | 2 | B24672 | Ig heavy chain pre |
| 65 | 45 | 47.4 | 139 | 2 | S54247 | Ig mu heavy chain |
| 66 | 45 | 47.4 | 253 | 2 | A70336 | heterodisulfide re |
| 67 | 44 | 46.3 | 97 | 2 | PL0118 | Ig heavy chain V-I |
| 68 | 44 | 46.3 | 97 | 2 | S26804 | Ig heavy chain V r |
| 69 | 44 | 46.3 | 97 | 2 | S26808 | Ig heavy chain V r |
| 70 | 44 | 46.3 | 98 | 2 | S26905 | Ig heavy chain V r |
| 71 | 44 | 46.3 | 98 | 2 | S26904 | Ig heavy chain V r |
| 72 | 44 | 46.3 | 99 | 2 | S26899 | Ig heavy chain V r |
| 73 | 44 | 46.3 | 109 | 2 | PH1673 | Ig heavy chain V r |
| 74 | 44 | 46.3 | 109 | 2 | PH1023 | Ig heavy chain V r |
| 75 | 44 | 46.3 | 116 | 2 | S18557 | Ig heavy chain V r |
| 76 | 44 | 46.3 | 119 | 2 | E25114 | Ig heavy chain V r |
| 77 | 44 | 46.3 | 130 | 2 | S30534 | Ig heavy chain V r |
| 78 | 44 | 46.3 | 137 | 2 | S31676 | Ig heavy chain V r |
| 79 | 44 | 46.3 | 139 | 2 | S31696 | Ig heavy chain V r |
| 80 | 44 | 46.3 | 139 | 2 | S31586 | Ig heavy chain V r |
| 81 | 44 | 46.3 | 145 | 2 | S78055 | Ig heavy chain pre |
| 82 | 44 | 46.3 | 156 | 2 | A75034 | hypothetical prote |
| 83 | 44 | 46.3 | 593 | 2 | F86441 | probable cytochrom |
| 84 | 44 | 46.3 | 597 | 2 | B71130 | probable oligopept |
| 85 | 44 | 46.3 | 2183 | 2 | S47307 | genome polyprotein |
| 86 | 43 | 45.3 | 115 | 2 | F25114 | Ig heavy chain V r |
| 87 | 43 | 45.3 | 135 | 2 | S78051 | Ig heavy chain pre |
| 88 | 43 | 45.3 | 136 | 2 | S07637 | Ig heavy chain V r |
| 89 | 43 | 45.3 | 155 | 2 | S31511 | Ig heavy chain - h |
| 90 | 43 | 45.3 | 383 | 2 | D75081 | phosphate abc tran |
| 91 | 43 | 45.3 | 492 | 2 | A81778 | UDP-N-acetylmutamo |
| 92 | 43 | 45.3 | 492 | 2 | C81202 | UDP-N-acetylmutamo |
| 93 | 43 | 45.3 | 938 | 2 | S55051 | Bicaudal-C - fruit |
| 94 | 43 | 45.3 | 1106 | 1 | A39299 | DNA-directed DNA p |
| 95 | 42.5 | 44.7 | 81 | 2 | AC2770 | hypothetical prote |
| 96 | 42.5 | 44.7 | 87 | 2 | D97550 | hypothetical prote |
| 97 | 42.5 | 44.7 | 368 | 2 | JC6081 | proximal sequence |
| 98 | 42.5 | 44.7 | 542 | 2 | T46464 | hypothetical prote |
| 99 | 42 | 44.2 | 74 | 2 | S26793 | Ig heavy chain V r |
| 100 | 42 | 44.2 | 98 | 2 | S26902 | Ig heavy chain V r |
| 101 | 42 | 44.2 | 98 | 2 | S12421 | Ig heavy chain V r |
| 102 | 42 | 44.2 | 119 | 2 | D25114 | Ig heavy chain V r |

| | | | | | | | | | | | | | |
|-----|------|------|------|---|--------|--------------------|-----|------|------|------|---|--------|--------------------|
| 103 | 42 | 44.2 | 130 | 2 | S31673 | Ig heavy chain V r | 176 | 39 | 41.1 | 114 | 2 | T01262 | Ig heavy chain V r |
| 104 | 42 | 44.2 | 140 | 2 | A24770 | hypothetical hybri | 177 | 39 | 41.1 | 115 | 2 | D33932 | Ig mu chain precu |
| 105 | 42 | 44.2 | 146 | 2 | S09710 | Ig heavy chain V r | 178 | 39 | 41.1 | 123 | 2 | S30529 | Ig heavy chain V r |
| 106 | 42 | 44.2 | 284 | 2 | T33586 | hypothetical prote | 179 | 39 | 41.1 | 134 | 2 | S54906 | Ig heavy chain V r |
| 107 | 42 | 44.2 | 298 | 2 | E70312 | hypothetical prote | 180 | 39 | 41.1 | 139 | 2 | A41287 | Ig heavy chain pre |
| 108 | 42 | 44.2 | 328 | 2 | C86351 | hypothetical prote | 181 | 39 | 41.1 | 153 | 2 | AC1286 | deoxyuridine triph |
| 109 | 42 | 44.2 | 389 | 1 | F64426 | phosphate-binding | 182 | 39 | 41.1 | 153 | 2 | AF1657 | deoxyuridine triph |
| 110 | 42 | 44.2 | 411 | 2 | T22290 | hypothetical prote | 183 | 39 | 41.1 | 201 | 2 | G97247 | intracellular prot |
| 111 | 42 | 44.2 | 472 | 2 | S31459 | Ig gamma-1 chain - | 184 | 39 | 41.1 | 210 | 2 | T40465 | probable mitosis a |
| 112 | 42 | 44.2 | 741 | 2 | T09015 | transketolase (EC | 185 | 39 | 41.1 | 240 | 2 | AD2006 | glucose-6-P-dehydr |
| 113 | 42 | 44.2 | 744 | 2 | T09541 | transketolase (EC | 186 | 39 | 41.1 | 243 | 1 | H64413 | probable phosphoe |
| 114 | 42 | 44.2 | 754 | 2 | T47886 | transketolase-like | 187 | 39 | 41.1 | 258 | 2 | H84905 | homodomain transc |
| 115 | 42 | 44.2 | 781 | 2 | JC7382 | DNA-directed DNA p | 188 | 39 | 41.1 | 259 | 2 | A64497 | precursor-3 methyl |
| 116 | 42 | 44.2 | 963 | 2 | E85055 | hypothetical prote | 189 | 39 | 41.1 | 267 | 2 | S47137 | homeotic protein A |
| 117 | 42 | 44.2 | 3191 | 2 | T22945 | hypothetical prote | 190 | 39 | 41.1 | 278 | 2 | T39517 | dual-specificity M |
| 118 | 41-5 | 43.7 | 251 | 1 | E69978 | conserved hypotet | 191 | 39 | 41.1 | 304 | 2 | T39016 | hypothetical prote |
| 119 | 41 | 43.2 | 102 | 2 | PH1235 | Ig heavy chain V r | 192 | 39 | 41.1 | 308 | 2 | T03862 | hypothetical prote |
| 120 | 41 | 43.2 | 121 | 2 | S37200 | Ig heavy chain V r | 193 | 39 | 41.1 | 311 | 2 | T0761 | chitinase (EC 3.2. |
| 121 | 41 | 43.2 | 122 | 2 | D41287 | Ig heavy chain V-I | 194 | 39 | 41.1 | 312 | 2 | T21992 | hypothetical prote |
| 122 | 41 | 43.2 | 122 | 2 | S69909 | Ig V-D-J region (M | 195 | 39 | 41.1 | 315 | 2 | T23824 | hypothetical prote |
| 123 | 41 | 43.2 | 137 | 1 | AVM335 | Ig heavy chain pre | 196 | 39 | 41.1 | 319 | 2 | B83370 | conserved hypotet |
| 124 | 41 | 43.2 | 155 | 2 | S31512 | Ig heavy chain - h | 197 | 39 | 41.1 | 323 | 2 | T41506 | probable phosphata |
| 125 | 41 | 43.2 | 222 | 2 | T46336 | hypothetical prote | 198 | 39 | 41.1 | 329 | 2 | F64356 | translation initia |
| 126 | 41 | 43.2 | 293 | 1 | RGBY54 | phosphate-binding | 199 | 39 | 41.1 | 351 | 2 | I64030 | hypothetical prote |
| 127 | 41 | 43.2 | 337 | 1 | C70473 | globoside alpha-N- | 200 | 39 | 41.1 | 363 | 2 | S37863 | hypothetical prote |
| 128 | 41 | 43.2 | 347 | 2 | AH1050 | conserved hypotet | 201 | 39 | 41.1 | 380 | 2 | S12839 | Ig heavy chain pre |
| 129 | 41 | 43.2 | 387 | 2 | S56411 | hypothetical 45K p | 202 | 39 | 41.1 | 426 | 2 | C69598 | spore maturation p |
| 130 | 41 | 43.2 | 387 | 2 | B86115 | probable synthetas | 203 | 39 | 41.1 | 464 | 2 | AG2769 | cytochrome P450 cy |
| 131 | 41 | 43.2 | 387 | 2 | B91274 | probable synthetas | 204 | 39 | 41.1 | 464 | 2 | H97549 | cytochrome p450 hy |
| 132 | 41 | 43.2 | 387 | 2 | C72254 | glycerol kinase - | 205 | 39 | 41.1 | 471 | 2 | H97200 | ferrichrome-bindin |
| 133 | 41 | 43.2 | 482 | 2 | AG3506 | phosphoenolpyruvat | 206 | 39 | 41.1 | 496 | 2 | B45868 | glycerol kinase (E |
| 134 | 41 | 43.2 | 491 | 2 | G75337 | glycerol kinase - | 207 | 39 | 41.1 | 508 | 2 | B79198 | glycerol kinase fi |
| 135 | 41 | 43.2 | 501 | 2 | T30398 | hypothetical prote | 208 | 39 | 41.1 | 560 | 2 | S27387 | interferon alpha r |
| 136 | 41 | 43.2 | 865 | 2 | F85875 | probable fibrial | 209 | 39 | 41.1 | 635 | 2 | T01311 | NAD ADP-ribosyltra |
| 137 | 41 | 43.2 | 879 | 2 | E91031 | probable outer mem | 210 | 39 | 41.1 | 642 | 2 | S53433 | plasma protein S p |
| 138 | 41 | 43.2 | 879 | 2 | S35362 | protein kinase C (| 211 | 39 | 41.1 | 655 | 2 | H82938 | probable ABC subst |
| 139 | 41 | 43.2 | 988 | 1 | MMHND | nidogen precursor | 212 | 39 | 41.1 | 694 | 2 | S58083 | transketolase (EC |
| 140 | 41 | 43.2 | 1245 | 1 | MMHND | nidogen precursor | 213 | 39 | 41.1 | 741 | 2 | B84888 | probable transketo |
| 141 | 41 | 43.2 | 1247 | 1 | S57198 | multidrug resistan | 214 | 39 | 41.1 | 803 | 2 | S56277 | DNA-directed DNA p |
| 142 | 41 | 43.2 | 1501 | 2 | T05658 | hypothetical prote | 215 | 39 | 41.1 | 831 | 2 | T00323 | chitinase (EC 3.2. |
| 143 | 40.5 | 42.6 | 277 | 2 | T05658 | hypothetical prote | 216 | 39 | 41.1 | 832 | 2 | T31288 | hypothetical prote |
| 144 | 40.5 | 42.6 | 433 | 2 | T05693 | hypothetical prote | 217 | 39 | 41.1 | 839 | 2 | F64171 | hypothetical prote |
| 145 | 40 | 42.1 | 89 | 2 | JC5633 | neuronal nitric ox | 218 | 39 | 41.1 | 924 | 1 | T27421 | cell division cont |
| 146 | 40 | 42.1 | 106 | 2 | S26464 | Ig heavy chain V r | 219 | 39 | 41.1 | 1200 | 2 | T43148 | probable protein-t |
| 147 | 40 | 42.1 | 116 | 2 | S38718 | Ig heavy chain V r | 220 | 39 | 41.1 | 1650 | 2 | S53457 | dominant autoantig |
| 148 | 40 | 42.1 | 117 | 2 | I57810 | gene C72-3A1 prote | 221 | 39 | 41.1 | 1660 | 2 | T42737 | gp330 protein prec |
| 149 | 40 | 42.1 | 129 | 2 | S44114 | Ig heavy chain V r | 222 | 38.5 | 40.5 | 117 | 2 | S19669 | Ig heavy chain V r |
| 150 | 40 | 42.1 | 141 | 2 | S54226 | Ig heavy chain pre | 223 | 38.5 | 40.5 | 126 | 2 | PH1416 | Ig heavy chain V r |
| 151 | 40 | 42.1 | 149 | 2 | S30752 | hypothetical prote | 224 | 38.5 | 40.5 | 126 | 2 | PH1417 | Ig heavy chain V r |
| 152 | 40 | 42.1 | 202 | 2 | T10547 | hypothetical prote | 225 | 38.5 | 40.5 | 126 | 2 | PH1418 | Ig heavy chain V r |
| 153 | 40 | 42.1 | 250 | 2 | T47611 | hypothetical prote | 226 | 38.5 | 40.5 | 126 | 2 | PH1419 | Ig heavy chain V r |
| 154 | 40 | 42.1 | 250 | 2 | E82014 | probable capsule b | 227 | 38.5 | 40.5 | 310 | 2 | T41985 | hypothetical prote |
| 155 | 40 | 42.1 | 357 | 2 | A72220 | conserved hypotet | 228 | 38.5 | 40.5 | 730 | 2 | A96788 | protein T4012.13 l |
| 156 | 40 | 42.1 | 409 | 2 | A95915 | probable TonB-depe | 229 | 38.5 | 40.5 | 870 | 2 | S27514 | mosquitocidal toxi |
| 157 | 40 | 42.1 | 437 | 2 | S67679 | probable membrane | 230 | 38 | 40.0 | 43 | 1 | A36939 | small acid-soluble |
| 158 | 40 | 42.1 | 569 | 2 | H59092 | hypothetical prote | 231 | 38 | 40.0 | 50 | 2 | AB1067 | hypothetical prote |
| 159 | 40 | 42.1 | 796 | 2 | T39962 | coatomer complex b | 232 | 38 | 40.0 | 82 | 2 | S16684 | hypothetical prote |
| 160 | 40 | 42.1 | 1291 | 2 | A49777 | botulinum neurotox | 233 | 38 | 40.0 | 96 | 2 | A28555 | Ig heavy chain V r |
| 161 | 40 | 42.1 | 1291 | 2 | S46431 | botulinum neurotox | 234 | 38 | 40.0 | 102 | 2 | PH1239 | Ig heavy chain V r |
| 162 | 40 | 42.1 | 1858 | 2 | T18273 | 1-phosphatidylinos | 235 | 38 | 40.0 | 117 | 1 | HVM573 | Ig heavy chain pre |
| 163 | 40 | 42.1 | 3079 | 1 | RGBY12 | probable GTPase-ac | 236 | 38 | 40.0 | 118 | 2 | S20780 | Ig heavy chain V r |
| 164 | 40 | 42.1 | 4427 | 2 | PN0637 | polyketide synthas | 237 | 38 | 40.0 | 135 | 2 | PL0100 | Ig heavy chain pre |
| 165 | 40 | 42.1 | 4543 | 1 | A53102 | alpha-2-macroglobu | 238 | 38 | 40.0 | 144 | 2 | S54244 | Ig mu heavy chain |
| 166 | 39.5 | 41.6 | 802 | 2 | C83588 | probable hydroxama | 239 | 38 | 40.0 | 148 | 2 | F83542 | hypothetical prote |
| 167 | 39 | 41.1 | 55 | 2 | D97080 | probable transcrip | 240 | 38 | 40.0 | 216 | 2 | B71231 | alanine-tRNA ligas |
| 168 | 39 | 41.1 | 56 | 2 | B86823 | hypothetical prote | 241 | 38 | 40.0 | 219 | 2 | D82603 | hypothetical prote |
| 169 | 39 | 41.1 | 94 | 2 | S26461 | Ig heavy chain V r | 242 | 38 | 40.0 | 227 | 2 | AH2705 | conserved hypotet |
| 170 | 39 | 41.1 | 99 | 2 | D34964 | Ig heavy chain V-V | 243 | 38 | 40.0 | 227 | 2 | H97487 | hypothetical 28.9K |
| 171 | 39 | 41.1 | 100 | 2 | S14485 | Ig heavy chain V r | 244 | 38 | 40.0 | 231 | 2 | T23136 | hypothetical prote |
| 172 | 39 | 41.1 | 101 | 2 | S14484 | Ig heavy chain V r | 245 | 38 | 40.0 | 259 | 2 | S14662 | hypothetical prote |
| 173 | 39 | 41.1 | 106 | 2 | S59639 | Ig heavy chain V r | 246 | 38 | 40.0 | 268 | 2 | I53413 | calcium sensor pro |
| 174 | 39 | 41.1 | 112 | 1 | ASLJGH | vpu protein - huma | 247 | 38 | 40.0 | 279 | 2 | C64244 | H+-transporting tw |
| 175 | 39 | 41.1 | 113 | 1 | G2MS60 | Ig heavy chain V r | 248 | 38 | 40.0 | 290 | 2 | H70117 | glycine betaine, L |

| | | | | | | | | | | | | | |
|-----|------|------|------|---|--------|---------------------|-----|----|------|-----|---|--------|---------------------|
| 249 | 38 | 40.0 | 291 | 2 | T37992 | probable tricarbox | 322 | 37 | 38.9 | 140 | 2 | S54245 | Ig mu heavy chain |
| 250 | 38 | 40.0 | 305 | 2 | JC5844 | chitinase (EC 3.2. | 323 | 37 | 38.9 | 140 | 2 | A75187 | hypothetical prote |
| 251 | 38 | 40.0 | 308 | 1 | CRH06 | carbonate dehydrat | 324 | 37 | 38.9 | 143 | 2 | B49028 | Ig heavy chain V-I |
| 252 | 38 | 40.0 | 316 | 1 | C97631 | probable 3',5'-cyc | 325 | 37 | 38.9 | 143 | 2 | S54249 | Ig mu heavy chain |
| 253 | 38 | 40.0 | 316 | 2 | AF2854 | conserved hypothet | 326 | 37 | 38.9 | 148 | 2 | B86741 | hypothetical prote |
| 254 | 38 | 40.0 | 380 | 2 | G64309 | hypothetical prote | 327 | 37 | 38.9 | 166 | 2 | A98310 | probable transcrip |
| 255 | 38 | 40.0 | 419 | 2 | S76571 | hypothetical prote | 328 | 37 | 38.9 | 166 | 2 | AB2973 | sigma factor [impo |
| 256 | 38 | 40.0 | 467 | 2 | AB1379 | glutamate decarbox | 329 | 37 | 38.9 | 168 | 2 | B84460 | Ac-like transposas |
| 257 | 38 | 40.0 | 481 | 2 | J50377 | p70 S6 kinase (EC | 330 | 37 | 38.9 | 173 | 2 | T06250 | probable resistanc |
| 258 | 38 | 40.0 | 500 | 2 | T10459 | probable cytochrom | 331 | 37 | 38.9 | 184 | 2 | H96718 | ACHA22C; 50565-49 |
| 259 | 38 | 40.0 | 570 | 2 | S42708 | proline transport | 332 | 37 | 38.9 | 184 | 2 | AG1260 | hypothetical prote |
| 260 | 38 | 40.0 | 570 | 2 | S04547 | proline transport | 333 | 37 | 38.9 | 191 | 2 | AC0273 | hypothetical prote |
| 261 | 38 | 40.0 | 592 | 2 | D88712 | protein C17H12.4 [| 334 | 37 | 38.9 | 209 | 2 | H86188 | probable exported |
| 262 | 38 | 40.0 | 621 | 2 | T13467 | low density lipopr | 335 | 37 | 38.9 | 217 | 2 | A81068 | protein T25N20.5 [|
| 263 | 38 | 40.0 | 623 | 2 | D71435 | hypothetical prote | 336 | 37 | 38.9 | 223 | 2 | A31583 | hypothetical prote |
| 264 | 38 | 40.0 | 658 | 2 | D81099 | membrane-bound lyc | 337 | 37 | 38.9 | 225 | 2 | B23746 | C-reactive protein |
| 265 | 38 | 40.0 | 658 | 2 | D81842 | probable membrane | 338 | 37 | 38.9 | 231 | 2 | D87218 | Ig Fab region IV-J |
| 266 | 38 | 40.0 | 692 | 2 | C81653 | probable thiol-dis | 339 | 37 | 38.9 | 248 | 1 | DFRTP | beta-neoendorphin |
| 267 | 38 | 40.0 | 760 | 1 | JXHU | transferrin recept | 340 | 37 | 38.9 | 254 | 1 | DFHU | beta-neoendorphin |
| 268 | 38 | 40.0 | 803 | 2 | AB0530 | outer membrane pro | 341 | 37 | 38.9 | 256 | 1 | DFPG | beta-neoendorphin |
| 269 | 38 | 40.0 | 893 | 2 | F86476 | protein F1504.39 [| 342 | 37 | 38.9 | 258 | 2 | JC6318 | gene B9R protein - |
| 270 | 38 | 40.0 | 933 | 2 | H69045 | hypothetical prote | 343 | 37 | 38.9 | 266 | 2 | I36855 | hypothetical prote |
| 271 | 38 | 40.0 | 1064 | 2 | H64516 | hypothetical prote | 344 | 37 | 38.9 | 266 | 2 | T28607 | H9R protein - vari |
| 272 | 38 | 40.0 | 1071 | 2 | S48378 | probable membrane | 345 | 37 | 38.9 | 266 | 2 | H72172 | hypothetical prote |
| 273 | 38 | 40.0 | 1210 | 2 | D88013 | protein K10B4.1 [i | 346 | 37 | 38.9 | 272 | 2 | I64245 | hypothetical prote |
| 274 | 38 | 40.0 | 1650 | 2 | T18444 | hypothetical prote | 347 | 37 | 38.9 | 272 | 2 | JQ1802 | B8R 31K protein pr |
| 275 | 38 | 40.0 | 1735 | 1 | S22812 | DNA-directed RNA p | 348 | 37 | 38.9 | 272 | 2 | A42526 | B8R protein - vacc |
| 276 | 38 | 40.0 | 4544 | 1 | S02332 | alpha-2-macroglobu | 349 | 37 | 38.9 | 285 | 2 | G86755 | prophage pi2 prote |
| 277 | 38 | 40.0 | 4545 | 1 | S25111 | alpha-2-macroglobu | 350 | 37 | 38.9 | 285 | 2 | T21802 | transcription regu |
| 278 | 37.5 | 39.5 | 204 | 2 | T08661 | anti-silencing pro | 351 | 37 | 38.9 | 341 | 2 | D71708 | nifH-like protein |
| 279 | 37.5 | 39.5 | 246 | 2 | A57484 | cell division cont | 352 | 37 | 38.9 | 367 | 2 | H85360 | hypothetical prote |
| 280 | 37.5 | 39.5 | 260 | 2 | G70568 | hypothetical prote | 353 | 37 | 38.9 | 376 | 2 | A75381 | peptide ABC transp |
| 281 | 37.5 | 39.5 | 373 | 2 | D64401 | hypothetical prote | 354 | 37 | 38.9 | 390 | 2 | T45789 | hypothetical prote |
| 282 | 37.5 | 39.5 | 419 | 1 | S32880 | lipB protein - Nei | 355 | 37 | 38.9 | 405 | 2 | S53040 | probable membrane |
| 283 | 37.5 | 39.5 | 419 | 2 | G82012 | capsule polysaccha | 356 | 37 | 38.9 | 424 | 2 | T35535 | probable secreted |
| 284 | 37.5 | 39.5 | 419 | 2 | B81240 | capsule polysaccha | 357 | 37 | 38.9 | 432 | 2 | AF0186 | probable sideropho |
| 285 | 37.5 | 39.5 | 421 | 1 | S70402 | zona pellucida gly | 358 | 37 | 38.9 | 432 | 2 | T27180 | hypothetical prote |
| 286 | 37.5 | 39.5 | 468 | 2 | S52495 | acid phosphatase h | 359 | 37 | 38.9 | 451 | 2 | S58653 | hypothetical prote |
| 287 | 37.5 | 39.5 | 642 | 2 | A11827 | cyclomaltodextrin | 360 | 37 | 38.9 | 451 | 2 | T16418 | hypothetical prote |
| 288 | 37.5 | 39.5 | 710 | 2 | A96540 | hypothetical prote | 361 | 37 | 38.9 | 464 | 2 | AC1370 | glutamate decarbox |
| 289 | 37.5 | 39.5 | 889 | 2 | F96637 | hypothetical prote | 362 | 37 | 38.9 | 464 | 2 | AB1740 | glutamate decarbox |
| 290 | 37.5 | 39.5 | 1103 | 2 | H82884 | multiple banded an | 363 | 37 | 38.9 | 467 | 2 | AC1748 | glutamate decarbox |
| 291 | 37.5 | 39.5 | 1118 | 2 | T28426 | probable DNA-direc | 364 | 37 | 38.9 | 484 | 2 | B86224 | hypothetical prote |
| 292 | 37.5 | 39.5 | 1400 | 2 | T20904 | hypothetical prote | 365 | 37 | 38.9 | 492 | 2 | S28007 | probable ATP-bind |
| 293 | 37.5 | 39.5 | 1404 | 2 | H89715 | protein F14F4.3 [i | 366 | 37 | 38.9 | 494 | 2 | T45480 | catalase (EC 1.11. |
| 294 | 37.5 | 39.5 | 1427 | 2 | T20903 | hypothetical prote | 367 | 37 | 38.9 | 517 | 2 | A70793 | probable glycerol |
| 295 | 37 | 38.9 | 63 | 2 | FC4336 | dymorphin precursor | 368 | 37 | 38.9 | 524 | 2 | D70861 | probable monoxigen |
| 296 | 37 | 38.9 | 64 | 2 | F97806 | hypothetical prote | 369 | 37 | 38.9 | 524 | 2 | B86628 | prophage psi prote |
| 297 | 37 | 38.9 | 65 | 2 | I36950 | urei protein - Bac | 370 | 37 | 38.9 | 560 | 2 | S54093 | hypothetical prote |
| 298 | 37 | 38.9 | 70 | 2 | JV0103 | hypothetical 8.5K | 371 | 37 | 38.9 | 569 | 2 | T07158 | amidophosphoribos |
| 299 | 37 | 38.9 | 97 | 2 | D81983 | hypothetical prote | 372 | 37 | 38.9 | 578 | 2 | H65006 | hypothetical prote |
| 300 | 37 | 38.9 | 97 | 2 | S26898 | Ig heavy chain V r | 373 | 37 | 38.9 | 610 | 2 | T47725 | hypothetical prote |
| 301 | 37 | 38.9 | 97 | 2 | S26806 | Ig heavy chain V r | 374 | 37 | 38.9 | 641 | 1 | JVBFAI | DNA-packaging prot |
| 302 | 37 | 38.9 | 97 | 2 | S26805 | Ig heavy chain V r | 375 | 37 | 38.9 | 641 | 1 | H85689 | DNA-packaging prot |
| 303 | 37 | 38.9 | 97 | 2 | S14474 | Ig heavy chain V-I | 376 | 37 | 38.9 | 641 | 2 | F90832 | terminase large su |
| 304 | 37 | 38.9 | 97 | 2 | G34964 | Ig heavy chain V-I | 377 | 37 | 38.9 | 641 | 2 | C90901 | terminase terminase |
| 305 | 37 | 38.9 | 102 | 2 | S14487 | Ig heavy chain V r | 378 | 37 | 38.9 | 676 | 2 | S54301 | transketolase (EC |
| 306 | 37 | 38.9 | 102 | 2 | S14488 | Ig heavy chain V r | 379 | 37 | 38.9 | 705 | 2 | T31261 | hypothetical prote |
| 307 | 37 | 38.9 | 106 | 2 | S37454 | Ig mu chain - huma | 380 | 37 | 38.9 | 708 | 2 | T50064 | probable transcrip |
| 308 | 37 | 38.9 | 114 | 2 | T72667 | cold agglutinin FS | 381 | 37 | 38.9 | 731 | 2 | AB1945 | hypothetical prote |
| 309 | 37 | 38.9 | 119 | 2 | C53285 | Ig heavy chain V a | 382 | 37 | 38.9 | 737 | 2 | A87626 | catalase/peroxidas |
| 310 | 37 | 38.9 | 121 | 2 | C55257 | Ig gamma heavy cha | 383 | 37 | 38.9 | 737 | 2 | C84232 | kinase anchor prot |
| 311 | 37 | 38.9 | 122 | 2 | JL0047 | Ig heavy chain V r | 384 | 37 | 38.9 | 754 | 2 | T00393 | Nijmegen breakage |
| 312 | 37 | 38.9 | 123 | 2 | S30530 | Ig heavy chain V r | 385 | 37 | 38.9 | 759 | 1 | A60011 | RNA-directed RNA p |
| 313 | 37 | 38.9 | 126 | 2 | S47010 | Ig heavy chain V4. | 386 | 37 | 38.9 | 759 | 1 | P31V2A | RNA-directed RNA p |
| 314 | 37 | 38.9 | 126 | 2 | T50826 | ribosomal protein | 387 | 37 | 38.9 | 759 | 2 | JN0435 | RNA-directed RNA p |
| 315 | 37 | 38.9 | 127 | 2 | S19668 | Ig variable region | 388 | 37 | 38.9 | 759 | 2 | T44142 | DR1 protein [impor |
| 316 | 37 | 38.9 | 129 | 2 | T37779 | Ig heavy chain V r | 389 | 37 | 38.9 | 775 | 1 | VPXRHK | outer layer protei |
| 317 | 37 | 38.9 | 133 | 2 | P80341 | Ig heavy chain V-D | 390 | 37 | 38.9 | 775 | 1 | VPXRW3 | outer layer protei |
| 318 | 37 | 38.9 | 133 | 2 | A64661 | biopolymer transpo | 391 | 37 | 38.9 | 775 | 1 | VPXRW4 | outer layer protei |
| 319 | 37 | 38.9 | 133 | 2 | A71855 | biopolymer transpo | 392 | 37 | 38.9 | 775 | 1 | VPXRW5 | outer layer protei |
| 320 | 37 | 38.9 | 140 | 2 | S78052 | Ig heavy chain pre | 393 | 37 | 38.9 | 775 | 1 | VPXRW6 | outer layer protei |
| 321 | 37 | 38.9 | 140 | 2 | A49045 | Ig heavy chain V r | 394 | 37 | 38.9 | 775 | 1 | VPXRWF | outer layer protei |

| | | | | | | | | | | | | |
|-----|------|------|------|---|--------|--------------------|-----|------|-----|---|--------|---------------------|
| 395 | 37 | 38.9 | 775 | 1 | VPXRWL | outer layer protei | 468 | 37.9 | 102 | 2 | PH1233 | Ig heavy chain V r |
| 396 | 37 | 38.9 | 775 | 1 | VPXRWM | outer layer protei | 469 | 37.9 | 102 | 2 | PH1273 | Ig heavy chain V r |
| 397 | 37 | 38.9 | 775 | 1 | S52165 | outer capsid prote | 470 | 37.9 | 102 | 2 | PH1265 | Ig heavy chain V r |
| 398 | 37 | 38.9 | 776 | 1 | IQ2022 | outer layer protei | 471 | 37.9 | 102 | 2 | PH1249 | Ig heavy chain V r |
| 399 | 37 | 38.9 | 778 | 1 | D95912 | probable membrane | 472 | 37.9 | 102 | 2 | PH1252 | Ig heavy chain V r |
| 400 | 37 | 38.9 | 780 | 1 | JC1368 | protein-tyrosine-p | 473 | 37.9 | 102 | 2 | PH1271 | Ig heavy chain V r |
| 401 | 37 | 38.9 | 841 | 2 | A90669 | probable enzyme [i | 474 | 37.9 | 102 | 2 | PH1278 | Ig heavy chain V r |
| 402 | 37 | 38.9 | 841 | 2 | D85519 | probable enzyme ya | 475 | 37.9 | 104 | 2 | B36006 | Ig heavy chain V r |
| 403 | 37 | 38.9 | 841 | 2 | C64755 | yagX protein - Eec | 476 | 37.9 | 113 | 2 | PH1428 | Ig heavy chain V r |
| 404 | 37 | 38.9 | 856 | 2 | T22575 | hypothetical prote | 477 | 37.9 | 115 | 2 | PH1557 | Ig heavy chain V r |
| 405 | 37 | 38.9 | 856 | 2 | D86258 | protein F5011.10 [| 478 | 37.9 | 116 | 2 | I49555 | gene C10 protein - |
| 406 | 37 | 38.9 | 912 | 2 | F71433 | probable growth re | 479 | 37.9 | 117 | 2 | A28846 | Ig heavy chain pre |
| 407 | 37 | 38.9 | 953 | 2 | T01093 | luminidependens pr | 480 | 37.9 | 117 | 2 | S19670 | Ig heavy chain V r |
| 408 | 37 | 38.9 | 1035 | 2 | F58409 | integrin alpha-9 c | 481 | 37.9 | 117 | 2 | I28195 | Ig heavy chain V r |
| 409 | 37 | 38.9 | 1042 | 2 | H70203 | isoleucine-tRNA li | 482 | 37.9 | 120 | 2 | G72727 | probable ribosomal |
| 410 | 37 | 38.9 | 1125 | 2 | T39052 | hypothetical serin | 483 | 37.9 | 122 | 2 | S36276 | Ig heavy chain V r |
| 411 | 37 | 38.9 | 1163 | 2 | T24855 | hypothetical prote | 484 | 37.9 | 123 | 2 | PH1423 | Ig heavy chain V r |
| 412 | 37 | 38.9 | 1296 | 2 | C82521 | hemolysin-type cal | 485 | 37.9 | 123 | 2 | S38492 | Ig heavy chain - h |
| 413 | 37 | 38.9 | 1345 | 2 | T41960 | major capsid prote | 486 | 37.9 | 123 | 2 | PH1413 | Ig heavy chain V r |
| 414 | 37 | 38.9 | 1469 | 2 | T19459 | hypothetical prote | 487 | 37.9 | 123 | 2 | C36006 | Ig heavy chain V r |
| 415 | 37 | 38.9 | 1490 | 2 | F88311 | protein T06D8.10 [| 488 | 37.9 | 126 | 1 | GIHUKL | Ig heavy chain V-I |
| 416 | 37 | 38.9 | 1490 | 2 | T24502 | hypothetical prote | 489 | 37.9 | 127 | 2 | PH1414 | Ig heavy chain V r |
| 417 | 37 | 38.9 | 1619 | 2 | T18499 | hypothetical prote | 490 | 37.9 | 127 | 2 | PH1420 | Ig heavy chain V r |
| 418 | 37 | 38.9 | 1757 | 2 | T14318 | ubiquitin-protein | 491 | 37.9 | 127 | 2 | PH1409 | Ig heavy chain V r |
| 419 | 37 | 38.9 | 1957 | 2 | A45627 | myosin heavy chain | 492 | 37.9 | 128 | 2 | S16685 | Ig heavy chain V r |
| 420 | 37 | 38.9 | 2048 | 1 | ZLN2SE | genome polyprotein | 493 | 37.9 | 130 | 2 | A83671 | ribosomal protein |
| 421 | 37 | 38.9 | 2228 | 1 | ZLN2SV | genome polyprotein | 494 | 37.9 | 132 | 2 | A83911 | Ig heavy chain V r |
| 422 | 37 | 38.9 | 2523 | 2 | T18477 | hypothetical prote | 495 | 37.9 | 134 | 2 | PH1422 | Ig heavy chain V r |
| 423 | 36.5 | 38.4 | 119 | 1 | GIHUDW | Ig heavy chain V-I | 496 | 37.9 | 136 | 2 | A49047 | Ig heavy chain V r |
| 424 | 36.5 | 38.4 | 125 | 2 | T08308 | hypothetical prote | 497 | 37.9 | 136 | 2 | PH1559 | Ig heavy chain V r |
| 425 | 36.5 | 38.4 | 154 | 2 | B37329 | antigen 5 - easter | 498 | 37.9 | 139 | 2 | PH1558 | Ig heavy chain V r |
| 426 | 36.5 | 38.4 | 204 | 2 | A44583 | venom allergen ant | 499 | 37.9 | 140 | 2 | S54240 | Ig mu heavy chain |
| 427 | 36.5 | 38.4 | 204 | 2 | B44583 | venom allergen ant | 500 | 37.9 | 140 | 2 | S54239 | Ig mu heavy chain |
| 428 | 36.5 | 38.4 | 204 | 2 | C44583 | venom allergen ant | 501 | 37.9 | 143 | 2 | A98093 | hypothetical prote |
| 429 | 36.5 | 38.4 | 204 | 2 | C44583 | venom allergen ant | 502 | 37.9 | 143 | 2 | F85938 | hypothetical prote |
| 430 | 36.5 | 38.4 | 237 | 2 | B59107 | hypothetical prote | 503 | 37.9 | 146 | 2 | F90337 | hypothetical prote |
| 431 | 36.5 | 38.4 | 247 | 2 | S72775 | probable glucose-6 | 504 | 37.9 | 170 | 2 | A12961 | conserved hypotet |
| 432 | 36.5 | 38.4 | 247 | 2 | H70916 | probable glucose-6 | 505 | 37.9 | 175 | 2 | E98321 | hypothetical prote |
| 433 | 36.5 | 38.4 | 400 | 2 | T18997 | nicotinic acetylch | 506 | 37.9 | 176 | 2 | AD1226 | hypothetical prote |
| 434 | 36.5 | 38.4 | 477 | 2 | I38409 | adenyl cyclase-a | 507 | 37.9 | 176 | 2 | AF1579 | hypothetical prote |
| 435 | 36.5 | 38.4 | 483 | 2 | S36470 | E2 protein - human | 508 | 37.9 | 182 | 2 | A64007 | hypothetical prote |
| 436 | 36.5 | 38.4 | 507 | 2 | S64507 | probable membrane | 509 | 37.9 | 185 | 2 | D85040 | hypothetical prote |
| 437 | 36.5 | 38.4 | 508 | 2 | T07277 | photosystem II chl | 510 | 37.9 | 192 | 2 | E69949 | hypothetical prote |
| 438 | 36.5 | 38.4 | 569 | 2 | E64427 | hypothetical prote | 511 | 37.9 | 202 | 2 | H97247 | S-adenosylmethioni |
| 439 | 36.5 | 38.4 | 644 | 2 | T37800 | probable lysophosp | 512 | 37.9 | 222 | 2 | AC1289 | hypothetical prote |
| 440 | 36.5 | 38.4 | 677 | 1 | CNRUB | chromogranin B pre | 513 | 37.9 | 232 | 2 | T16315 | hypothetical prote |
| 441 | 36.5 | 38.4 | 972 | 2 | A30363 | glycoprotein GP330 | 514 | 37.9 | 250 | 2 | F86761 | nucleotidase [impo |
| 442 | 36.5 | 38.4 | 1173 | 2 | B97208 | pyruvate ferredoxi | 515 | 37.9 | 256 | 2 | E89769 | hypothetical prote |
| 443 | 36.5 | 38.4 | 1235 | 2 | T17457 | SARA protein - Afr | 516 | 37.9 | 257 | 2 | G90051 | hypothetical prote |
| 444 | 36 | 37.9 | 82 | 2 | E95891 | conserved hypotet | 517 | 37.9 | 258 | 2 | H90051 | hypothetical prote |
| 445 | 36 | 37.9 | 97 | 1 | ZCBPT9 | gene 55.5 protein | 518 | 37.9 | 264 | 2 | F90051 | hypothetical prote |
| 446 | 36 | 37.9 | 98 | 2 | PH1274 | Ig heavy chain V r | 519 | 37.9 | 264 | 2 | B90051 | hypothetical prote |
| 447 | 36 | 37.9 | 98 | 2 | S26907 | Ig heavy chain V r | 520 | 37.9 | 266 | 2 | H69189 | hypothetical prote |
| 448 | 36 | 37.9 | 101 | 2 | S12428 | Ig heavy chain V r | 521 | 37.9 | 278 | 2 | G69399 | conserved hypotet |
| 449 | 36 | 37.9 | 101 | 2 | S12424 | Ig heavy chain V r | 522 | 37.9 | 285 | 2 | T15252 | hypothetical prote |
| 450 | 36 | 37.9 | 102 | 2 | PH1266 | Ig heavy chain V r | 523 | 37.9 | 293 | 2 | H72064 | hypothetical prote |
| 451 | 36 | 37.9 | 102 | 2 | PH1279 | Ig heavy chain V r | 524 | 37.9 | 293 | 2 | C86558 | ABC transporter, p |
| 452 | 36 | 37.9 | 102 | 2 | PH1281 | Ig heavy chain V r | 525 | 37.9 | 293 | 2 | C86558 | metal transport, pr |
| 453 | 36 | 37.9 | 102 | 2 | PH1277 | Ig heavy chain V r | 526 | 37.9 | 293 | 2 | C85898 | probable proteinas |
| 454 | 36 | 37.9 | 102 | 2 | PH1244 | Ig heavy chain V r | 527 | 37.9 | 293 | 2 | E65030 | hypothetical prote |
| 455 | 36 | 37.9 | 102 | 2 | PH1267 | Ig heavy chain V r | 528 | 37.9 | 293 | 2 | H91053 | probable enzyme [i |
| 456 | 36 | 37.9 | 102 | 2 | PH1247 | Ig heavy chain V r | 529 | 37.9 | 293 | 2 | D95919 | hypothetical prote |
| 457 | 36 | 37.9 | 102 | 2 | PH1272 | Ig heavy chain V r | 530 | 37.9 | 294 | 2 | D96560 | hypothetical prote |
| 458 | 36 | 37.9 | 102 | 2 | PH1282 | Ig heavy chain V r | 531 | 37.9 | 302 | 2 | A45511 | chitinase (EC 3.2. |
| 459 | 36 | 37.9 | 102 | 2 | PH1268 | Ig heavy chain V r | 532 | 37.9 | 303 | 2 | A41036 | cell-division inhi |
| 460 | 36 | 37.9 | 102 | 2 | PH1248 | Ig heavy chain V r | 533 | 37.9 | 305 | 2 | T41040 | conserved hypotet |
| 461 | 36 | 37.9 | 102 | 2 | PH1236 | Ig heavy chain V r | 534 | 37.9 | 306 | 2 | G61169 | hypothetical prote |
| 462 | 36 | 37.9 | 102 | 2 | PH1280 | Ig heavy chain V r | 535 | 37.9 | 310 | 2 | T35417 | probable beta-lact |
| 463 | 36 | 37.9 | 102 | 2 | PH1258 | Ig heavy chain V r | 536 | 37.9 | 315 | 2 | A72282 | oligopeptide ABC t |
| 464 | 36 | 37.9 | 102 | 2 | PH1276 | Ig heavy chain V r | 537 | 37.9 | 318 | 2 | T44792 | 2-keto-3-deoxygluc |
| 465 | 36 | 37.9 | 102 | 2 | PH1264 | Ig heavy chain V r | 538 | 37.9 | 319 | 2 | S71877 | carbonate dehydrat |
| 466 | 36 | 37.9 | 102 | 2 | PH1259 | Ig heavy chain V r | 539 | 37.9 | 324 | 2 | A99284 | hypothetical prote |
| 467 | 36 | 37.9 | 102 | 2 | PH1243 | Ig heavy chain V r | 540 | 37.9 | 325 | 2 | S46760 | hypothetical prote |

| | | | | | | | | | | | | | |
|-----|----|------|------|---|--------|---------------------|-----|------|------|------|---|--------|--------------------|
| 541 | 36 | 37.9 | 333 | 2 | AG1205 | molybdenum cofactor | 614 | 36 | 37.9 | 1083 | 2 | C88854 | protein F11A10.3 (|
| 542 | 36 | 37.9 | 342 | 2 | T44229 | hypothetical prote | 615 | 36 | 37.9 | 1131 | 2 | F82875 | hypothetical prote |
| 543 | 36 | 37.9 | 342 | 2 | T44043 | hypothetical prote | 616 | 36 | 37.9 | 1197 | 2 | T28628 | Y4CA protein - Rhi |
| 544 | 36 | 37.9 | 343 | 2 | F64011 | hypothetical prote | 617 | 36 | 37.9 | 1321 | 2 | T42238 | P-glycoprotein sis |
| 545 | 36 | 37.9 | 344 | 2 | E84181 | hypothetical prote | 618 | 36 | 37.9 | 1321 | 2 | T42842 | hile salt transpor |
| 546 | 36 | 37.9 | 346 | 1 | BXCPR | phosphate-repressi | 619 | 36 | 37.9 | 1327 | 2 | T21268 | hypothetical prote |
| 547 | 36 | 37.9 | 346 | 2 | H86057 | phosphate-binding | 620 | 36 | 37.9 | 1384 | 2 | T26656 | hypothetical prote |
| 548 | 36 | 37.9 | 346 | 2 | H91211 | phosphate-binding | 621 | 36 | 37.9 | 1576 | 1 | A23662 | myosin I, high mol |
| 549 | 36 | 37.9 | 357 | 2 | JC4753 | RecF protein - Lac | 622 | 36 | 37.9 | 1584 | 2 | T22674 | hypothetical prote |
| 550 | 36 | 37.9 | 358 | 2 | G86871 | RecF protein [impo | 623 | 36 | 37.9 | 1613 | 2 | JE0272 | low density lipopr |
| 551 | 36 | 37.9 | 409 | 1 | VH1HAI | nucleocapsid prote | 624 | 36 | 37.9 | 1613 | 2 | JE0273 | low density lipopr |
| 552 | 36 | 37.9 | 411 | 2 | S40064 | 3-deoxy-manno-octu | 625 | 36 | 37.9 | 1807 | 2 | T30940 | vitellogenin - Pim |
| 553 | 36 | 37.9 | 413 | 2 | D83310 | conserved hypothet | 626 | 36 | 37.9 | 1933 | 2 | F72648 | hypothetical prote |
| 554 | 36 | 37.9 | 421 | 2 | T00598 | hypothetical prote | 627 | 36 | 37.9 | 2105 | 2 | T18968 | probable serine-ty |
| 555 | 36 | 37.9 | 426 | 2 | E84531 | hypothetical prote | 628 | 36 | 37.9 | 2229 | 2 | T16199 | hypothetical prote |
| 556 | 36 | 37.9 | 427 | 2 | D84540 | hypothetical prote | 629 | 36 | 37.9 | 2288 | 2 | T30568 | acetyl-CoA carboxy |
| 557 | 36 | 37.9 | 441 | 2 | T49113 | hypothetical prote | 630 | 36 | 37.9 | 4869 | 2 | S66572 | ryanodine receptor |
| 558 | 36 | 37.9 | 481 | 2 | B97348 | hypothetical prote | 631 | 35.5 | 37.4 | 102 | 2 | PH1240 | Ig heavy chain V r |
| 559 | 36 | 37.9 | 483 | 2 | F75360 | hypothetical prote | 632 | 35.5 | 37.4 | 221 | 1 | S71905 | probable nonhiston |
| 560 | 36 | 37.9 | 498 | 2 | F84667 | hypothetical prote | 633 | 35.5 | 37.4 | 226 | 2 | S61182 | hypothetical prote |
| 561 | 36 | 37.9 | 499 | 2 | AD3035 | probable cytochrom | 634 | 35.5 | 37.4 | 259 | 2 | B82348 | probable lipopolys |
| 562 | 36 | 37.9 | 507 | 2 | G38250 | glycerol kinase gl | 635 | 35.5 | 37.4 | 344 | 1 | S46020 | probable aldehyde |
| 563 | 36 | 37.9 | 514 | 2 | T46131 | probable carbohydr | 636 | 35.5 | 37.4 | 344 | 2 | A42883 | ferrochelatase (bc |
| 564 | 36 | 37.9 | 531 | 2 | B84442 | hypothetical prote | 637 | 35.5 | 37.4 | 390 | 2 | G75037 | probable aromatic- |
| 565 | 36 | 37.9 | 531 | 2 | S76616 | hypothetical prote | 638 | 35.5 | 37.4 | 409 | 1 | PAWTF | fructose-bisphosph |
| 566 | 36 | 37.9 | 550 | 1 | A26772 | photinus-luciferin | 639 | 35.5 | 37.4 | 427 | 2 | AH0377 | probable exported |
| 567 | 36 | 37.9 | 556 | 2 | C75202 | dipeptide abc tran | 640 | 35.5 | 37.4 | 469 | 1 | NNIVEA | exo-alpha-sialidas |
| 568 | 36 | 37.9 | 567 | 2 | T35771 | hypothetical prote | 641 | 35.5 | 37.4 | 489 | 2 | H89979 | hypothetical prote |
| 569 | 36 | 37.9 | 572 | 2 | F90297 | ATP-dependent RNA | 642 | 35.5 | 37.4 | 508 | 1 | QJSP8A | photosystem II chl |
| 570 | 36 | 37.9 | 572 | 2 | S72249 | trithorax protein | 643 | 35.5 | 37.4 | 508 | 1 | QJLV6A | photosystem II chl |
| 571 | 36 | 37.9 | 582 | 2 | AG0650 | periplasmic oligop | 644 | 35.5 | 37.4 | 508 | 1 | QJNT6A | photosystem II chl |
| 572 | 36 | 37.9 | 590 | 2 | I46687 | complement compone | 645 | 35.5 | 37.4 | 508 | 1 | QJRT6A | photosystem II chl |
| 573 | 36 | 37.9 | 591 | 1 | CBHUB | complement C8 beta | 646 | 35.5 | 37.4 | 508 | 1 | QJZMBB | photosystem II chl |
| 574 | 36 | 37.9 | 608 | 2 | T40814 | probable nucleolar | 647 | 35.5 | 37.4 | 508 | 2 | S12132 | photosystem II chl |
| 575 | 36 | 37.9 | 616 | 2 | JC7776 | matrix metalloprot | 648 | 35.5 | 37.4 | 508 | 2 | S04100 | photosystem II chl |
| 576 | 36 | 37.9 | 642 | 2 | B90767 | probable terminase | 649 | 35.5 | 37.4 | 508 | 2 | S01385 | photosystem II chl |
| 577 | 36 | 37.9 | 642 | 2 | G90970 | probable terminase | 650 | 35.5 | 37.4 | 508 | 2 | S14140 | photosystem II chl |
| 578 | 36 | 37.9 | 646 | 1 | B49849 | terminase large ch | 651 | 35.5 | 37.4 | 508 | 2 | S12129 | photosystem II chl |
| 579 | 36 | 37.9 | 646 | 1 | A55093 | fatty acid transpo | 652 | 35.5 | 37.4 | 534 | 2 | S61228 | DNA (cytosine-5)- |
| 580 | 36 | 37.9 | 648 | 2 | E75038 | indolepyruvate fer | 653 | 35.5 | 37.4 | 536 | 2 | B84327 | phytoene dehydroge |
| 581 | 36 | 37.9 | 654 | 2 | A85717 | hypothetical prote | 654 | 35.5 | 37.4 | 841 | 1 | S24462 | probable 3',5'-cyc |
| 582 | 36 | 37.9 | 666 | 2 | E82619 | transketolase 1 XF | 655 | 35.5 | 37.4 | 918 | 2 | D88544 | protein R08D7.6 li |
| 583 | 36 | 37.9 | 674 | 2 | T19780 | hypothetical prote | 656 | 35.5 | 37.4 | 1201 | 2 | A57369 | anillin - fruit fl |
| 584 | 36 | 37.9 | 676 | 2 | H96970 | endo-arabinase rel | 657 | 35.5 | 37.4 | 1201 | 2 | F96907 | phage-related prot |
| 585 | 36 | 37.9 | 692 | 2 | E96841 | hypothetical prote | 658 | 35 | 36.8 | 1645 | 2 | T16215 | hypothetical prote |
| 586 | 36 | 37.9 | 697 | 2 | H70177 | N-acetylmuramoyl-L | 659 | 35 | 36.8 | 31 | 2 | B26815 | peptide PXL-amide |
| 587 | 36 | 37.9 | 706 | 2 | D83112 | elongation factor | 660 | 35 | 36.8 | 49 | 2 | B26815 | peptide PGLa precu |
| 588 | 36 | 37.9 | 715 | 2 | A34408 | peroxidase (EC 1.1 | 661 | 35 | 36.8 | 64 | 2 | A26815 | probable transcrip |
| 589 | 36 | 37.9 | 730 | 2 | A75486 | hypothetical prote | 662 | 35 | 36.8 | 71 | 2 | F97207 | repressor protein |
| 590 | 36 | 37.9 | 775 | 2 | S55345 | protein-tyrosine-p | 663 | 35 | 36.8 | 86 | 2 | B69453 | Ig heavy chain V r |
| 591 | 36 | 37.9 | 776 | 2 | T20738 | hypothetical prote | 664 | 35 | 36.8 | 86 | 2 | S12580 | Ig heavy chain V-I |
| 592 | 36 | 37.9 | 813 | 2 | JG6569 | translation initia | 665 | 35 | 36.8 | 86 | 2 | F34964 | Ig heavy chain V r |
| 593 | 36 | 37.9 | 814 | 1 | C3CLEM | cellulase (EC 3.2. | 666 | 35 | 36.8 | 94 | 2 | T10250 | lectin homolog 2 - |
| 594 | 36 | 37.9 | 833 | 1 | S20387 | outer membrane pro | 667 | 35 | 36.8 | 102 | 2 | S14486 | Ig heavy chain V r |
| 595 | 36 | 37.9 | 833 | 2 | T14703 | F1 capsule anchori | 668 | 35 | 36.8 | 123 | 2 | G84592 | hypothetical prote |
| 596 | 36 | 37.9 | 881 | 2 | T31818 | hypothetical prote | 669 | 35 | 36.8 | 124 | 2 | B55257 | Ig gamma heavy cha |
| 597 | 36 | 37.9 | 883 | 2 | A96662 | hypothetical prote | 670 | 35 | 36.8 | 126 | 2 | PH1412 | Ig heavy chain V r |
| 598 | 36 | 37.9 | 896 | 2 | A12733 | glutamate receptor | 671 | 35 | 36.8 | 129 | 1 | D2HWA | Ig heavy chain V-I |
| 599 | 36 | 37.9 | 906 | 2 | A40222 | glutamate receptor | 672 | 35 | 36.8 | 132 | 2 | T09626 | outer membrane pro |
| 600 | 36 | 37.9 | 906 | 2 | S38723 | glutamate receptor | 673 | 35 | 36.8 | 132 | 2 | B65069 | hypothetical prote |
| 601 | 36 | 37.9 | 906 | 2 | S25852 | glutamate receptor | 674 | 35 | 36.8 | 145 | 2 | T15788 | hypothetical prote |
| 602 | 36 | 37.9 | 907 | 1 | ACRTK1 | glutamate receptor | 675 | 35 | 36.8 | 145 | 2 | S68215 | Mas 20 protein - h |
| 603 | 36 | 37.9 | 907 | 2 | A40170 | glutamate receptor | 676 | 35 | 36.8 | 147 | 2 | T41271 | hypothetical prote |
| 604 | 36 | 37.9 | 907 | 2 | S12874 | glutamate receptor | 677 | 35 | 36.8 | 149 | 2 | G71162 | hypothetical prote |
| 605 | 36 | 37.9 | 910 | 2 | S38167 | hypothetical prote | 678 | 35 | 36.8 | 161 | 2 | F75633 | hypothetical prote |
| 606 | 36 | 37.9 | 966 | 2 | G69189 | hypothetical prote | 679 | 35 | 36.8 | 179 | 2 | AB3199 | haloacid dehalogen |
| 607 | 36 | 37.9 | 967 | 1 | HXAD2 | hexon protein - hu | 680 | 35 | 36.8 | 180 | 2 | T36827 | hypothetical prote |
| 608 | 36 | 37.9 | 976 | 2 | G87389 | TonB-dependent rec | 681 | 35 | 36.8 | 184 | 2 | D83234 | hypothetical prote |
| 609 | 36 | 37.9 | 995 | 2 | AB1398 | formate dehydrogen | 682 | 35 | 36.8 | 186 | 2 | H75106 | hypothetical prote |
| 610 | 36 | 37.9 | 995 | 2 | AB1773 | formate dehydrogen | 683 | 35 | 36.8 | 202 | 2 | T18495 | hypothetical prote |
| 611 | 36 | 37.9 | 1016 | 2 | H71460 | probable outer mem | 684 | 35 | 36.8 | 210 | 2 | AH2147 | hypothetical prote |
| 612 | 36 | 37.9 | 1035 | 2 | S56285 | sulfite reductase | 685 | 35 | 36.8 | 212 | 2 | C90905 | hypothetical prote |
| 613 | 36 | 37.9 | 1040 | 2 | T40859 | silencing protein | 686 | 35 | 36.8 | 216 | 2 | S50760 | lectin 2, phloem-s |
| | | | | | | | | | | 216 | 2 | S50761 | lectin 2, phloem-s |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|--------|--------------------|-----|----|------|------|---|--------|--------------------|
| 687 | 35 | 36.8 | 216 | 2 | B85712 | unknown protein en | 760 | 35 | 36.8 | 578 | 1 | BVBYD1 | GCD1 protein - Yea |
| 688 | 35 | 36.8 | 218 | 2 | S38462 | lectin PP2 - winte | 761 | 35 | 36.8 | 595 | 1 | A35919 | carotenoid biosynt |
| 689 | 35 | 36.8 | 218 | 2 | JQ1731 | phloem-specific le | 762 | 35 | 36.8 | 597 | 1 | NBHUC4 | C4b-binding protei |
| 690 | 35 | 36.8 | 218 | 2 | C72255 | hypothetical prote | 763 | 35 | 36.8 | 597 | 2 | T08681 | adenosylhomocyste |
| 691 | 35 | 36.8 | 221 | 2 | S84675 | hypothetical prote | 764 | 35 | 36.8 | 601 | 1 | B56564 | transcription fact |
| 692 | 35 | 36.8 | 223 | 2 | H64314 | hypothetical prote | 765 | 35 | 36.8 | 625 | 1 | H90533 | hypothetical prote |
| 693 | 35 | 36.8 | 236 | 2 | B69090 | conserved hypotet | 766 | 35 | 36.8 | 626 | 2 | E95250 | glycosyl hydrolase |
| 694 | 35 | 36.8 | 240 | 2 | AH0749 | cell-division regu | 767 | 35 | 36.8 | 626 | 2 | B98115 | hypothetical prote |
| 695 | 35 | 36.8 | 248 | 2 | B81002 | conserved hypotet | 768 | 35 | 36.8 | 626 | 2 | JQ0706 | alcohol dehydrogen |
| 696 | 35 | 36.8 | 248 | 2 | E82017 | hypothetical prote | 769 | 35 | 36.8 | 635 | 2 | T27014 | hypothetical prote |
| 697 | 35 | 36.8 | 255 | 2 | H89769 | hypothetical prote | 770 | 35 | 36.8 | 640 | 2 | B96502 | hypothetical prote |
| 698 | 35 | 36.8 | 256 | 2 | D89769 | hypothetical prote | 771 | 35 | 36.8 | 641 | 2 | JC7142 | dextranase (EC 3.2 |
| 699 | 35 | 36.8 | 256 | 2 | D89769 | hypothetical prote | 772 | 35 | 36.8 | 648 | 1 | G64826 | probable ABC trans |
| 700 | 35 | 36.8 | 259 | 2 | C64481 | conserved hypotet | 773 | 35 | 36.8 | 648 | 2 | A85600 | hypothetical prote |
| 701 | 35 | 36.8 | 263 | 2 | B81148 | probable transfera | 774 | 35 | 36.8 | 648 | 2 | E90749 | hypothetical prote |
| 702 | 35 | 36.8 | 267 | 2 | T21274 | hypothetical prote | 775 | 35 | 36.8 | 648 | 2 | F71124 | probable indolepyr |
| 703 | 35 | 36.8 | 268 | 2 | C90484 | hypothetical prote | 776 | 35 | 36.8 | 658 | 2 | H84385 | dipeptide ABC tran |
| 704 | 35 | 36.8 | 270 | 2 | T37814 | DNA damage checkp | 777 | 35 | 36.8 | 661 | 2 | S67177 | hypothetical prote |
| 705 | 35 | 36.8 | 281 | 2 | S32566 | actin-binding prot | 778 | 35 | 36.8 | 662 | 2 | E64650 | acetyl-CoA synthet |
| 706 | 35 | 36.8 | 283 | 2 | S44948 | KO6H7.8 protein - | 779 | 35 | 36.8 | 662 | 2 | JC7906 | sucrose 1F-fructos |
| 707 | 35 | 36.8 | 285 | 1 | EDBBD9 | immediate-early pr | 780 | 35 | 36.8 | 665 | 2 | C82192 | tail-specific prot |
| 708 | 35 | 36.8 | 285 | 2 | T20237 | hypothetical prote | 781 | 35 | 36.8 | 673 | 1 | VCPVB5 | coat protein VP1 - |
| 709 | 35 | 36.8 | 286 | 1 | I53714 | 3,4-dihydroxy-5-he | 782 | 35 | 36.8 | 682 | 2 | B70121 | hypothetical prote |
| 710 | 35 | 36.8 | 291 | 2 | C72762 | hypothetical prote | 783 | 35 | 36.8 | 682 | 2 | G86300 | R19K19.13 protein |
| 711 | 35 | 36.8 | 296 | 2 | AD2434 | hypothetical prote | 784 | 35 | 36.8 | 683 | 2 | T40780 | beta adaptin-like |
| 712 | 35 | 36.8 | 299 | 2 | D86199 | hypothetical prote | 785 | 35 | 36.8 | 688 | 2 | B86448 | hypothetical prote |
| 713 | 35 | 36.8 | 300 | 2 | AG3199 | transcription regu | 786 | 35 | 36.8 | 694 | 2 | B84331 | phosphorylated car |
| 714 | 35 | 36.8 | 306 | 2 | S32834 | methylviologen-red | 787 | 35 | 36.8 | 704 | 2 | JC7932 | hypothetical prote |
| 715 | 35 | 36.8 | 309 | 2 | G87498 | hypothetical prote | 788 | 35 | 36.8 | 706 | 2 | F87683 | peptidase M13 fami |
| 716 | 35 | 36.8 | 311 | 2 | F69820 | conserved hypotet | 789 | 35 | 36.8 | 728 | 2 | A86453 | CDS protein F9L11. |
| 717 | 35 | 36.8 | 312 | 2 | AC1385 | HPR-P(Ser) kinase/ | 790 | 35 | 36.8 | 730 | 2 | H86295 | hypothetical prote |
| 718 | 35 | 36.8 | 312 | 2 | AE1760 | HPR-P(Ser) kinase/ | 791 | 35 | 36.8 | 745 | 2 | D86461 | hypothetical prote |
| 719 | 35 | 36.8 | 312 | 2 | T05377 | probable glucose 6 | 792 | 35 | 36.8 | 765 | 2 | T29582 | hypothetical prote |
| 720 | 35 | 36.8 | 314 | 2 | T08065 | protein kinase (EC | 793 | 35 | 36.8 | 775 | 2 | E84828 | probable WD-40 rep |
| 721 | 35 | 36.8 | 330 | 2 | F81656 | conserved hypotet | 794 | 35 | 36.8 | 783 | 2 | B91124 | probable isomerase |
| 722 | 35 | 36.8 | 333 | 2 | AF1562 | molybdenum cofacto | 795 | 35 | 36.8 | 783 | 2 | A85969 | probable isomerase |
| 723 | 35 | 36.8 | 334 | 2 | B81406 | probable integral | 796 | 35 | 36.8 | 783 | 2 | E65096 | hypothetical 88.3K |
| 724 | 35 | 36.8 | 356 | 2 | G88968 | protein T27B7.5 [i | 797 | 35 | 36.8 | 783 | 2 | F84514 | hypothetical prote |
| 725 | 35 | 36.8 | 369 | 2 | T16506 | hypothetical prote | 798 | 35 | 36.8 | 818 | 2 | S64251 | SAP4 protein - yea |
| 726 | 35 | 36.8 | 372 | 2 | F86189 | hypothetical prote | 799 | 35 | 36.8 | 820 | 2 | T04570 | hypothetical prote |
| 727 | 35 | 36.8 | 376 | 2 | S75438 | hypothetical prote | 800 | 35 | 36.8 | 830 | 2 | S54547 | PAM1 protein - yea |
| 728 | 35 | 36.8 | 376 | 2 | T48714 | hypothetical prote | 801 | 35 | 36.8 | 837 | 1 | A29512 | LDL receptor precu |
| 729 | 35 | 36.8 | 379 | 2 | AB2423 | hypothetical prote | 802 | 35 | 36.8 | 840 | 2 | C70131 | leucine-tRNA ligas |
| 730 | 35 | 36.8 | 381 | 2 | T29826 | hypothetical prote | 803 | 35 | 36.8 | 861 | 1 | S01142 | lipoxigenase (EC 1 |
| 731 | 35 | 36.8 | 381 | 2 | G71130 | hypothetical prote | 804 | 35 | 36.8 | 866 | 2 | F64625 | type I restriction |
| 732 | 35 | 36.8 | 382 | 2 | G96641 | hypothetical prote | 805 | 35 | 36.8 | 887 | 2 | B96598 | hypothetical prote |
| 733 | 35 | 36.8 | 385 | 2 | G83817 | coproporphyrinogen | 806 | 35 | 36.8 | 894 | 1 | A65146 | probable ABC trans |
| 734 | 35 | 36.8 | 389 | 2 | T18574 | hypothetical prote | 807 | 35 | 36.8 | 894 | 2 | G86019 | hypothetical prote |
| 735 | 35 | 36.8 | 390 | 2 | AG0929 | probable major tai | 808 | 35 | 36.8 | 894 | 2 | G91173 | hypothetical prote |
| 736 | 35 | 36.8 | 390 | 2 | AI0836 | probable bacteriop | 809 | 35 | 36.8 | 902 | 2 | B84652 | hypothetical prote |
| 737 | 35 | 36.8 | 405 | 2 | G84200 | cytochrome P450 [i | 810 | 35 | 36.8 | 913 | 2 | AH0989 | hypothetical ABC t |
| 738 | 35 | 36.8 | 413 | 1 | XNPGDC | aspartate transami | 811 | 35 | 36.8 | 917 | 1 | VGBBHH | glycoprotein B pre |
| 739 | 35 | 36.8 | 413 | 2 | S01076 | aspartate transami | 812 | 35 | 36.8 | 922 | 2 | T03854 | hypothetical prote |
| 740 | 35 | 36.8 | 413 | 2 | H75357 | tRNA (5-methylamin | 813 | 35 | 36.8 | 925 | 2 | AG3130 | hypothetical prote |
| 741 | 35 | 36.8 | 431 | 1 | G69259 | hypothetical prote | 814 | 35 | 36.8 | 930 | 2 | B98157 | hypothetical prote |
| 742 | 35 | 36.8 | 431 | 1 | G69259 | conserved hypotet | 815 | 35 | 36.8 | 939 | 2 | S75908 | hypothetical prote |
| 743 | 35 | 36.8 | 454 | 2 | A64305 | conserved hypotet | 816 | 35 | 36.8 | 944 | 2 | G90205 | leucyl-tRNA synthe |
| 744 | 35 | 36.8 | 458 | 2 | C69421 | methylviologen-red | 817 | 35 | 36.8 | 968 | 2 | T39908 | probable coiled co |
| 745 | 35 | 36.8 | 466 | 2 | G84476 | probable retroelem | 818 | 35 | 36.8 | 982 | 2 | S10340 | DNA-directed RNA p |
| 746 | 35 | 36.8 | 469 | 2 | G86638 | cationic amino aci | 819 | 35 | 36.8 | 982 | 2 | S00964 | hypothetical prote |
| 747 | 35 | 36.8 | 484 | 2 | S60943 | RUD3 protein - yea | 820 | 35 | 36.8 | 984 | 2 | T44608 | pyruvate carboxyla |
| 748 | 35 | 36.8 | 491 | 2 | I40455 | penicillin binding | 821 | 35 | 36.8 | 996 | 2 | JE0237 | apolipoprotein E r |
| 749 | 35 | 36.8 | 498 | 2 | AI1140 | hypothetical secre | 822 | 35 | 36.8 | 1004 | 2 | A71617 | SERA antigen/papai |
| 750 | 35 | 36.8 | 501 | 2 | T10493 | probable cytochrom | 823 | 35 | 36.8 | 1016 | 1 | A46079 | protein kinase C (|
| 751 | 35 | 36.8 | 525 | 2 | H70982 | probable fadD7 pro | 824 | 35 | 36.8 | 1018 | 2 | T22318 | hypothetical prote |
| 752 | 35 | 36.8 | 535 | 2 | A46101 | protein-tyrosine-p | 825 | 35 | 36.8 | 1024 | 2 | C64208 | hypothetical prote |
| 753 | 35 | 36.8 | 535 | 2 | S31097 | cold acclimation p | 826 | 35 | 36.8 | 1025 | 2 | T21319 | hypothetical prote |
| 754 | 35 | 36.8 | 548 | 2 | B46101 | protein-tyrosine-p | 827 | 35 | 36.8 | 1032 | 1 | G7BPT4 | baseplate protein |
| 755 | 35 | 36.8 | 549 | 2 | S37914 | MF2 protein - yea | 828 | 35 | 36.8 | 1035 | 2 | S61342 | sulfite reductase |
| 756 | 35 | 36.8 | 561 | 2 | AD2581 | phosphoenolpyruvat | 829 | 35 | 36.8 | 1052 | 2 | E71422 | hypothetical prote |
| 757 | 35 | 36.8 | 562 | 2 | B97363 | phosphoenolpyruvat | 830 | 35 | 36.8 | 1131 | 2 | S22266 | enamelin precursor |
| 758 | 35 | 36.8 | 566 | 2 | T31364 | hypothetical prote | 831 | 35 | 36.8 | 1142 | 2 | T37455 | adenosinetriphosph |
| 759 | 35 | 36.8 | 569 | 2 | C89993 | endo-beta-1,4-gluc | 832 | 35 | 36.8 | 1149 | 2 | T18515 | |

| | | | | | | | | | | | | | |
|-----|------|------|------|---|--------|--------------------|-----|----|------|-----|---|--------|---------------------|
| 833 | 35 | 36.8 | 1149 | 2 | T30869 | probable adenosine | 106 | 34 | 35.8 | 86 | 2 | B69895 | spore coat protein |
| 834 | 35 | 36.8 | 1153 | 2 | A49676 | nitric-oxide synth | 907 | 34 | 35.8 | 89 | 2 | T34388 | hypothetical prote |
| 835 | 35 | 36.8 | 1160 | 2 | A46423 | transcription fact | 908 | 34 | 35.8 | 91 | 2 | T02103 | hypothetical prote |
| 836 | 35 | 36.8 | 1244 | 2 | S37034 | DNA-directed DNA p | 909 | 34 | 35.8 | 96 | 2 | S03096 | transition state r |
| 837 | 35 | 36.8 | 1289 | 2 | S70582 | botulinum neurotox | 910 | 34 | 35.8 | 105 | 2 | A71460 | hypothetical prote |
| 838 | 35 | 36.8 | 1285 | 1 | RMXRR3 | mRNA guanylyltrans | 911 | 34 | 35.8 | 106 | 2 | D71622 | probable integral |
| 839 | 35 | 36.8 | 1335 | 2 | H75511 | DNA polymerase III | 912 | 34 | 35.8 | 112 | 1 | ASLJST | vpu protein - simi |
| 840 | 35 | 36.8 | 1370 | 1 | VCBECA | major capsid prote | 913 | 34 | 35.8 | 119 | 2 | C84504 | probable CCHC-type |
| 841 | 35 | 36.8 | 1442 | 2 | B18538 | patched protein - | 914 | 34 | 35.8 | 126 | 2 | S70624 | cytochrome P450 Cy |
| 842 | 35 | 36.8 | 1449 | 2 | B81963 | IgA-specific serin | 915 | 34 | 35.8 | 127 | 2 | PH1415 | Ig heavy chain V r |
| 843 | 35 | 36.8 | 1501 | 1 | B29813 | 174K hnaC protein | 916 | 34 | 35.8 | 131 | 2 | AG2034 | hypothetical prote |
| 844 | 35 | 36.8 | 1502 | 2 | T14278 | myosin-like protei | 917 | 34 | 35.8 | 138 | 2 | S54225 | Ig mu heavy chain |
| 845 | 35 | 36.8 | 1529 | 2 | T02730 | RNA-directed DNA p | 918 | 34 | 35.8 | 138 | 2 | AD2156 | hypothetical prote |
| 846 | 35 | 36.8 | 1609 | 2 | B87243 | probable cation tr | 919 | 34 | 35.8 | 139 | 2 | S54231 | Ig mu heavy chain |
| 847 | 35 | 36.8 | 1615 | 2 | JB0372 | low density lipopr | 920 | 34 | 35.8 | 139 | 2 | S54229 | Ig mu heavy chain |
| 848 | 35 | 36.8 | 1632 | 2 | C70752 | probable ctpi prot | 921 | 34 | 35.8 | 139 | 2 | S54233 | Ig mu heavy chain |
| 849 | 35 | 36.8 | 1643 | 2 | T07961 | myosin heavy chain | 922 | 34 | 35.8 | 142 | 2 | S54243 | Ig mu heavy chain |
| 850 | 35 | 36.8 | 1691 | 1 | D54689 | protein-tyrosine-p | 923 | 34 | 35.8 | 143 | 2 | T22164 | hypothetical prote |
| 851 | 35 | 36.8 | 1772 | 2 | A45532 | major merozoite su | 924 | 34 | 35.8 | 145 | 2 | S54237 | Ig mu heavy chain |
| 852 | 35 | 36.8 | 1777 | 2 | T00490 | nonstructural prot | 925 | 34 | 35.8 | 145 | 2 | S54230 | Ig mu heavy chain |
| 853 | 35 | 36.8 | 1832 | 2 | AC2594 | glutamate synthase | 926 | 34 | 35.8 | 145 | 2 | T50276 | hypothetical prote |
| 854 | 35 | 36.8 | 1858 | 2 | D97376 | hypothetical prote | 927 | 34 | 35.8 | 147 | 1 | RPBPF5 | immunity repressor |
| 855 | 35 | 36.8 | 1894 | 2 | C34689 | protein-tyrosine-p | 928 | 34 | 35.8 | 152 | 2 | AG2211 | hypothetical prote |
| 856 | 35 | 36.8 | 1957 | 2 | A59294 | skeletal myosin - | 929 | 34 | 35.8 | 160 | 2 | AD2490 | hypothetical prote |
| 857 | 35 | 36.8 | 2057 | 2 | F90109 | splicing factor Pr | 930 | 34 | 35.8 | 171 | 2 | A37110 | protein phosphatas |
| 858 | 35 | 36.8 | 2218 | 2 | B84683 | hypothetical prote | 931 | 34 | 35.8 | 171 | 2 | C64247 | conserved hypoteth |
| 859 | 35 | 36.8 | 2434 | 2 | S44861 | DNA topoisomerase | 932 | 34 | 35.8 | 184 | 2 | H86629 | prophage psi prote |
| 860 | 35 | 36.8 | 3085 | 2 | T00327 | polyprotein - infe | 933 | 34 | 35.8 | 186 | 2 | T32528 | hypothetical prote |
| 861 | 35 | 36.8 | 3069 | 2 | T17464 | rifamycin polyketi | 934 | 34 | 35.8 | 194 | 2 | E75083 | hypothetical prote |
| 862 | 34.5 | 36.3 | 104 | 2 | S16761 | cytochrome c - yea | 935 | 34 | 35.8 | 201 | 2 | C96634 | hypothetical prote |
| 863 | 34.5 | 36.3 | 112 | 2 | T36440 | hypothetical prote | 936 | 34 | 35.8 | 209 | 2 | T47244 | blt-3 protein, blu |
| 864 | 34.5 | 36.3 | 113 | 1 | C6BYBC | cytochrome c2 - ye | 937 | 34 | 35.8 | 211 | 2 | S12252 | self incompatible |
| 865 | 34.5 | 36.3 | 127 | 2 | PH1421 | Ig heavy chain V r | 938 | 34 | 35.8 | 213 | 2 | B27898 | beta-crystallin B3 |
| 866 | 34.5 | 36.3 | 151 | 2 | C82464 | acetyltransferase, | 939 | 34 | 35.8 | 217 | 2 | G71807 | ribulose-phosphate |
| 867 | 34.5 | 36.3 | 160 | 2 | A84104 | hypothetical prote | 940 | 34 | 35.8 | 217 | 2 | B64693 | D-ribulose-5-phosp |
| 868 | 34.5 | 36.3 | 203 | 2 | B87461 | hypothetical prote | 941 | 34 | 35.8 | 221 | 2 | A11660 | hypothetical prote |
| 869 | 34.5 | 36.3 | 229 | 2 | I64017 | hypothetical prote | 942 | 34 | 35.8 | 232 | 2 | C83249 | 3-demethylubiquin |
| 870 | 34.5 | 36.3 | 263 | 2 | JC5283 | proopiomelanocorti | 943 | 34 | 35.8 | 237 | 2 | T34473 | hypothetical prote |
| 871 | 34.5 | 36.3 | 298 | 2 | F83777 | hypothetical prote | 944 | 34 | 35.8 | 238 | 2 | S44969 | lmbv protein - Str |
| 872 | 34.5 | 36.3 | 368 | 2 | F64017 | hypothetical prote | 945 | 34 | 35.8 | 243 | 2 | AD1238 | arginine N-methylt |
| 873 | 34.5 | 36.3 | 423 | 2 | S11974 | polyketide beta-ke | 946 | 34 | 35.8 | 243 | 2 | AH1600 | weakly arginine N- |
| 874 | 34.5 | 36.3 | 439 | 2 | G97159 | contains cell adhe | 947 | 34 | 35.8 | 244 | 2 | T28175 | hypothetical prote |
| 875 | 34.5 | 36.3 | 442 | 2 | T18507 | hypothetical prote | 948 | 34 | 35.8 | 245 | 2 | JB0179 | protein-glutamine |
| 876 | 34.5 | 36.3 | 454 | 2 | F83748 | hypothetical prote | 949 | 34 | 35.8 | 248 | 2 | D86012 | probable membrane |
| 877 | 34.5 | 36.3 | 458 | 2 | F97146 | probable iron-sulf | 950 | 34 | 35.8 | 248 | 2 | D91166 | probable membrane |
| 878 | 34.5 | 36.3 | 500 | 2 | A83536 | probable 3-hydroxy | 951 | 34 | 35.8 | 249 | 2 | C95188 | acyltransferase fa |
| 879 | 34.5 | 36.3 | 528 | 1 | ALBSK | alpha-amylase (EC | 952 | 34 | 35.8 | 250 | 2 | AD3461 | hypothetical prote |
| 880 | 34.5 | 36.3 | 548 | 2 | S22615 | triacylglycerol li | 953 | 34 | 35.8 | 251 | 2 | A90424 | carboxylesterase (|
| 881 | 34.5 | 36.3 | 556 | 2 | A85867 | 2-oxoglutarate dec | 954 | 34 | 35.8 | 252 | 2 | T16405 | hypothetical prote |
| 882 | 34.5 | 36.3 | 556 | 2 | F64997 | 2-succinyl-6-hydro | 955 | 34 | 35.8 | 252 | 2 | D32252 | gene I protein - A |
| 883 | 34.5 | 36.3 | 556 | 2 | H91022 | 2-oxoglutarate dec | 956 | 34 | 35.8 | 254 | 2 | S76814 | hypothetical prote |
| 884 | 34.5 | 36.3 | 678 | 2 | S82939 | hypothetical prote | 957 | 34 | 35.8 | 256 | 2 | T40964 | probable hydroxyc |
| 885 | 34.5 | 36.3 | 702 | 2 | D90886 | VgrG protein [limp | 958 | 34 | 35.8 | 257 | 2 | A85515 | unknown protein fr |
| 886 | 34.5 | 36.3 | 704 | 2 | J39805 | cyclomaltodextrin | 959 | 34 | 35.8 | 257 | 2 | E90664 | hypothetical prote |
| 887 | 34.5 | 36.3 | 710 | 2 | S63598 | cyclomaltodextrin | 960 | 34 | 35.8 | 262 | 2 | F89809 | hypothetical prote |
| 888 | 34.5 | 36.3 | 713 | 2 | D90658 | VgrG protein [limp | 961 | 34 | 35.8 | 262 | 2 | A88482 | protein C05D11.5 [|
| 889 | 34.5 | 36.3 | 713 | 2 | D85509 | hypothetical prote | 962 | 34 | 35.8 | 264 | 2 | A11802 | an E. coli protein |
| 890 | 34.5 | 36.3 | 714 | 2 | B85732 | Rhs element associ | 963 | 34 | 35.8 | 264 | 2 | AB1429 | an E. coli protein |
| 891 | 34.5 | 36.3 | 728 | 1 | A35644 | hepatocyte growth | 964 | 34 | 35.8 | 264 | 2 | H98054 | conserved hypoteth |
| 892 | 34.5 | 36.3 | 728 | 1 | A60185 | hepatocyte growth | 965 | 34 | 35.8 | 266 | 2 | AB2270 | hypothetical prote |
| 893 | 34.5 | 36.3 | 806 | 2 | A12428 | sucrose synthase [| 966 | 34 | 35.8 | 267 | 2 | C83242 | conserved hypoteth |
| 894 | 34.5 | 36.3 | 875 | 2 | F96027 | probable maltoolig | 967 | 34 | 35.8 | 271 | 2 | D96995 | ATP-utilizing enzy |
| 895 | 34.5 | 36.3 | 946 | 2 | F88196 | ribonucleoside-dip | 968 | 34 | 35.8 | 275 | 2 | H87546 | enoyl-CoA hydratase |
| 896 | 34.5 | 36.3 | 1047 | 2 | F81728 | hypothetical prote | 969 | 34 | 35.8 | 276 | 2 | D71835 | ribosomal protein |
| 897 | 34.5 | 36.3 | 1269 | 2 | T00443 | hypothetical prote | 970 | 34 | 35.8 | 276 | 2 | D64684 | hypothetical prote |
| 898 | 34.5 | 36.3 | 1389 | 2 | H84914 | probable WD-40 rep | 971 | 34 | 35.8 | 276 | 2 | T22267 | conserved hypoteth |
| 899 | 34.5 | 36.3 | 1524 | 2 | A36950 | DNA segregation AT | 972 | 34 | 35.8 | 278 | 2 | D69959 | conserved hypoteth |
| 900 | 34.5 | 36.3 | 1548 | 2 | T04456 | hypothetical prote | 973 | 34 | 35.8 | 281 | 2 | T50351 | transcription regu |
| 901 | 34.5 | 36.3 | 3461 | 2 | S58870 | reslin precursor - | 974 | 34 | 35.8 | 285 | 2 | H86894 | probable methyltra |
| 902 | 34 | 35.8 | 67 | 2 | F81037 | hypothetical prote | 975 | 34 | 35.8 | 285 | 2 | A45854 | leucocyte common a |
| 903 | 34 | 35.8 | 70 | 2 | E96930 | uncharacterized Fe | 976 | 34 | 35.8 | 287 | 2 | T30208 | hypothetical prote |
| 904 | 34 | 35.8 | 74 | 2 | F70526 | hypothetical prote | 977 | 34 | 35.8 | 292 | 2 | A13042 | hypothetical prote |
| 905 | 34 | 35.8 | 84 | 2 | D82518 | hypothetical prote | 978 | 34 | 35.8 | 293 | 2 | S50051 | restriction endonu |

979 34 35.8 294 2 AC3642
980 34 35.8 295 2 F70936
981 34 35.8 304 1 CRV27P
982 34 35.8 304 1 CRVZW
983 34 35.8 304 2 H72162
984 34 35.8 304 2 T28536
985 34 35.8 304 2 E36847
986 34 35.8 304 2 C98243
987 34 35.8 306 2 H69966
988 34 35.8 310 2 E83326
989 34 35.8 313 2 JC7817
990 34 35.8 317 2 I59379
991 34 35.8 327 2 F87541
992 34 35.8 327 2 F84610
993 34 35.8 329 2 T22497
994 34 35.8 331 2 S74910
995 34 35.8 337 2 H64332
996 34 35.8 340 2 A89798
997 34 35.8 342 2 H72111
998 34 35.8 342 2 B86511
999 34 35.8 346 2 A45885
1000 34 35.8 347 1 S55143

ALIGNMENTS

RESULT 1
S11740
IG heavy chain precursor V-D-J region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S11740
R;Hayakawa, K.; Carnarck, C.E.; Hyman, R.; Hardy, R.R.
submitted to the EMBL Data Library, May 1990
A;Description: Natural autoantibodies to thymocytes: Origin, VH genes, fine specificities
A;Reference number: S11740
A;Accession: S11740
A;Molecule type: mRNA
A;Residues: 1-122 <EMB>
A;Cross-references: UNIPARC:UPI000011D085; EMBL:X53097; NID:g52368; PIDN:CAA37261.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;22-106/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 95; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 9.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HIYDDDKRYNPSLSKS 16
|||:|||||:|||||
Db 59 HIYDDDKRYNPSLSKS 74
|||:|||||:|||||
RESULT 2
A49442
IG heavy chain V region (50.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: A49442
R;Stura, E.A.; Stanfield, R.L.; Fieser, G.G.; Silver, S.; Roguska, M.; Hincapié, L.M.; S
Proteins 14, 499-508, 1992
A;Title: Crystallization, sequence, and preliminary crystallographic data for an antipep
A;Reference number: A49442; MUID:93066166; PMID:1438187
A;Accession: A49442
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-107 <STU>
A;Cross-references: UNIPARC:UPI00001768FD
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-91/Domain: immunoglobulin homology <IMM>

Query Match 88.4%; Score 84; DB 2; Length 107;
Best Local Similarity 87.5%; Pred. No. 4.5e-06;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 HIYDDDKRYNPSLSKS 16
|||:|||||:|||||
Db 44 HIFWDGDKRYNPSLSKS 59
|||:|||||:|||||
RESULT 3
S26465
IG heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S26465
R;Kavaler, J.
submitted to the EMBL Data Library, April 1991
A;Reference number: S26459
A;Accession: S26465
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-113 <KAV>
A;Cross-references: UNIPARC:UPI0000115F69; EMBL:X59115; NID:g51928; PIDN:CAA41841.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;6-90/Domain: immunoglobulin homology <IMM>

Query Match 87.4%; Score 83; DB 2; Length 113;
Best Local Similarity 87.5%; Pred. No. 6.8e-06;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HIYDDDKRYNPSLSKS 16
|||:|||||:|||||
Db 43 HIWDDDKRYNPSLSKS 58
|||:|||||:|||||

RESULT 4
S26936
IG heavy chain V region (DP-76) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26936
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26936
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-41 <TOM>
A;Cross-references: UNIPARC:UPI0000116448; EMBL:Z14072; NID:g32971; PIDN:CAA78452.1; PID
C;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 86.3%; Score 82; DB 2; Length 41;
Best Local Similarity 93.3%; Pred. No. 3.2e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IYWDDDKRYNPSLSKS 16
|||:|||||:|||||
Db 23 IYWDDDKRYNPSLSKS 37
|||:|||||:|||||

RESULT 5
S18556
IG heavy chain V region precursor (VII-5b) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C;Accession: S18556
R;Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H
EMBO J. 10, 3641-3645, 1991
A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: clu

A;Reference number: S18551; MUID:92037524; PMID:1935893
A;Accession: S18556
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-118 <SHI>
A;Cross-references: UNIPARC:UPI0000115FEC; EMBL:X62108; NID:G37840; PIDN:CAA44018.1; PID
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-118/Product: Ig heavy chain V region (VII-5b) #status predicted <MAT>
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 86.3%; Score 82; DB 2; Length 118;
Best Local Similarity 93.3%; Pred. No. 1e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IYWDGKRYNPSLKS 16
|||:|||||:|||||
Db 71 IYWDGKRYNPSLKS 85

RESULT 6

S1513
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S1513
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A;Reference number: S31509
A;Accession: S31513
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-138 <CHA>
A;Cross-references: UNIPARC:UPI00001160FA; EMBL:X69861; NID:G33084; PIDN:CAA49495.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;30-114/Domain: immunoglobulin homology <IMM>

Query Match 86.3%; Score 82; DB 2; Length 138;
Best Local Similarity 93.3%; Pred. No. 1.2e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IYWDGKRYNPSLKS 16
|||:|||||:|||||
Db 68 IYWDGKRYNPSLKS 82

RESULT 7

S18555
Ig heavy chain V region precursor (VII-5) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 21-Jul-2000
C;Accession: S18555
R;Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H
EMBO J. 10, 3641-3645, 1991
A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A;Reference number: S18551; MUID:92037524; PMID:1935893
A;Accession: S18555
A;Molecule type: DNA
A;Residues: 1-119 <SHI>
A;Cross-references: UNIPARC:UPI0000115FEP; EMBL:X62111; NID:G37839; PIDN:CAA44021.1; PID
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-119/Product: Ig heavy chain V region (VII-5) #status predicted <MAT>
F;34-118/Domain: immunoglobulin homology <IMM>

Query Match 81.1%; Score 77; DB 2; Length 119;
Best Local Similarity 86.7%; Pred. No. 6.3e-05;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IYWDGKRYNPSLKS 16
|||:|||||:|||||
Db 72 IYWDGKRYNPSLKS 86

RESULT 8

GIHUE
Ig heavy chain V-II region (He) - human
C;Species: Homo sapiens (man)
C;Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 09-Jul-2004
C;Accession: A02093
R;Cunningham, B.A.; Pflumm, M.N.; Rutishauser, U.; Edelman, G.M.
Proc. Natl. Acad. Sci. U.S.A. 64, 997-1003, 1969
A;Title: Subgroups of amino acid sequences in the variable regions of immunoglobulin hea
A;Reference number: A02093; MUID:70114712; PMID:5264153
A;Accession: A02093
A;Molecule type: protein
A;Residues: 1-121 <CUN>
A;Cross-references: UNIPROT:P01818; UNIPARC:UPI000012CEE8
C;Comment: This gamma-1 chain was isolated from a myeloma protein.
C;Genetics:
A;Gene: GDB:IGHV@
A;Cross-references: GDB:128528; OMIM:147070
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: blocked amino end; heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>
F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #statu

Query Match 80.0%; Score 76; DB 1; Length 121;
Best Local Similarity 80.0%; Pred. No. 9.1e-05;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IYWDGKRYNPSLKS 16
|||:|||||:|||||
Db 54 IYWDGKRYNPSLKS 68

RESULT 9

A49002
Ig heavy chain V region, rheumatoid factor RF antibody - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C;Accession: A49002
R;Stuber, F.; Lee, S.K.; Bridges Jr., S.L.; Koopman, W.J.; Schroeder, H.W.J.; Gaskin, F.
Arthritis Rheum. 35, 900-904, 1992
A;Title: A rheumatoid factor from a normal individual encoded by VH2 and V kappa II gene
A;Reference number: A49002; MUID:92352481; PMID:1322670
A;Accession: A49002
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-124 <STU>
A;Cross-references: UNIPARC:UPI0000176978; GB:M30808; NID:G185515; PIDN:AAA52989.1; PID:
A;Experimental source: EBV-transformed lymphoblastoid cell line SSH23
A;Note: sequence extracted from NCBI backbone (NCBI:110261, NCBI:110262)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 77.9%; Score 74; DB 2; Length 124;
Best Local Similarity 80.0%; Pred. No. 0.00019;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IYWDGKRYNPSLKS 16
|||:|||||:|||||
Db 53 IYWDGKRYNPSLKS 67

RESULT 10

PT0174
IG heavy chain precursor V region (IdB5.7) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996
C/Accession: PT0174
R/Perfetti, V.; Borden, P.; Tao, M.H.; Morrison, S.L.; Kabat, E.A.
Mol. Immunol. 28, 505-515, 1991
A/Title: Specificity and variable region cDNA sequence of an isogeneic monoclonal antiid
A/Reference number: PT0174; MUID:91287738; PMID:1712074
A/Accession: PT0174
A/Molecule type: mRNA
A/Residues: 1-143 <PER>
A/Cross-references: UNIPARC:UPI0000176976
A/Experimental source: strain BALB/c
C/Comment: IdB5.7 is an antibody to anti-alpha (1-6) dextran.
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/34-118/Domain: immunoglobulin homology <IMM>

Query Match 77.9%; Score 74; DB 2; Length 143;
Best Local Similarity 81.2%; Pred. No. 0.0023;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 HIYDDDKRYNPSLKS 16
DB 71 HISWDDDLNYPNLSKS 86
|| |||| |||||
|| |||| |||||

RESULT 11
S69339
IG heavy chain V region precursor - human
C/Species: Homo sapiens (man)
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C/Accession: S69339; S72664
R/Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A/Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A/Reference number: S69339; MUID:95262687; PMID:7744049
A/Accession: S69339
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-374 <KHA>
A/Cross-references: UNIPARC:UPI0000176F24; EMBL:X81695
R/Khamilichi, A.A.
submitted to the EMBL Data Library, September 1994
A/Reference number: S72664
A/Accession: S72664
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-140, 'C', 142-374 <KH2>
A/Cross-references: UNIPARC:UPI0000176F25; EMBL:X81695
C/Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 75.8%; Score 72; DB 2; Length 374;
Best Local Similarity 73.3%; Pred. No. 0.0013;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 IYWDKKRYNPSLKS 16
DB 72 IFWDDDKRYSPSLRT 86
|:|||||:|:|:
|:|||||:|:|:

RESULT 12
B25913
IG heavy chain precursor V region (BFL23) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 16-Aug-1996
C/Accession: B25913
R/Lawler, A.M.; Lin, P.S.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 2454-2458, 1987
A/Title: Adult B-cell repertoire is biased toward two heavy-chain variable-region genes
A/Reference number: A94148; MUID:87175692; PMID:3104915
A/Accession: B25913

A/Molecule type: DNA
A/Residues: 1-103 <LAW>
A/Cross-references: UNIPARC:UPI00001768FE
A/Note: the authors translated the codon TGT for residue 11 as Ser
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/19-103/Domain: immunoglobulin homology <IMM>

Query Match 69.5%; Score 66; DB 2; Length 103;
Best Local Similarity 68.8%; Pred. No. 0.0028;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 HIYDDDKRYNPSLKS 16
DB 56 HILWDSKYNPALKS 71
||:|:|:|:|:|:
||:|:|:|:|:|:

RESULT 13
S26328
IG heavy chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C/Accession: S26328
R/Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A/Title: Antibodies that are specific for a single amino acid interchange in a protein e
A/Reference number: S26309; MUID:91341421; PMID:1908510
A/Accession: S26328
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-116 <STA>
A/Cross-references: UNIPARC:UPI0000115F83; EMBL:X59198; NID:g52074; PIDN:CAA41908.1; PID
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/11-95/Domain: immunoglobulin homology <IMM>

Query Match 69.5%; Score 66; DB 2; Length 116;
Best Local Similarity 68.8%; Pred. No. 0.0032;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 HIYDDDKRYNPSLKS 16
DB 48 HILWDSKYNPALKS 63
||:|:|:|:|:|:
||:|:|:|:|:|:

RESULT 14
MHUMC
IG heavy chain V-II region (McE) - human
C/Species: Homo sapiens (man)
C/Date: 14-Nov-1983 #sequence_revision 22-Nov-1983 #text_change 09-Jul-2004
C/Accession: A02092
R/Gerber-Jenson, B.; Kazin, A.; Kehoe, J.M.; Scheffel, C.; Brickson, B.W.; Litman, G.W.
J. Immunol. 126, 1212-1216, 1981
A/Title: Molecular basis for the temperature-dependent insolubility of cryoglobulins. X.
A/Reference number: A02092; MUID:8118242; PMID:6780622
A/Accession: A02092
A/Molecule type: protein
A/Residues: 1-125 <GER>
A/Cross-references: UNIPROT:P01817; UNIPARC:UPI000012CEED
A/Note: this chain was derived from a monoclonal IgM cryoimmunoglobulin
C/Genetics:
A/Gene: GDB:IGHV@
A/Cross-references: GDB:128528; OMIM:147070
A/Map position: 14q32.33-14q32.33
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F/15-99/Domain: immunoglobulin homology <IMM>
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 68.4%; Score 65; DB 1; Length 125;
Best Local Similarity 73.3%; Pred. No. 0.005;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Eur. J. Immunol. 20, 771-777, 1990

A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies

A;Reference number: S09955; MUID:90269328; PMID:2347362

A;Accession: S09959

A;Molecule type: mRNA

A;Residues: 1-121 <REI>

A;Cross-references: UNIPARC:UPI0000115E5E; EMBL:X51847; NID:G55247; PID:CA36140.1; PID:CA36140.1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-99/Domain: immunoglobulin homology <IMM>

A;Accession: A5005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-121 <SCH>
A;Cross-references: UNIPARC:UPI0000176977; GB:M34027
C;Genetics:
A;Gene: GDB:IGH@; IGHDI1
A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

C>Date: 03-Dec-1998 #sequence_revision 03-Dec-1998 #text_change 07-May
C/Accession: S46471
A/Cook, G.P.; Tomlinson, I.M.; Walter, G.; Riethman, H.; Carter, N.P.; Buluwela, L.; Win
Nature Genet. 7, 162-168, 1994
A>Title: A map of the human immunoglobulin V(H) locus completed by analysis of the telom
A/Reference number: S46460; MUID:95004581; PMID:7920835
A/Accession: S46471
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-56 <COO>
A/Cross-references: UNIPARC:UPI00001768FF; EMBL:Z29983
C/Superfamily: immunoglobulin V region; immunoglobulin homology

A;Residues: 1-36 8000
A;Cross-references: UNIPARC:UPI00001768FF; EMBL:Z29983
C;Superfamily: immunoglobulin V region; immunoglobulin homology

| | | | | |
|-----------------------|-----------------|-----------------|-----------|------------|
| Query Match | 55.8% | Score 53; | DB 2; | Length 56; |
| Best Local Similarity | 66.7% | Pred. No. 0.16; | | |
| Matches 10; | Conservative 2; | Mismatches 3; | Indels 0; | Gaps 0; |

EMBO J. 8, 3741-3748, 1989
A;Title: The smaller human V(H) gene families display remarkably little polymorphism.
A;Reference number: S09421; MUID:90059975; PMID:2511001

A;Accession: S12416
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-97 <SAN>
A;Cross-references: UNIPROT:Q9UL73; UNIPARC:UPI0000176565; EMBL:X56360
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 52.6%; Score 50; DB 2; Length 97;
Best Local Similarity 56.2%; Pred. No. 0.85;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 HIYWDDDKRYNPISLKS 16
:|: |||||
Db 50 YIYSGSTNYNPISLKS 65

RESULT 25

S12412
Ig heavy chain V region (4.12) - human
C;Species: Homo sapiens (man)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C;Accession: S12412
R;Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.

EMBO J. 8, 3741-3748, 1989
A;Title: The smaller human V(H) gene families display remarkably little polymorphism.
A;Reference number: S09421; MUID:90059975; PMID:2511001

A;Accession: S12412
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-99 <SAN>
A;Cross-references: UNIPARC:UPI0000176562; EMBL:X56356
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 52.6%; Score 50; DB 2; Length 99;
Best Local Similarity 56.2%; Pred. No. 0.87;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 HIYWDDDKRYNPISLKS 16
:|: |||||
Db 52 YIYSGSTNYNPISLKS 67

RESULT 26

S44125
Ig lambda chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44125
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.

A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable region
A;Reference number: S44105

A;Accession: S44125
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-105 <HAW>
A;Cross-references: UNIPARC:UPI000011662A; EMBL:Z31383; NID:9472978; PIDN:CAA83258.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 52.6%; Score 50; DB 2; Length 105;
Best Local Similarity 56.2%; Pred. No. 0.93;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 HIYWDDDKRYNPISLKS 16

Db 50 YIYSGSTNYNPISLKS 65
:|: |||||

RESULT 27

S57464
Ig heavy chain V-J region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S57464
R;Paterson, G.; Wilson, G.; Kennedy, P.G.E.; Willison, H.J.

submitted to the EMBL Data Library, June 1995
A;Description: Analysis of anti-GM1 ganglioside IgM antibodies cloned from motor neuropathy
A;Reference number: S57408
A;Accession: S57464
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-115 <PAT>
A;Cross-references: UNIPARC:UPI00001137AD; EMBL:X87897; NID:9871273; PIDN:CAA61148.1; PI

C;Genetics:
A;Introns: 100/2
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 52.6%; Score 50; DB 2; Length 115;
Best Local Similarity 56.2%; Pred. No. 1;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 HIYWDDDKRYNPISLKS 16
:|: |||||
Db 52 YIYSGSTNYNPISLKS 67

RESULT 28

B26340
Ig heavy chain precursor V-II region (71-4) - human
C;Species: Homo sapiens (man)
C;Date: 05-Jun-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
C;Accession: B26340

R;Kodaira, M.; Kinashi, T.; Umemura, I.; Matsuura, F.; Noma, T.; Ono, Y.; Honjo, T.
J. Mol. Biol. 190, 529-541, 1986
A;Title: Organization and evolution of variable region genes of the human immunoglobulin
A;Reference number: A26340; MUID:87061007; PMID:3097326

A;Accession: B26340
A;Molecule type: DNA
A;Residues: 1-116 <KOD>
A;Cross-references: UNIPARC:UPI0000115D70; GB:X05711; NID:933602; PIDN:CAA29183.1; PID:9
A;Note: the authors translated the codon GAG for residue 25 as Gln
C;Genetics:

A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;120-116/Product: Ig heavy chain V region 71-4 #status predicted <MAT>
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 52.6%; Score 50; DB 2; Length 116;
Best Local Similarity 56.2%; Pred. No. 1;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 HIYWDDDKRYNPISLKS 16
:|: |||||
Db 69 YIYSGSTNYNPISLKS 84

RESULT 29...

A26340
Ig heavy chain precursor V-II region (71-2) - human
N;Alternate names: Ig heavy chain V region (DP-66)
C;Species: Homo sapiens (man)
C;Date: 05-Jun-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
C;Accession: A26340; S26901
R;Kodaira, M.; Kinashi, T.; Umemura, I.; Matsuura, F.; Noma, T.; Ono, Y.; Honjo, T.

C:Species: Homo sapiens (man)

SECRET

SECRET

A;Residues: 1-99 <WEN>
A;Cross-references: UNIPARC:UPI0000116484; EMBL:Z14236; NID:g37702; PIDN:CAA78605.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 48.4%; Score 46; DB 2; Length 99;
Best Local Similarity 60.0%; Pred. No. 3.7;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 IYWDDDKRYNPSLKS 16
Db 53 IYSGSTYYPNPSLKS 67
||: |||||

RESULT 49

S12418
Ig heavy chain V region (4.18) - human
C;Species: Homo sapiens (man)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C;Accession: S12418
R;Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A;Title: The smaller human V(H) gene families display remarkably little polymorphism.
A;Reference number: S09421; MUID:90059975; PMID:2511001
A;Accession: S12418
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-99 <SAN>
A;Cross-references: UNIPARC:UPI0000176E61; EMBL:X56362
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 48.4%; Score 46; DB 2; Length 99;
Best Local Similarity 60.0%; Pred. No. 3.7;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 IYWDDDKRYNPSLKS 16
Db 53 IYSGSTYYPNPSLKS 67
||: |||||

RESULT 50

S78056
Ig heavy chain V region (clone MLH4-1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 31-Dec-2004
C;Accession: S78056; S23721
R;Harindranath, N.
submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78056
A;Molecule type: DNA
A;Residues: 1-100 <HAR>
A;Cross-references: UNIPROT:O95973; UNIPARC:UPI00001769D3; EMBL:X54447
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Norkkine
Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and H
patient.
A;Reference number: S23716; MUID:92031262; PMID:1718404
A;Accession: S23721
A;Molecule type: DNA
A;Residues: 5-100 <HAW>
A;Cross-references: UNIPARC:UPI00001769D4; EMBL:X54447
C;Superfamily: immunoglobulin homology
C;Keywords: immunoglobulin
F;19-100/Domain: immunoglobulin homology (fragment) <IMM>

Query Match 48.4%; Score 46; DB 2; Length 100;
Best Local Similarity 60.0%; Pred. No. 3.7;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 IYWDDDKRYNPSLKS 16
Db 57 IYSGSTYYPNPSLKS 71
||: |||||

Search completed: February 23, 2006, 09:51:44
Job time : 32.6462 secs

OM protein - protein search, using sw model

Run on: February 23, 2006, 09:29:53 ; Search time 137.846 Seconds
(without alignments)
81.892 Million cell updates/sec

Title: US-10-723-872-24
Perfect score: 95
Sequence: 1 HIYWDKDRNPSTLKS 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 95 | 100.0 | 485 | 2 | Q561m5 mus musculus |
| 2 | 87 | 91.6 | 118 | 2 | Q811u5 mouse |
| 3 | 82 | 86.3 | 121 | 2 | Q9ul96 homo sapien |
| 4 | 78 | 82.1 | 487 | 2 | Q58e53 mouse |
| 5 | 76 | 80.0 | 121 | 1 | HV2E_HUMAN |
| 6 | 73 | 76.8 | 617 | 2 | Q569B3 RAT |
| 7 | 71 | 74.7 | 493 | 2 | Q569J1 HUMAN |
| 8 | 68 | 71.6 | 482 | 2 | Q5VLR6 RAT |
| 9 | 65 | 68.4 | 125 | 1 | HV2D_HUMAN |
| 10 | 62 | 65.3 | 485 | 2 | Q58E54_MOUSE |
| 11 | 55 | 57.9 | 120 | 1 | HV2B_HUMAN |
| 12 | 51 | 53.7 | 145 | 2 | Q8IEB8_PLAF7 |
| 13 | 51 | 53.7 | 357 | 2 | Q4XWY4_PLACH |
| 14 | 50 | 52.6 | 139 | 2 | Q86SX2_HUMAN |
| 15 | 50 | 52.6 | 801 | 2 | Q5G7N6_9CAUD |
| 16 | 49 | 51.6 | 97 | 2 | Q43234_HUMAN |
| 17 | 49 | 51.6 | 147 | 1 | HV2H_HUMAN |
| 18 | 49 | 51.6 | 167 | 2 | Q5XN06_ANOGA |
| 19 | 49 | 51.6 | 383 | 2 | Q5JEL9_PYRKO |
| 20 | 49 | 51.6 | 426 | 2 | Q6CVD3_KLULA |
| 21 | 49 | 51.6 | 462 | 2 | Q7OHX0_ANOGA |
| 22 | 49 | 51.6 | 497 | 2 | Q5TW91_ANOGA |
| 23 | 48 | 50.5 | 476 | 2 | Q6GMX1_HUMAN |
| 24 | 48 | 50.5 | 549 | 2 | Q8LEX3_BACCR |
| 25 | 47.5 | 50.0 | 288 | 2 | Q6LZD6_METMP |
| 26 | 47.5 | 50.0 | 288 | 2 | Q6LZD6_METMP |
| 27 | 47 | 49.5 | 400 | 2 | Q621X9_CAEBR |
| 28 | 47 | 49.5 | 778 | 2 | Q7XPL1_ORISA |
| 29 | 46 | 48.4 | 208 | 2 | Q99JU0_MOUSE |
| 30 | 46 | 48.4 | 485 | 1 | K56B2_MOUSE |
| 31 | 46 | 48.4 | 492 | 2 | Q72374_HUMAN |

| | | | | | | | | | | | | | | | | |
|-----|------|------|------|---|--------------|--------|--------------|---|-----|------|------|------|---|--------------|---------|--------------|
| 105 | 46 | 48.4 | 642 | 2 | Q70AE1_9LUTE | Q70ae1 | sugarcane | Y | 178 | 43 | 45.3 | 98 | 2 | Q53VQ0_MOUSE | O53vq0 | mus musculus |
| 106 | 46 | 48.4 | 642 | 2 | Q70AF9_9LUTE | Q70af9 | sugarcane | Y | 179 | 43 | 45.3 | 108 | 2 | Q853D6_9CAUD | O853d6 | mycobacteri |
| 107 | 46 | 48.4 | 642 | 2 | Q70AF6_9LUTE | Q70af6 | sugarcane | Y | 180 | 43 | 45.3 | 115 | 2 | Q53VQ1_MOUSE | O53vq1 | mus musculus |
| 108 | 46 | 48.4 | 642 | 2 | Q70AF3_9LUTE | Q70af3 | sugarcane | Y | 181 | 43 | 45.3 | 136 | 2 | Q6LBQ5_MOUSE | O6lbq5 | mus musculus |
| 109 | 46 | 48.4 | 642 | 2 | Q70AF0_9LUTE | Q70af0 | sugarcane | Y | 182 | 43 | 45.3 | 143 | 2 | Q5J303_PYROC | O5jj303 | pyrococcus |
| 110 | 46 | 48.4 | 642 | 2 | Q70AE7_9LUTE | Q70ae7 | sugarcane | Y | 183 | 43 | 45.3 | 217 | 2 | Q728U7_COPCI | O728u7 | coprinus ci |
| 111 | 46 | 48.4 | 642 | 2 | Q70AE4_9LUTE | Q70ae4 | sugarcane | Y | 184 | 43 | 45.3 | 221 | 2 | Q89J52_BRAJA | O89j52 | bradyrhizob |
| 112 | 46 | 48.4 | 642 | 2 | Q70AD9_9LUTE | Q70ad9 | sugarcane | Y | 185 | 43 | 45.3 | 221 | 2 | Q5EJX6_9VIBR | O5ejx6 | vibrio salm |
| 113 | 46 | 48.4 | 650 | 2 | Q9JH79_9LUTE | Q9jh79 | sugarcane | Y | 186 | 43 | 45.3 | 283 | 2 | Q72W64_LEPIC | O72w64 | leptospira |
| 114 | 46 | 48.4 | 650 | 2 | Q9QKN9_9LUTE | Q9qkn9 | sugarcane | Y | 187 | 43 | 45.3 | 283 | 2 | Q8F9V6_LEPIN | O8f9v6 | leptospira |
| 115 | 46 | 48.4 | 650 | 2 | Q80FH9_9LUTE | Q80fh9 | sugarcane | Y | 188 | 43 | 45.3 | 342 | 2 | Q5FSF4_GLNOX | O5fsf4 | gluconobact |
| 116 | 46 | 48.4 | 720 | 2 | Q581T3_9TRYF | Q581t3 | trypanosoma | Y | 189 | 43 | 45.3 | 383 | 2 | Q9UZV3_PYRAB | O9uzv3 | pyrococcus |
| 117 | 46 | 48.4 | 747 | 2 | Q55UL0_CRYNE | O55ul0 | cryptococcu | Y | 190 | 43 | 45.3 | 398 | 2 | Q6CV71_KLJLA | O6cv71 | kluyveromyc |
| 118 | 46 | 48.4 | 747 | 2 | Q5KHT4_CRYNE | O5kht4 | cryptococcu | Y | 191 | 43 | 45.3 | 492 | 1 | MURE_NEIMA | O9j8z0 | neiseeria m |
| 119 | 46 | 48.4 | 815 | 2 | Q70AE3_9LUTE | Q70ae3 | sugarcane | Y | 192 | 43 | 45.3 | 492 | 1 | MURE_NEIMB | O9k0y9 | neiseeria m |
| 120 | 46 | 48.4 | 815 | 2 | Q70AF5_9LUTE | Q70af5 | sugarcane | Y | 193 | 43 | 45.3 | 511 | 2 | Q9UIR5_CABEL | O9uir5 | caenorhabdi |
| 121 | 46 | 48.4 | 815 | 2 | Q70AF8_9LUTE | Q70af8 | sugarcane | Y | 194 | 43 | 45.3 | 557 | 2 | Q51IB9_MAGGR | O51ib9 | magnaporth |
| 122 | 46 | 48.4 | 815 | 2 | Q70AF2_9LUTE | Q70af2 | sugarcane | Y | 195 | 43 | 45.3 | 560 | 2 | Q871X9_VIBPA | O871x9 | vibrio para |
| 123 | 46 | 48.4 | 815 | 2 | Q70AE9_9LUTE | Q70ae9 | sugarcane | Y | 196 | 43 | 45.3 | 626 | 1 | DHML_METOR | P15279 | methylobact |
| 124 | 46 | 48.4 | 815 | 2 | Q70AE6_9LUTE | Q70ae6 | sugarcane | Y | 197 | 43 | 45.3 | 665 | 2 | Q8D6R2_VIBVU | O8d6r2 | vibrio vuln |
| 125 | 46 | 48.4 | 815 | 2 | Q70AD8_9LUTE | Q70ad8 | sugarcane | Y | 198 | 43 | 45.3 | 665 | 2 | Q7MDM1_VIBVY | O7mdm1 | vibrio vuln |
| 126 | 46 | 48.4 | 857 | 2 | Q526C4_MAGGR | O526c4 | magnaporth | Y | 199 | 43 | 45.3 | 785 | 2 | Q8IP26_DROME | O8ip26 | drosophila |
| 127 | 46 | 48.4 | 1110 | 2 | Q94J89_ORYSA | Q94j89 | oryza sativ | Y | 200 | 43 | 45.3 | 865 | 2 | Q7PVI4_ANOGA | O7pvi4 | anopheles g |
| 128 | 46 | 48.4 | 1320 | 2 | Q9T100_9CAUD | Q9t100 | bacterioph | Y | 201 | 43 | 45.3 | 905 | 2 | Q24009_DROME | O24009 | drosophila |
| 129 | 46 | 48.4 | 2304 | 2 | Q4RW33_TETNG | Q4rw33 | tetraodon n | Y | 202 | 43 | 45.3 | 991 | 2 | Q8SS94_ENCCU | O8ss94 | encephalito |
| 130 | 45.5 | 47.9 | 363 | 1 | RA51C_ARATH | O8gxf0 | arabidopsis | Y | 203 | 43 | 45.3 | 996 | 2 | Q4MX24_THRPA | O4mx24 | thellieria p |
| 131 | 45.5 | 47.9 | 1197 | 2 | Q4T281_TETNG | O4t281 | tetraodon n | Y | 204 | 43 | 45.3 | 1067 | 2 | Q54YD4_DICDI | O54yd4 | dictyosteli |
| 132 | 45 | 47.4 | 98 | 2 | Q53VR2_MOUSE | O53vr2 | mus musculus | Y | 205 | 43 | 45.3 | 1106 | 1 | DPD01_BOVIN | P28339 | bos taurus |
| 133 | 45 | 47.4 | 98 | 2 | Q53VR6_MOUSE | P18531 | mus musculus | Y | 206 | 43 | 45.3 | 1350 | 2 | Q8I447_PLAP7 | O8i447 | plasmodium |
| 134 | 45 | 47.4 | 116 | 1 | HV60_MOUSE | P18531 | mus musculus | Y | 207 | 43 | 45.3 | 2294 | 2 | Q7RJK4_PLAP7 | O7rjk4 | plasmodium |
| 135 | 45 | 47.4 | 116 | 1 | HV61_MOUSE | P18532 | mus musculus | Y | 208 | 43 | 45.3 | 2745 | 2 | Q7R6Q2_GIALA | O7r6q2 | giardia lam |
| 136 | 45 | 47.4 | 119 | 2 | Q53VR3_MOUSE | O53vr3 | mus musculus | Y | 209 | 42.5 | 44.7 | 81 | 2 | Q8UF27_AGR5 | O8uf27 | agrobacteri |
| 137 | 45 | 47.4 | 120 | 2 | Q53VR7_MOUSE | O53vr7 | mus musculus | Y | 210 | 42.5 | 44.7 | 87 | 2 | Q7CY33_AGR5 | O7cy33 | agrobacteri |
| 138 | 45 | 47.4 | 229 | 2 | Q74WU9_NANRQ | Q74wu9 | nanarchaetu | Y | 211 | 42.5 | 44.7 | 334 | 2 | Q8ERN3_OCEIH | O8ern3 | oceanobacil |
| 139 | 45 | 47.4 | 253 | 2 | Q66717_AQUAE | O66717 | aquifex aeo | Y | 212 | 42.5 | 44.7 | 350 | 2 | Q7S6N8_NEUCR | O7s6n8 | neurospora |
| 140 | 45 | 47.4 | 262 | 2 | Q65211_MOUSE | O65x11 | mus musculus | Y | 213 | 42.5 | 44.7 | 366 | 2 | Q29988_HUMAN | O29988 | homo sapien |
| 141 | 45 | 47.4 | 347 | 2 | O5TT37_ANOGA | O5tt37 | anopheles g | Y | 214 | 42.5 | 44.7 | 367 | 2 | Q4R6W9_MAFCA | O4r6w9 | macaca fasc |
| 142 | 45 | 47.4 | 479 | 2 | Q99M22_MOUSE | O99m22 | mus musculus | Y | 215 | 42.5 | 44.7 | 368 | 1 | SNPC1_HUMAN | O16533 | h snrna act |
| 143 | 45 | 47.4 | 506 | 2 | Q70AG8_ANOGA | O7qag8 | anopheles g | Y | 216 | 42.5 | 44.7 | 541 | 2 | Q6PKH5_HUMAN | O6pkh5 | homo sapien |
| 144 | 45 | 47.4 | 572 | 2 | Q6BZK0_DEBHA | O6bzk0 | debariomyce | Y | 217 | 42.5 | 44.7 | 542 | 2 | Q9NTB1_HUMAN | O9ntb1 | homo sapien |
| 145 | 44.5 | 46.8 | 1163 | 2 | Q4IG17_GIBZE | O4ig17 | gibberella | Y | 218 | 42.5 | 44.7 | 557 | 2 | O8BY56_MOUSE | O8by56 | mus musculus |
| 146 | 44 | 46.3 | 98 | 2 | Q53VQ4_MOUSE | O53vq4 | mus musculus | Y | 219 | 42.5 | 44.7 | 591 | 2 | O566J0_MOUSE | O566j0 | mus musculus |
| 147 | 44 | 46.3 | 119 | 2 | Q9UL73_HUMAN | O9ul73 | homo sapien | Y | 220 | 42.5 | 44.7 | 692 | 2 | Q4IF30_GIBZE | O4if30 | gibberella |
| 148 | 44 | 46.3 | 119 | 2 | Q53VQ5_MOUSE | O53vq5 | mus musculus | Y | 221 | 42.5 | 44.7 | 852 | 1 | RBW10_FAT | P70501 | rattus norv |
| 149 | 44 | 46.3 | 156 | 2 | Q9UZ93_PYRAB | O9uz93 | pyrococcus | Y | 222 | 42.5 | 44.7 | 852 | 2 | Q9BTK0_HUMAN | O9btk0 | homo sapien |
| 150 | 44 | 46.3 | 222 | 1 | 6PGL_ACTAC | P70715 | actinobacil | Y | 223 | 42.5 | 44.7 | 853 | 2 | Q5JRR2_HUMAN | O5jrr2 | homo sapien |
| 151 | 44 | 46.3 | 288 | 2 | Q9LQA0_COXBU | O9laq0 | coxiella bu | Y | 224 | 42.5 | 44.7 | 853 | 2 | O8BTP8_MOUSE | O8btp8 | mus musculus |
| 152 | 44 | 46.3 | 298 | 2 | Q63UX6_BURPS | O63ux6 | burkholderi | Y | 225 | 42.5 | 44.7 | 857 | 2 | Q80U75_MOUSE | O80u75 | mus musculus |
| 153 | 44 | 46.3 | 298 | 2 | Q62JR9_BURMA | O62jr9 | burkholderi | Y | 226 | 42.5 | 44.7 | 929 | 1 | RBW10_HUMAN | P98175 | homo sapien |
| 154 | 44 | 46.3 | 321 | 2 | Q4XUQ2_PLACH | O4xuq2 | plasmodium | Y | 227 | 42.5 | 44.7 | 930 | 2 | Q9BTE4_HUMAN | O9bte4 | homo sapien |
| 155 | 44 | 46.3 | 463 | 2 | O522P3_MYCHY | O5z2p3 | mycoplasma | Y | 228 | 42.5 | 44.7 | 930 | 2 | Q99KG3_MOUSE | O99kg3 | mus musculus |
| 156 | 44 | 46.3 | 455 | 2 | Q6GMX6_HUMAN | O6gmx6 | homo sapien | Y | 229 | 42.5 | 44.7 | 995 | 2 | Q7Z3D7_HUMAN | O7z3d7 | homo sapien |
| 157 | 44 | 46.3 | 478 | 2 | Q72379_HUMAN | Q72379 | homo sapien | Y | 230 | 42 | 44.2 | 98 | 2 | Q53VQ8_MOUSE | O53vq8 | mus musculus |
| 158 | 44 | 46.3 | 576 | 2 | Q6P418_HUMAN | O6p418 | homo sapien | Y | 231 | 42 | 44.2 | 119 | 2 | Q53VQ9_MOUSE | O53vq9 | mus musculus |
| 159 | 44 | 46.3 | 656 | 2 | Q5LB34_BACFN | O5lb34 | bacteroides | Y | 232 | 42 | 44.2 | 186 | 2 | Q7QID9_ANOGA | O7qid9 | anopheles g |
| 160 | 44 | 46.3 | 593 | 2 | Q9C6S0_ARATH | O9c6s0 | arabidopsis | Y | 233 | 42 | 44.2 | 221 | 2 | Q4XP07_PLACH | O4xp07 | plasmodium |
| 161 | 44 | 46.3 | 593 | 2 | Q93VK5_ARATH | O93vk5 | arabidopsis | Y | 234 | 42 | 44.2 | 249 | 2 | Q4SB57_TETNG | O4sb57 | tetraodon n |
| 162 | 44 | 46.3 | 597 | 2 | O58537_PYRHO | O58537 | pyrococcus | Y | 235 | 42 | 44.2 | 264 | 2 | Q8ENW2_OCEIH | O8enw2 | oceanobacil |
| 163 | 44 | 46.3 | 620 | 2 | Q96EY0_HUMAN | Q96ey0 | homo sapien | Y | 236 | 42 | 44.2 | 284 | 2 | Q9TZB2_CABEL | O9tzb2 | caenorhabdi |
| 164 | 44 | 46.3 | 656 | 2 | Q6MDH8_BACFR | O6mdh8 | bacteroides | Y | 237 | 42 | 44.2 | 286 | 2 | Q4QQ33_DROME | O4qq33 | drosophila |
| 165 | 44 | 46.3 | 764 | 2 | Q6MD03_PAPUR | O6md03 | parachlamyd | Y | 238 | 42 | 44.2 | 298 | 2 | P71702_MYCTU | P71702 | mycobacteri |
| 166 | 44 | 46.3 | 794 | 2 | Q6FSB5_CANGA | O6fbs5 | candida gla | Y | 239 | 42 | 44.2 | 298 | 2 | Q7U2Y9_MYCBO | O7u2y9 | mycobacteri |
| 167 | 44 | 46.3 | 802 | 2 | Q9C1R8_CANGA | O9c1r8 | candida gla | Y | 240 | 42 | 44.2 | 312 | 2 | Q60UY8_CAEBR | O60uy8 | caenorhabdi |
| 168 | 44 | 46.3 | 833 | 2 | Q5B418_EMENI | O5b418 | aspergillus | Y | 241 | 42 | 44.2 | 328 | 2 | Q9X100_ARATH | O9x100 | arabidopsis |
| 169 | 44 | 46.3 | 943 | 2 | Q60D35_SOLDE | O60d35 | solanum dem | Y | 242 | 42 | 44.2 | 329 | 2 | Q4YWX2_PLABE | O4ywx2 | plasmodium |
| 170 | 44 | 46.3 | 1345 | 2 | Q9QBUR_9VIRU | Q9qbur | oat golden | Y | 243 | 42 | 44.2 | 330 | 2 | O8DYM6_STRAS | O8dym6 | streptococc |
| 171 | 44 | 46.3 | 1725 | 2 | Q7RT66_PLAYO | Q7rt66 | plasmodium | Y | 244 | 42 | 44.2 | 330 | 2 | O8E483_STRAS | O8e483 | streptococc |
| 172 | 44 | 46.3 | 1782 | 2 | Q4SHC2_TETNG | O4shc2 | tetraodon n | Y | 245 | 42 | 44.2 | 348 | 2 | O19481_HETFR | O19481 | heterodontu |
| 173 | 44 | 46.3 | 1834 | 2 | Q8I5C8_PLAP7 | O8i5c8 | plasmodium | Y | 246 | 42 | 44.2 | 374 | 2 | P7RX50_NEUCR | P7rx50 | neurospora |
| 174 | 44 | 46.3 | 1853 | 2 | Q9IWA9_9VIRU | Q9iwa9 | oat golden | Y | 247 | 42 | 44.2 | 389 | 1 | PSFS_WETJA | O58421 | methanococc |
| 175 | 44 | 46.3 | 2183 | 1 | L_RINDR | F41357 | rinderpest | Y | 248 | 42 | 44.2 | 393 | 2 | Q5AA57_CANAL | O5aa57 | candida alb |
| 176 | 44 | 46.3 | 2183 | 2 | Q86499_RINDR | O86499 | rinderpest | Y | 249 | 42 | 44.2 | 407 | 2 | Q5WCA6_BACSK | O5wca6 | bacillus cl |
| 177 | 43.5 | 45.8 | 464 | 2 | Q62YN0_HYDRK | O62yn0 | hydractinia | Y | 250 | 42 | 44.2 | 408 | 2 | Q75AW2_ASHGO | O75aw2 | ashhya goss |

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|-----|------|------|------|---|--------|-------------|
| 251 | 42 | 44.2 | 411 | 2 | Q20449 | CABEL |
| 252 | 42 | 44.2 | 412 | 2 | Q60VW0 | CAENORHABDI |
| 253 | 42 | 44.2 | 422 | 2 | Q4KVC0 | TETNG |
| 254 | 42 | 44.2 | 454 | 2 | Q6CHC9 | YARROWIA LI |
| 255 | 42 | 44.2 | 462 | 2 | Q944P9 | ARABIDOPSIS |
| 256 | 42 | 44.2 | 470 | 2 | Q55999 | SPHINGOMONA |
| 257 | 42 | 44.2 | 475 | 2 | Q79C40 | SPHINGOMONA |
| 258 | 42 | 44.2 | 470 | 2 | Q81E06 | PLAF7 |
| 259 | 42 | 44.2 | 483 | 2 | Q5U413 | MOUSE |
| 260 | 42 | 44.2 | 483 | 2 | Q5AB16 | CANAL |
| 261 | 42 | 44.2 | 514 | 2 | Q5V3W2 | HALMA |
| 262 | 42 | 44.2 | 580 | 2 | Q4WR17 | ASPERGILLUS |
| 263 | 42 | 44.2 | 585 | 2 | Q7PDW2 | PLAYO |
| 264 | 42 | 44.2 | 592 | 2 | Q7UL40 | RHODOPRELL |
| 265 | 42 | 44.2 | 633 | 2 | Q5VNM1 | ORYZA |
| 266 | 42 | 44.2 | 639 | 2 | Q7XW04 | ORYZA |
| 267 | 42 | 44.2 | 741 | 1 | TKTC | SP10L |
| 268 | 42 | 44.2 | 741 | 2 | Q84W15 | ARATH |
| 269 | 42 | 44.2 | 741 | 2 | Q8LE99 | ARATH |
| 270 | 42 | 44.2 | 741 | 2 | Q8RW00 | ARATH |
| 271 | 42 | 44.2 | 743 | 2 | Q842Y2 | ORYZA |
| 272 | 42 | 44.2 | 744 | 2 | Q78327 | CAPAN |
| 273 | 42 | 44.2 | 754 | 2 | Q9LZV8 | ARATH |
| 274 | 42 | 44.2 | 765 | 2 | Q73K54 | TREDE |
| 275 | 42 | 44.2 | 781 | 2 | Q9P9N1 | SULOH |
| 276 | 42 | 44.2 | 781 | 2 | Q96YV1 | SULTO |
| 277 | 42 | 44.2 | 861 | 2 | Q8IN52 | DROME |
| 278 | 42 | 44.2 | 897 | 2 | Q5UL65 | DROME |
| 279 | 42 | 44.2 | 963 | 2 | Q8XE96 | ARATH |
| 280 | 42 | 44.2 | 1424 | 2 | Q61P83 | CABER |
| 281 | 42 | 44.2 | 1429 | 2 | Q4PF57 | USTMA |
| 282 | 42 | 44.2 | 1450 | 2 | Q86A05 | DICDI |
| 283 | 42 | 44.2 | 1527 | 2 | Q81425 | PLAF7 |
| 284 | 42 | 44.2 | 1719 | 2 | Q8TL36 | 9HIVA |
| 285 | 42 | 44.2 | 3165 | 2 | Q8IJ18 | PLAF7 |
| 286 | 42 | 44.2 | 3191 | 2 | Q01335 | CABEL |
| 287 | 41.5 | 43.7 | 166 | 2 | Q4RHE3 | TETNG |
| 288 | 41.5 | 43.7 | 251 | 1 | YRPE | BACSU |
| 289 | 41.5 | 43.7 | 333 | 1 | Q5W129 | BACSK |
| 290 | 41.5 | 43.7 | 375 | 1 | DAPE | BUCAP |
| 291 | 41.5 | 43.7 | 377 | 1 | CDG37 | TETFL |
| 292 | 41.5 | 43.7 | 405 | 2 | Q9NVF0 | HUMAN |
| 293 | 41.5 | 43.7 | 473 | 2 | Q4UTV3 | ORYZA |
| 294 | 41.5 | 43.7 | 484 | 2 | Q5U472 | MOUSE |
| 295 | 41.5 | 43.7 | 532 | 2 | Q4WLC3 | ASPFU |
| 296 | 41.5 | 43.7 | 545 | 2 | Q9H8Y4 | HUMAN |
| 297 | 41.5 | 43.7 | 573 | 2 | Q9NVN9 | HUMAN |
| 298 | 41.5 | 43.7 | 643 | 2 | Q56U81 | EMENI |
| 299 | 41.5 | 43.7 | 663 | 2 | Q4P788 | USTMA |
| 300 | 41.5 | 43.7 | 666 | 2 | Q8ILE1 | PLAF7 |
| 301 | 41.5 | 43.7 | 667 | 2 | Q5B5B7 | EMENI |
| 302 | 41.5 | 43.7 | 718 | 2 | Q4YV87 | PLABE |
| 303 | 41.5 | 43.7 | 871 | 2 | Q5CZ78 | HUMAN |
| 304 | 41.5 | 43.7 | 901 | 2 | Q4XZM4 | PLACH |
| 305 | 41.5 | 43.7 | 906 | 2 | Q61GH5 | CABER |
| 306 | 41.5 | 43.7 | 1087 | 2 | Q6NSK5 | HUMAN |
| 307 | 41.5 | 43.7 | 1125 | 2 | Q9N0M6 | HUMAN |
| 308 | 41 | 43.2 | 93 | 2 | Q7F210 | ORYZA |
| 309 | 41 | 43.2 | 112 | 2 | Q90DD0 | SIVCZ |
| 310 | 41 | 43.2 | 116 | 2 | Q8GHX0 | PSERE |
| 311 | 41 | 43.2 | 137 | 1 | HV46 | MOUSE |
| 312 | 41 | 43.2 | 148 | 2 | Q5L2F5 | GEOKA |
| 313 | 41 | 43.2 | 149 | 2 | Q51PC3 | WAGGR |
| 314 | 41 | 43.2 | 162 | 2 | Q8D413 | VIBVU |
| 315 | 41 | 43.2 | 194 | 2 | Q9W692 | ACITR |
| 316 | 41 | 43.2 | 230 | 2 | Q8IND7 | BACAN |
| 317 | 41 | 43.2 | 230 | 2 | Q638X4 | BACCZ |
| 318 | 41 | 43.2 | 232 | 1 | 6PGL | HABIN |
| 319 | 41 | 43.2 | 241 | 2 | Q8RCJ3 | THETN |
| 320 | 41 | 43.2 | 245 | 2 | Q4QM22 | HAB18 |
| 321 | 41 | 43.2 | 287 | 2 | Q6CG89 | YARLI |
| 322 | 41 | 43.2 | 293 | 1 | PET54 | YEAST |
| 323 | 41 | 43.2 | 297 | 2 | Q4GY59 | 9TRYPP |

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|-----|----|------|------|---|--------|------------|
| 324 | 41 | 43.2 | 297 | 2 | Q84S31 | VITVI |
| 325 | 41 | 43.2 | 301 | 1 | CHIT3 | VITVI |
| 326 | 41 | 43.2 | 305 | 2 | Q7MG16 | VIBVU |
| 327 | 41 | 43.2 | 323 | 2 | Q9H635 | HUMAN |
| 328 | 41 | 43.2 | 323 | 2 | Q6K837 | ORYZA |
| 329 | 41 | 43.2 | 335 | 2 | Q6BXT3 | DEBHA |
| 330 | 41 | 43.2 | 337 | 2 | Q67815 | AQUAE |
| 331 | 41 | 43.2 | 346 | 2 | Q7MMK8 | PORGI |
| 332 | 41 | 43.2 | 347 | 1 | GBGT1 | CANFA |
| 333 | 41 | 43.2 | 347 | 1 | GBGT1 | HUMAN |
| 334 | 41 | 43.2 | 353 | 2 | Q5V3C7 | HALMA |
| 335 | 41 | 43.2 | 384 | 2 | Q4RJ33 | TETNG |
| 336 | 41 | 43.2 | 387 | 1 | YJFC | ECOLI |
| 337 | 41 | 43.2 | 387 | 2 | Q5PIP6 | SALPA |
| 338 | 41 | 43.2 | 387 | 2 | Q8Z177 | SALMONELLA |
| 339 | 41 | 43.2 | 387 | 2 | Q8ZK95 | SALTY |
| 340 | 41 | 43.2 | 387 | 2 | Q83P32 | SHIFL |
| 341 | 41 | 43.2 | 387 | 2 | Q8XDK6 | ECOS7 |
| 342 | 41 | 43.2 | 400 | 2 | Q8FW29 | BRUSU |
| 343 | 41 | 43.2 | 431 | 2 | Q4INK1 | GIBZE |
| 344 | 41 | 43.2 | 441 | 2 | Q51Y48 | WAGGR |
| 345 | 41 | 43.2 | 496 | 1 | GLPK2 | THEMA |
| 346 | 41 | 43.2 | 501 | 1 | GLPK | DEIRA |
| 347 | 41 | 43.2 | 532 | 2 | Q8BGU0 | MOUSE |
| 348 | 41 | 43.2 | 534 | 2 | Q4QH21 | LEIMA |
| 349 | 41 | 43.2 | 536 | 1 | PPCK | BRUSE |
| 350 | 41 | 43.2 | 536 | 1 | PPCK | BRUSE |
| 351 | 41 | 43.2 | 542 | 2 | Q5UQ24 | MIMIV |
| 352 | 41 | 43.2 | 544 | 2 | Q4MMP6 | BACCE |
| 353 | 41 | 43.2 | 544 | 2 | Q73920 | BACCI |
| 354 | 41 | 43.2 | 566 | 2 | Q55S21 | CRYNE |
| 355 | 41 | 43.2 | 566 | 2 | Q5KHC3 | CRYNE |
| 356 | 41 | 43.2 | 578 | 2 | Q64YP4 | BACPR |
| 357 | 41 | 43.2 | 582 | 2 | Q55Z47 | CRYNE |
| 358 | 41 | 43.2 | 582 | 2 | Q5KNG2 | CRYNE |
| 359 | 41 | 43.2 | 608 | 2 | Q5LSN2 | CHLAB |
| 360 | 41 | 43.2 | 616 | 2 | Q4QRI1 | XENTR |
| 361 | 41 | 43.2 | 620 | 1 | VLCS | RAT |
| 362 | 41 | 43.2 | 620 | 2 | Q66HN6 | RAT |
| 363 | 41 | 43.2 | 632 | 2 | Q4WU86 | ASPFU |
| 364 | 41 | 43.2 | 633 | 2 | Q5B1L1 | EMENI |
| 365 | 41 | 43.2 | 636 | 2 | Q756E3 | ASHGO |
| 366 | 41 | 43.2 | 646 | 2 | Q4MH68 | BACCE |
| 367 | 41 | 43.2 | 646 | 2 | Q6HIG7 | BACHK |
| 368 | 41 | 43.2 | 646 | 2 | Q81D87 | BACCR |
| 369 | 41 | 43.2 | 646 | 2 | Q63B36 | BACCZ |
| 370 | 41 | 43.2 | 646 | 2 | Q737U2 | BACCI |
| 371 | 41 | 43.2 | 646 | 2 | Q81Q80 | BACAN |
| 372 | 41 | 43.2 | 650 | 2 | Q6NRP6 | XENLA |
| 373 | 41 | 43.2 | 652 | 2 | Q6PIU3 | XENTR |
| 374 | 41 | 43.2 | 660 | 2 | Q8RF34 | FUSNN |
| 375 | 41 | 43.2 | 675 | 2 | Q7SIC9 | MAIZE |
| 376 | 41 | 43.2 | 719 | 2 | Q6C9P9 | YARLI |
| 377 | 41 | 43.2 | 725 | 2 | Q55VR0 | CRYNE |
| 378 | 41 | 43.2 | 725 | 2 | Q5KKH9 | CRYNE |
| 379 | 41 | 43.2 | 766 | 2 | Q5BRR1 | EMENI |
| 380 | 41 | 43.2 | 792 | 2 | Q4UCD5 | THEAN |
| 381 | 41 | 43.2 | 806 | 2 | Q4LV04 | 9BURK |
| 382 | 41 | 43.2 | 814 | 2 | Q4V875 | XENLA |
| 383 | 41 | 43.2 | 828 | 1 | DYRK3 | DROME |
| 384 | 41 | 43.2 | 829 | 2 | Q5LJP2 | DROME |
| 385 | 41 | 43.2 | 865 | 2 | P90740 | CAEEL |
| 386 | 41 | 43.2 | 869 | 2 | Q6DCZ0 | XENLA |
| 387 | 41 | 43.2 | 876 | 2 | Q9LAW2 | CLOCL |
| 388 | 41 | 43.2 | 879 | 2 | Q7ABX8 | ECOS7 |
| 389 | 41 | 43.2 | 879 | 2 | Q8XCP4 | ECOS7 |
| 390 | 41 | 43.2 | 988 | 1 | PKC1 | SCHPO |
| 391 | 41 | 43.2 | 1114 | 2 | Q5TAF3 | HUMAN |
| 392 | 41 | 43.2 | 1114 | 2 | Q86XD7 | HUMAN |
| 393 | 41 | 43.2 | 1241 | 2 | Q59FL2 | HUMAN |
| 394 | 41 | 43.2 | 1245 | 1 | NIDO | MOUSE |
| 395 | 41 | 43.2 | 1247 | 1 | NIDO | HUMAN |
| 396 | 41 | 43.2 | 1247 | 2 | Q5TAF2 | HUMAN |

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|--------|--------------|
| Q84S31 | vitis vinif |
| P51614 | vitis vinif |
| Q7MG16 | vibrio vuln |
| Q9H635 | homo sapien |
| Q6K837 | oryza sativ |
| Q6BXT3 | debaromyce |
| Q67815 | aquifex aeo |
| Q7MMK8 | porphyromon |
| Q51518 | canis famil |
| Q8N5D6 | homo sapien |
| Q5V3C7 | haloarcuila |
| Q4RJ33 | tetradodon n |
| P33222 | escherichia |
| Q5PIP6 | salmonella |
| Q8Z177 | salmonella |
| Q8ZK95 | salmonella |
| Q83P32 | shigella fl |
| Q8XDK6 | escherichia |
| Q8FW29 | bruceila su |
| Q4INK1 | gibberella |
| Q51Y48 | magnaporthe |
| Q8X1E4 | thermotoga |
| Q9RT38 | deinococcus |
| Q8BGU0 | m mus muscu |
| Q4QH21 | leishmania |
| PPCK | bruceila me |
| Q8YE41 | bruceila su |
| Q8FY05 | bruceila su |
| Q5UQ24 | mimivirus |
| Q4MMF6 | bacillus ce |
| Q73920 | bacillus ce |
| Q55S21 | cryptococu |
| Q5KHC3 | cryptococu |
| Q64YP4 | bacteroides |
| Q55Z47 | cryptococu |
| Q5KNG2 | cryptococu |
| Q5LSN2 | chlamydomphi |
| Q4QRI1 | xenopus tro |
| P97524 | rattus norv |
| Q66HN6 | rattus norv |
| Q4WU86 | aspergillus |
| Q5B1L1 | aspergillus |
| Q756E3 | ashbya goas |
| Q4MH68 | bacillus ce |
| Q6HIG7 | bacillus th |
| Q81D87 | bacillus ce |
| Q63B36 | bacillus ce |
| Q737U2 | bacillus ce |
| Q81Q80 | bacillus an |
| Q6NRP6 | xenopus lae |
| Q6PIU3 | xenopus tro |
| Q8RF34 | fusobacteri |
| Q7SIC9 | zea mays (m |
| Q6C9P9 | yarrowia li |
| Q55VR0 | cryptococu |
| Q5KKH9 | cryptococu |
| Q5BRR1 | aspergillus |
| Q4UCD5 | theileria a |
| Q4LV04 | burkholderi |
| Q4V875 | xenopus lae |
| P83102 | drosophila |
| Q5LJP2 | drosophila |
| P90740 | caenorhabdi |
| Q6DCZ0 | xenopus lae |
| Q9LAW2 | clostridium |
| Q7ABX8 | escherichia |
| Q8XCP4 | escherichia |
| P36582 | schizosacch |
| Q5TAF3 | homo sapien |
| Q86XD7 | homo sapien |
| Q59FL2 | homo sapien |
| P10493 | mus musculu |
| P14543 | homo sapien |
| Q5TAF2 | homo sapien |

| | | | | | | | | | | | | | | | |
|-----|------|------|------|---|---------------|---------|--------------|-----|----|------|-----|---|--------------|---------|--------------|
| 397 | 41 | 43.2 | 1340 | 2 | Q51C25_ENTHI | O51C25_ | entamoeba h | 470 | 40 | 42.1 | 361 | 2 | Q4XSG8_PLACH | O4XSG8_ | plasmodium |
| 398 | 41 | 43.2 | 1355 | 2 | Q6C4M7_YARLI | O6C4M7_ | yarrowia li | 471 | 40 | 42.1 | 372 | 2 | Q8PKC3_XANAC | Q8PKC3_ | xanthomonas |
| 399 | 41 | 43.2 | 1372 | 2 | Q948C1_ORYSA | Q948C1_ | oryza sativ | 472 | 40 | 42.1 | 383 | 2 | Q92NA9_RHINE | Q92NA9_ | rhizobium m |
| 400 | 41 | 43.2 | 1501 | 1 | CDR1_CANAL | P43071 | candida alb | 473 | 40 | 42.1 | 388 | 2 | Q9GRU2_LEIME | Q9GRU2_ | leishmania |
| 401 | 41 | 43.2 | 1501 | 2 | Q5ANA3_CANAL | Q5ANA3_ | candida alb | 474 | 40 | 42.1 | 388 | 2 | Q4QHG6_LEIMA | Q4QHG6_ | leishmania |
| 402 | 41 | 43.2 | 1846 | 2 | Q6BWN2_DEBHA | Q6BWN2_ | debaryomyce | 475 | 40 | 42.1 | 391 | 2 | Q83CF8_COXBU | Q83CF8_ | coxiiella bu |
| 403 | 41 | 43.2 | 2537 | 2 | Q95P34_MACRS | Q95P34_ | macrobrachi | 476 | 40 | 42.1 | 395 | 2 | Q5QMG7_9CORA | Q5QMG7_ | pigeon coro |
| 404 | 41 | 43.2 | 5276 | 2 | Q7QJA9_ANOGA | Q7QJA9_ | anopheles g | 477 | 40 | 42.1 | 405 | 2 | Q7LGS2_YEAST | Q7LGS2_ | saccharomyc |
| 405 | 40.5 | 42.6 | 122 | 2 | Q9G0H2_9CAUD | Q9G0H2_ | roseophage | 478 | 40 | 42.1 | 409 | 2 | Q92VM2_RHINE | Q92VM2_ | rhizobium m |
| 406 | 40.5 | 42.6 | 139 | 2 | Q7RP21_PLAYO | Q7RP21_ | plasmodium | 479 | 40 | 42.1 | 409 | 2 | Q64FY7_9CORA | Q64FY7_ | avian infec |
| 407 | 40.5 | 42.6 | 219 | 2 | Q6W1S3_BPKV4 | Q6W1S3_ | bacterioph | 480 | 40 | 42.1 | 409 | 2 | Q6DTU5_9CORA | Q6DTU5_ | avian infec |
| 408 | 40.5 | 42.6 | 242 | 2 | Q6PDX5_MOUSE | Q6PDX5_ | mus musculu | 481 | 40 | 42.1 | 409 | 2 | Q9QCQ4_9CORA | Q9QCQ4_ | avian infec |
| 409 | 40.5 | 42.6 | 267 | 2 | Q80X10_MOUSE | Q80X10_ | mus musculu | 482 | 40 | 42.1 | 409 | 2 | Q4G2X2_9CORA | Q4G2X2_ | avian infec |
| 410 | 40.5 | 42.6 | 277 | 2 | Q9SVF5_ARATH | Q9SVF5_ | arabidopsis | 483 | 40 | 42.1 | 410 | 2 | Q9VA30_DROME | Q9VA30_ | drosophila |
| 411 | 40.5 | 42.6 | 433 | 2 | Q9SZP3_ARATH | Q9SZP3_ | arabidopsis | 484 | 40 | 42.1 | 411 | 2 | Q9VZX6_DROME | Q9VZX6_ | drosophila |
| 412 | 40.5 | 42.6 | 520 | 1 | CP4P2_DROME | Q9V557_ | drosophila | 485 | 40 | 42.1 | 412 | 1 | DAD3A_RHILIO | DAD3A_ | rhizobium l |
| 413 | 40.5 | 42.6 | 562 | 2 | Q84VX1_ARATH | Q84VX1_ | arabidopsis | 486 | 40 | 42.1 | 417 | 2 | Q5GMY9_9CORA | Q5GMY9_ | pigeon coro |
| 414 | 40.5 | 42.6 | 589 | 2 | Q4YU51_PLABE | Q4YU51_ | plasmodium | 487 | 40 | 42.1 | 419 | 2 | Q4YUY2_PLABE | Q4YUY2_ | plasmodium |
| 415 | 40.5 | 42.6 | 593 | 2 | Q86G53_PLABE | Q86G53_ | plasmodium | 488 | 40 | 42.1 | 419 | 2 | Q9LQG6_ORYSA | Q9LQG6_ | oryza sativ |
| 416 | 40.5 | 42.6 | 595 | 2 | Q4Y678_PLACH | Q4Y678_ | plasmodium | 489 | 40 | 42.1 | 421 | 2 | Q95T10_DROME | Q95T10_ | drosophila |
| 417 | 40.5 | 42.6 | 738 | 2 | Q7XUQ4_ORYSA | Q7XUQ4_ | oryza sativ | 490 | 40 | 42.1 | 426 | 2 | Q76MR4_POEGU | Q76MR4_ | poephila gu |
| 418 | 40.5 | 42.6 | 864 | 2 | Q8CVM4_ECOL6 | Q8CVM4_ | escherichia | 491 | 40 | 42.1 | 427 | 1 | EXG23_HANAN | EXG23_ | hansenula a |
| 419 | 40.5 | 42.6 | 929 | 2 | Q4RW90_TETNG | Q4RW90_ | tetraodon n | 492 | 40 | 42.1 | 437 | 2 | Q12516_YEAST | Q12516_ | saccharomyc |
| 420 | 40.5 | 42.6 | 938 | 2 | Q7RMR9_PLAYO | Q7RMR9_ | plasmodium | 493 | 40 | 42.1 | 437 | 2 | Q8FM46_COREF | Q8FM46_ | corynebacte |
| 421 | 40 | 42.1 | 70 | 2 | Q4MK34_BACCE | Q4MK34_ | bacillus ce | 494 | 40 | 42.1 | 442 | 2 | Q6BJ53_DEBHA | Q6BJ53_ | debaryomyce |
| 422 | 40 | 42.1 | 78 | 2 | Q862K7_BOVIN | Q862K7_ | bos taurus | 495 | 40 | 42.1 | 451 | 2 | Q4NA38_9MICC | Q4NA38_ | arthrobacte |
| 423 | 40 | 42.1 | 78 | 2 | Q862U7_BOVIN | Q862U7_ | bos taurus | 496 | 40 | 42.1 | 455 | 2 | Q61WH6_CAEBR | Q61WH6_ | caenorhabdi |
| 424 | 40 | 42.1 | 79 | 2 | Q7TUA2_PROMP | Q7TUA2_ | prochloroco | 497 | 40 | 42.1 | 466 | 2 | Q60VC7_CAEBR | Q60VC7_ | caenorhabdi |
| 425 | 40 | 42.1 | 89 | 1 | DYLI_HUMAN | P61285_ | bos taurus | 498 | 40 | 42.1 | 467 | 2 | Q9N3W9_CAEEL | Q9N3W9_ | caenorhabdi |
| 426 | 40 | 42.1 | 89 | 1 | DYLI_BOVIN | P63167_ | homo sapien | 499 | 40 | 42.1 | 476 | 2 | Q4UHI1_THEAN | Q4UHI1_ | theileria a |
| 427 | 40 | 42.1 | 89 | 1 | DYLI_MACFA | P61273_ | macaca fasc | 500 | 40 | 42.1 | 489 | 2 | Q6YV92_ORYSA | Q6YV92_ | oryza sativ |
| 428 | 40 | 42.1 | 89 | 1 | DYLI_MOUSE | P63168_ | mus musculu | 501 | 40 | 42.1 | 502 | 2 | Q9VFF4_DROME | Q9VFF4_ | drosophila |
| 429 | 40 | 42.1 | 89 | 1 | DYLI_RABIT | P63169_ | oryctolagus | 502 | 40 | 42.1 | 504 | 2 | Q4ND37_9MICC | Q4ND37_ | arthrobacte |
| 430 | 40 | 42.1 | 89 | 1 | DYLI_RAT | P63170_ | rattus norv | 503 | 40 | 42.1 | 511 | 2 | Q6YU9_ORYSA | Q6YU9_ | oryza sativ |
| 431 | 40 | 42.1 | 89 | 2 | Q6FGH9_HUMAN | Q6FGH9_ | homo sapien | 504 | 40 | 42.1 | 513 | 2 | Q9XHC6_SOYBN | Q9XHC6_ | glycine max |
| 432 | 40 | 42.1 | 89 | 2 | Q6B859_BOVIN | Q6B859_ | bos taurus | 505 | 40 | 42.1 | 514 | 1 | CP6W1_DROME | CP6W1_ | drosophila |
| 433 | 40 | 42.1 | 89 | 2 | Q4R7J2_MACFA | Q4R7J2_ | macaca fasc | 506 | 40 | 42.1 | 519 | 2 | Q6ZII0_ORYSA | Q6ZII0_ | oryza sativ |
| 434 | 40 | 42.1 | 89 | 2 | Q80Z57_MOUSE | Q80Z57_ | mus musculu | 507 | 40 | 42.1 | 522 | 2 | Q9BMX7_APICA | Q9BMX7_ | aplycia cal |
| 435 | 40 | 42.1 | 89 | 2 | Q9D6F6_MOUSE | Q9D6F6_ | mus musculu | 508 | 40 | 42.1 | 524 | 2 | Q61LJ0_CAEBR | Q61LJ0_ | caenorhabdi |
| 436 | 40 | 42.1 | 89 | 2 | Q5F412_CHICK | Q5F412_ | gallus gall | 509 | 40 | 42.1 | 538 | 2 | Q81EQ4_BACCR | Q81EQ4_ | bacillus ce |
| 437 | 40 | 42.1 | 93 | 2 | Q8WNY6_PIG | Q8WNY6_ | sus scrofa | 510 | 40 | 42.1 | 540 | 2 | Q7T6H9_9LUTE | Q7T6H9_ | sugarcane y |
| 438 | 40 | 42.1 | 98 | 2 | Q5W1J2_BACSK | Q5W1J2_ | bacillus cl | 511 | 40 | 42.1 | 544 | 2 | Q6HK41_BACHK | Q6HK41_ | bacillus th |
| 439 | 40 | 42.1 | 106 | 2 | Q6H818_ORYSA | Q6H818_ | oryza sativ | 512 | 40 | 42.1 | 544 | 2 | Q81RX5_BACAN | Q81RX5_ | bacillus an |
| 440 | 40 | 42.1 | 121 | 2 | Q54RZ0_DICDI | Q54RZ0_ | dictyosteli | 513 | 40 | 42.1 | 547 | 2 | Q63CP1_BACCC | Q63CP1_ | bacillus ce |
| 441 | 40 | 42.1 | 132 | 2 | Q4KSV7_9NUCL | Q4KSV7_ | chrysoideixi | 514 | 40 | 42.1 | 560 | 2 | Q4Q6Z7_LEIMA | Q4Q6Z7_ | leishmania |
| 442 | 40 | 42.1 | 133 | 2 | Q5A7A1_CANAL | Q5A7A1_ | candida alb | 515 | 40 | 42.1 | 567 | 2 | Q6PF09_HUMAN | Q6PF09_ | homo sapien |
| 443 | 40 | 42.1 | 163 | 2 | Q8CIA4_MOUSE | Q8CIA4_ | mus musculu | 516 | 40 | 42.1 | 569 | 2 | Q7CMJ8_BACAN | Q7CMJ8_ | bacillus an |
| 444 | 40 | 42.1 | 173 | 2 | Q8LAA7_ARATH | Q8LAA7_ | arabidopsis | 517 | 40 | 42.1 | 569 | 2 | Q4MP20_BACCE | Q4MP20_ | bacillus ce |
| 445 | 40 | 42.1 | 187 | 2 | Q4XBC3_PLACH | Q4XBC3_ | plasmodium | 518 | 40 | 42.1 | 569 | 2 | Q9X2Y7_BACAN | Q9X2Y7_ | bacillus an |
| 446 | 40 | 42.1 | 192 | 2 | Q6J1C9_9CORA | Q6J1C9_ | avian infec | 519 | 40 | 42.1 | 581 | 2 | Q6AD78_LEITX | Q6AD78_ | leifaonia x |
| 447 | 40 | 42.1 | 192 | 2 | Q6J1D1_9CORA | Q6J1D1_ | avian infec | 520 | 40 | 42.1 | 583 | 2 | Q6C634_YARLI | Q6C634_ | yarrowia li |
| 448 | 40 | 42.1 | 202 | 2 | Q9SUG0_ARATH | Q9SUG0_ | arabidopsis | 521 | 40 | 42.1 | 583 | 2 | Q9VHN8_DROME | Q9VHN8_ | drosophila |
| 449 | 40 | 42.1 | 221 | 2 | Q71YV1_LISNF | Q71YV1_ | listeria mo | 522 | 40 | 42.1 | 602 | 2 | Q8XMT5_CLOPE | Q8XMT5_ | clostridium |
| 450 | 40 | 42.1 | 231 | 2 | Q7RJ37_PLAYO | Q7RJ37_ | plasmodium | 523 | 40 | 42.1 | 604 | 1 | MMP21_XENLA | MMP21_ | xenopus lae |
| 451 | 40 | 42.1 | 232 | 2 | Q65WN8_MANSN | Q65WN8_ | mannheimia | 524 | 40 | 42.1 | 604 | 2 | Q4P139_USTWA | Q4P139_ | ustilago m |
| 452 | 40 | 42.1 | 238 | 2 | Q5PPV3_XENLA | Q5PPV3_ | xenopus lae | 525 | 40 | 42.1 | 619 | 2 | Q74GH2_GEOSL | Q74GH2_ | geobacter s |
| 453 | 40 | 42.1 | 250 | 2 | Q9M1H5_ARATH | Q9M1H5_ | arabidopsis | 526 | 40 | 42.1 | 620 | 1 | VLCS_MOUSE | VLCS_ | homo sapien |
| 454 | 40 | 42.1 | 255 | 2 | Q8EFW6_OCEIH | Q8EFW6_ | oceanobacil | 527 | 40 | 42.1 | 620 | 1 | VLCS_MOUSE | VLCS_ | homo sapien |
| 455 | 40 | 42.1 | 262 | 2 | Q9FH41_ARATH | Q9FH41_ | arabidopsis | 528 | 40 | 42.1 | 620 | 2 | Q53FY6_HUMAN | Q53FY6_ | homo sapien |
| 456 | 40 | 42.1 | 281 | 2 | Q65JB5_BACLD | Q65JB5_ | bacillus li | 529 | 40 | 42.1 | 620 | 2 | Q53GS2_HUMAN | Q53GS2_ | homo sapien |
| 457 | 40 | 42.1 | 284 | 2 | Q6CDI2_YARLI | Q6CDI2_ | yarrowia li | 530 | 40 | 42.1 | 620 | 2 | Q91WV6_MOUSE | Q91WV6_ | mus musculu |
| 458 | 40 | 42.1 | 285 | 2 | Q4HL81_CAMLA | Q4HL81_ | campylobact | 531 | 40 | 42.1 | 620 | 2 | Q5PRD9_BRARE | Q5PRD9_ | brachydanio |
| 459 | 40 | 42.1 | 287 | 2 | Q7BSK2_NEIME | Q7BSK2_ | neisseria m | 532 | 40 | 42.1 | 625 | 2 | Q8AVCS_XENLA | Q8AVCS_ | xenopus lae |
| 460 | 40 | 42.1 | 287 | 2 | Q68217_NEIMA | Q68217_ | neisseria m | 533 | 40 | 42.1 | 650 | 1 | TDRD3_MOUSE | TDRD3_ | mus musculu |
| 461 | 40 | 42.1 | 293 | 2 | Q83DK6_COXBU | Q83DK6_ | coxiiella bu | 534 | 40 | 42.1 | 650 | 2 | Q6P992_HUMAN | Q6P992_ | homo sapien |
| 462 | 40 | 42.1 | 299 | 2 | Q6DYCS_ARATH | Q6DYCS_ | arabidopsis | 535 | 40 | 42.1 | 650 | 2 | Q6NZG7_MOUSE | Q6NZG7_ | mus musculu |
| 463 | 40 | 42.1 | 307 | 2 | Q566X7_BRARE | Q566X7_ | brachydanio | 536 | 40 | 42.1 | 651 | 1 | TDRD3_HUMAN | TDRD3_ | homo sapien |
| 464 | 40 | 42.1 | 315 | 2 | Q8TOS1_DROME | Q8TOS1_ | drosophila | 537 | 40 | 42.1 | 651 | 2 | Q5VUZ2_HUMAN | Q5VUZ2_ | homo sapien |
| 465 | 40 | 42.1 | 322 | 2 | Q7QFH6_ANOGA | Q7QFH6_ | anopheles g | 538 | 40 | 42.1 | 651 | 2 | Q66HCL_RAT | Q66HCL_ | rattus norv |
| 466 | 40 | 42.1 | 328 | 2 | Q5P383_AZOSE | Q5P383_ | azoarcus sp | 539 | 40 | 42.1 | 652 | 2 | Q9VME6_DROME | Q9VME6_ | drosophila |
| 467 | 40 | 42.1 | 340 | 2 | Q4Q149_LEIMA | Q4Q149_ | leishmania | 540 | 40 | 42.1 | 655 | 2 | Q8IM63_PLAP7 | Q8IM63_ | plasmodium |
| 468 | 40 | 42.1 | 343 | 2 | Q6W9J8_MOUSE | Q6W9J8_ | mus musculu | 541 | 40 | 42.1 | 687 | 2 | Q529B3_MAGGR | Q529B3_ | magnaporthe |
| 469 | 40 | 42.1 | 357 | 2 | Q9X221_THEMEA | Q9X221_ | thermotoga | 542 | 40 | 42.1 | 690 | 1 | GS11_CANAL | GS11_ | candida alb |

| | | | | | | | | | | | | | |
|-----|------|------|------|---|--------------|---------------------|-----|------|------|------|---|--------------|---------------------|
| 543 | 40 | 42.1 | 700 | 2 | QBXP08_NEUCR | QBXP08_neurospora | 616 | 39.5 | 41.6 | 1645 | 2 | Q5A667_CANAL | Q5A667_candida alb |
| 544 | 40 | 42.1 | 728 | 2 | QB12W7_PLAF7 | QB12w7 plasmidium | 617 | 39 | 41.1 | 55 | 2 | Q97J23_CLOAB | Q97J23_clostridium |
| 545 | 40 | 42.1 | 741 | 2 | Q5ZM36_CHICK | Q5zme6 gallus gall | 618 | 39 | 41.1 | 56 | 2 | Q9CF95_LACLA | Q9CF95_lactococcus |
| 546 | 40 | 42.1 | 759 | 2 | Q8UW73_9INFA | Q8uwt3 influenza a | 619 | 39 | 41.1 | 67 | 2 | Q5FAB6_NEIGI | Q5fae6 neisseria g |
| 547 | 40 | 42.1 | 759 | 2 | Q8UW76_9INFA | Q8uwt6 influenza a | 620 | 39 | 41.1 | 81 | 2 | Q6L210_PICTO | Q6L210_picrophilus |
| 548 | 40 | 42.1 | 777 | 1 | PTK2_CANGA | Q6tre7 candida gla | 621 | 39 | 41.1 | 81 | 2 | Q92Q68_RHIME | Q92q68 rhizobium m |
| 549 | 40 | 42.1 | 794 | 2 | Q9U110_LEIMA | Q9u110 leishmania | 622 | 39 | 41.1 | 101 | 2 | Q93EH9_HELHP | Q93eh9 helicobacte |
| 550 | 40 | 42.1 | 796 | 1 | COPB2_SCHPO | Q42937 schizosacch | 623 | 39 | 41.1 | 112 | 1 | VPX_HV2G1 | P18045 human immun |
| 551 | 40 | 42.1 | 802 | 2 | Q7XMG8_ORYSA | Q7xmg8 oryza sativ | 624 | 39 | 41.1 | 113 | 1 | HV47_MOUSE | P18023 mus musculus |
| 552 | 40 | 42.1 | 954 | 2 | Q4T7P8_TFTNG | Q4t7p8 tetradodon n | 625 | 39 | 41.1 | 116 | 2 | P96983_RHOCA | P96983 rhodobacter |
| 553 | 40 | 42.1 | 966 | 2 | Q5X4S1_LEGPA | Q5x4s1 legionella | 626 | 39 | 41.1 | 128 | 2 | Q6MT08_MYCMS | Q6mt08 mycoplasma |
| 554 | 40 | 42.1 | 1002 | 1 | INVS2_XENLA | Q7ls21 xenopus lae | 627 | 39 | 41.1 | 143 | 2 | Q64BY4_9ARCH | Q64by4 uncultured |
| 555 | 40 | 42.1 | 1011 | 2 | Q5AD63_CANAL | Q5ad63 candida alb | 628 | 39 | 41.1 | 143 | 2 | Q64DH3_9ARCH | Q64dh3 uncultured |
| 556 | 40 | 42.1 | 1013 | 2 | Q5ADJ2_CANAL | Q5adj2 candida alb | 629 | 39 | 41.1 | 153 | 2 | Q8Y6J3_LISMO | Q8y6j3 listeria mo |
| 557 | 40 | 42.1 | 1055 | 2 | Q5QY28_IDILO | Q5qy28 idiomarina | 630 | 39 | 41.1 | 153 | 2 | Q92AW9_LISIN | Q92aw9 listeria in |
| 558 | 40 | 42.1 | 1073 | 2 | Q6CMG0_KIULA | Q6cmg0 kluyveromyc | 631 | 39 | 41.1 | 156 | 2 | Q71YX6_LISMF | Q71yx6 listeria mo |
| 559 | 40 | 42.1 | 1175 | 2 | Q5UYX8_HALMA | Q5uyx8 haloarcula | 632 | 39 | 41.1 | 170 | 2 | Q81CH7_BACCR | Q81ch7 bacillus ce |
| 560 | 40 | 42.1 | 1246 | 2 | Q6AWJ8_DROME | Q6awj8 drosophila | 633 | 39 | 41.1 | 183 | 2 | Q63AG4_BACCC | Q63ag4 bacillus ce |
| 561 | 40 | 42.1 | 1268 | 2 | Q8IL41_PLAF7 | Q8il41 plasmidium | 634 | 39 | 41.1 | 188 | 2 | Q4MK10_BACCE | Q4mk10 bacillus ce |
| 562 | 40 | 42.1 | 1275 | 2 | Q6L2P1_PICTO | Q6l2p1 picrophilus | 635 | 39 | 41.1 | 190 | 2 | Q52004_9Z2Z2 | Q52004 plasmid pip |
| 563 | 40 | 42.1 | 1290 | 1 | BXC1_CLOBO | P18640 clostridium | 636 | 39 | 41.1 | 190 | 2 | Q79A48_ENTFA | Q79a48 enterococu |
| 564 | 40 | 42.1 | 1291 | 2 | Q3HT3_CLOBO | Q3ht3 clostridium | 637 | 39 | 41.1 | 191 | 2 | Q72QC2_LEPIC | Q72qc2 leptospira |
| 565 | 40 | 42.1 | 1303 | 2 | Q5AOK7_CANAL | Q5aok7 candida alb | 638 | 39 | 41.1 | 201 | 2 | Q97FB4_CLOAB | Q97fb4 clostridium |
| 566 | 40 | 42.1 | 1382 | 2 | Q5KNN0_CRYNE | Q5knn0 cryptococcus | 639 | 39 | 41.1 | 210 | 1 | MOB1_SCHPO | Q94360 schizosacch |
| 567 | 40 | 42.1 | 1382 | 2 | Q5ZB55_CRYNE | Q5zbs5 cryptococcus | 640 | 39 | 41.1 | 210 | 1 | Q83A79_COXBU | Q83a79 coxiella bu |
| 568 | 40 | 42.1 | 1631 | 2 | Q57ZB9_9TRYP | Q57ze9 trypanosoma | 641 | 39 | 41.1 | 221 | 2 | Q8F5S7_LEPIN | Q8f5s7 leptospira |
| 569 | 40 | 42.1 | 1678 | 2 | Q95V09_DROME | Q95v09 drosophila | 642 | 39 | 41.1 | 228 | 2 | Q89C16_BRAJA | Q89c16 bradyrhizob |
| 570 | 40 | 42.1 | 1678 | 2 | Q3NH89_DROME | Q3nh89 drosophila | 643 | 39 | 41.1 | 232 | 1 | UBIG_CHRVO | Q7n291 chromobacte |
| 571 | 40 | 42.1 | 1678 | 2 | Q3V600_DROME | Q3v6q0 drosophila | 644 | 39 | 41.1 | 240 | 1 | GFGL_ANASP | P46016 anabaena sp |
| 572 | 40 | 42.1 | 1723 | 2 | Q60S90_CABBR | Q60s90 caenorhabdi | 645 | 39 | 41.1 | 240 | 1 | Q61PD1_CABBR | Q61pd1 caenorhabdi |
| 573 | 40 | 42.1 | 1857 | 2 | Q54R78_DICDI | Q54r78 dictyosteli | 646 | 39 | 41.1 | 243 | 1 | Y912_METJA | Q58322 methanococc |
| 574 | 40 | 42.1 | 1858 | 1 | P13K2_DICDI | P54674 dictyosteli | 647 | 39 | 41.1 | 249 | 2 | Q63YF5_BURPS | Q63yp5 burkholderi |
| 575 | 40 | 42.1 | 1900 | 2 | Q54K67_DICDI | Q54kf7 dictyosteli | 648 | 39 | 41.1 | 254 | 2 | Q8EMA6_OCEIH | Q8ema6 oceanobacil |
| 576 | 40 | 42.1 | 2040 | 2 | Q7RE46_PLAYO | Q7raf6 plasmidium | 649 | 39 | 41.1 | 258 | 2 | ATHB7_ARATH | P46897 arabidopsis |
| 577 | 40 | 42.1 | 2465 | 2 | Q4RXZ7_TETNG | Q4rxz7 tetradodon n | 650 | 39 | 41.1 | 258 | 2 | Q7ZVS6_LEPIC | Q7zvs6 leptospira |
| 578 | 40 | 42.1 | 3079 | 1 | IRA2_YEAST | P19158 saccharomyc | 651 | 39 | 41.1 | 258 | 2 | Q8F9E0_LEPIN | Q8f9e0 leptospira |
| 579 | 40 | 42.1 | 3452 | 2 | Q3IEA3_PLAF7 | Q3iea3 plasmidium | 652 | 39 | 41.1 | 259 | 1 | CBIF_METJA | Q58973 methanococc |
| 580 | 40 | 42.1 | 4081 | 2 | Q9VW23_DROME | Q9vw23 drosophila | 653 | 39 | 41.1 | 267 | 2 | Q6SVA8_NEOPS | Q6sva8 neoceratodu |
| 581 | 40 | 42.1 | 4538 | 1 | PKSL_BACSU | Q5470 bacillus su | 654 | 39 | 41.1 | 269 | 2 | Q5D8E9_SCHJA | Q5d8e9 schistosoma |
| 582 | 40 | 42.1 | 4543 | 1 | L3P1_CHICK | P98157 gallus gall | 655 | 39 | 41.1 | 274 | 2 | Q65H20_BACLD | Q65h20 bacillus li |
| 583 | 39.5 | 41.6 | 108 | 2 | Q90XW8_9ACTI | Q90xm8 polypterus | 656 | 39 | 41.1 | 276 | 2 | Q5R110_BRARE | Q5r110 brachydanio |
| 584 | 39.5 | 41.6 | 110 | 2 | Q6BM76_DEBHA | Q6bm76 debaryomyce | 657 | 39 | 41.1 | 278 | 1 | PMP1_SCHPO | Q13453 schizosacch |
| 585 | 39.5 | 41.6 | 142 | 2 | Q5F997_NEIGI | Q5f997 neisseria g | 658 | 39 | 41.1 | 279 | 2 | Q734N7_BACCI | Q734n7 bacillus ce |
| 586 | 39.5 | 41.6 | 178 | 2 | Q9AG35_BACTN | Q9ag35 bacteroides | 659 | 39 | 41.1 | 280 | 2 | Q9FK57_ARATH | Q9fk57 arabidopsis |
| 587 | 39.5 | 41.6 | 244 | 2 | Q9AN08_BRAJA | Q9anq8 bradyrhizob | 660 | 39 | 41.1 | 294 | 2 | Q84U85_9LAMI | Q84u85 rehmannia g |
| 588 | 39.5 | 41.6 | 246 | 2 | Q8VU42_ECOLI | Q8vu42 escherichia | 661 | 39 | 41.1 | 294 | 2 | Q662L9_BORGA | Q662l9 borrelia ga |
| 589 | 39.5 | 41.6 | 256 | 2 | Q22F70_MAGGR | Q22fj0 magnaporthe | 662 | 39 | 41.1 | 294 | 2 | Q638N8_BACCC | Q638n8 bacillus ce |
| 590 | 39.5 | 41.6 | 259 | 2 | Q8UVB6_POLSE | Q8uvb6 polypterus n | 663 | 39 | 41.1 | 296 | 2 | Q4LK58_9BURK | Q4lk58 burkholderi |
| 591 | 39.5 | 41.6 | 310 | 2 | Q8MC80_ASPND | Q8mc80 asplenium n | 664 | 39 | 41.1 | 297 | 2 | Q84ZH2_ORYSA | Q84zh2 oryza sativ |
| 592 | 39.5 | 41.6 | 319 | 2 | Q8MC92_MARMI | Q8mc92 marsilea mu | 665 | 39 | 41.1 | 298 | 2 | Q4LXC9_9BURK | Q4lxc9 burkholderi |
| 593 | 39.5 | 41.6 | 346 | 2 | Q5EB71_RAT | Q5eb71 rattus norv | 666 | 39 | 41.1 | 300 | 2 | Q73KK0_TREDE | Q73kk0 treponema d |
| 594 | 39.5 | 41.6 | 437 | 2 | Q5EYC5_TAXBR | Q5eyc5 taxus brevi | 667 | 39 | 41.1 | 303 | 2 | Q5V2S2_HALMA | Q5v2s2 haloarcula |
| 595 | 39.5 | 41.6 | 452 | 2 | Q8M8W2_TAXBR | Q8m8w2 taxus brevi | 668 | 39 | 41.1 | 303 | 2 | Q6Z2F3_PICJA | Q6z2f3 pichia jadi |
| 596 | 39.5 | 41.6 | 462 | 2 | Q9MUC5_TORCL | Q9muc5 torreyia cal | 669 | 39 | 41.1 | 304 | 2 | Q14214_SCHPO | Q14214 schizosacch |
| 597 | 39.5 | 41.6 | 480 | 2 | Q4L7M7_STAHL | Q4l7m7 staphylococ | 670 | 39 | 41.1 | 309 | 2 | Q4HLJ8_CAMLA | Q4hlj8 campylobact |
| 598 | 39.5 | 41.6 | 484 | 2 | Q5YL79_SCIVE | Q5ylt9 sciadophytys | 671 | 39 | 41.1 | 311 | 1 | CHLY_HEYBR | P23472 hevea bras |
| 599 | 39.5 | 41.6 | 495 | 2 | Q5V531_HALMA | Q5v531 haloarcula | 672 | 39 | 41.1 | 312 | 1 | MTX1_CABEL | Q45503 caenorhabdi |
| 600 | 39.5 | 41.6 | 502 | 2 | Q8EYK4_9CONI | Q8eyk4 cephalotaxu | 673 | 39 | 41.1 | 319 | 2 | Q911Q6_PSEAB | Q911q6 pseudomonas |
| 601 | 39.5 | 41.6 | 505 | 2 | Q59H86_HUMAN | Q59he6 homo sapien | 674 | 39 | 41.1 | 323 | 1 | YCU5_SCHPO | Q9y7t1 schizosacch |
| 602 | 39.5 | 41.6 | 509 | 1 | P5BB_ADICA | Q8sfj7 adiantum ca | 675 | 39 | 41.1 | 328 | 2 | Q9J518_FOWPV | Q9j518 fowlpox vir |
| 603 | 39.5 | 41.6 | 508 | 1 | P5BB_POPDE | Q03061 populus del | 676 | 39 | 41.1 | 328 | 2 | Q70GU2_FOWPV | Q70gu2 fowlpox vir |
| 604 | 39.5 | 41.6 | 737 | 2 | Q9P1H2_ENTFA | Q9p1h2 enterococu | 677 | 39 | 41.1 | 329 | 1 | E12B1_METJA | Q57896 methanococc |
| 605 | 39.5 | 41.6 | 737 | 2 | Q82YT5_ENTFA | Q82yt5 enterococu | 678 | 39 | 41.1 | 333 | 2 | Q4FN51_9RICK | Q4fn51 candidatus |
| 606 | 39.5 | 41.6 | 747 | 2 | Q8VT41_ENTFA | Q8vt41 enterococu | 679 | 39 | 41.1 | 341 | 2 | Q89VF5_BRAJA | Q89vf5 bradyrhizob |
| 607 | 39.5 | 41.6 | 752 | 2 | Q8KUC2_ENTFA | Q8kuc2 enterococu | 680 | 39 | 41.1 | 350 | 2 | Q8GIH1_9BACT | Q8gih1 uncultured |
| 608 | 39.5 | 41.6 | 801 | 2 | Q88HB0_PSEPK | Q88hb0 pseudomonas | 681 | 39 | 41.1 | 350 | 2 | Q8GI16_9BACT | Q8gi16 uncultured |
| 609 | 39.5 | 41.6 | 802 | 2 | Q68595_PSEAE | Q68595 pseudomonas | 682 | 39 | 41.1 | 351 | 2 | Q8GIJ3_9BACT | Q8gij3 uncultured |
| 610 | 39.5 | 41.6 | 802 | 2 | Q91648_PSEAE | Q91648 pseudomonas | 683 | 39 | 41.1 | 351 | 1 | Y1472_HABIN | P44206 haemophilus |
| 611 | 39.5 | 41.6 | 815 | 1 | REM5_HUMAN | P52756 homo sapien | 684 | 39 | 41.1 | 352 | 2 | Q98DF1_RHILO | Q98df1 rhizobium l |
| 612 | 39.5 | 41.6 | 1259 | 2 | Q932J7_ENTFA | Q932j7 enterococu | 685 | 39 | 41.1 | 362 | 2 | Q5N4B2_SYNP6 | Q5n4b2 synecococc |
| 613 | 39.5 | 41.6 | 1427 | 2 | Q34UV2_DICDI | Q34uv2 dictyosteli | 686 | 39 | 41.1 | 363 | 1 | SPC42_YEAST | P36094 saccharomyc |
| 614 | 39.5 | 41.6 | 1543 | 2 | Q55X09_CRYNE | Q55xd9 cryptococcus | 687 | 39 | 41.1 | 378 | 2 | Q58FT6_ARATH | Q58ft6 arabidopsis |
| 615 | 39.5 | 41.6 | 1543 | 2 | Q5KMJ4_CRYNE | Q5kmj4 cryptococcus | 688 | 39 | 41.1 | 379 | 1 | SGAA_METEX | P55819 methylobact |

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|-----|----|------|-----|---|---------------|---------------------|-----|------|------|------|---|--------------|---------------------|
| 689 | 39 | 41.1 | 379 | 2 | Q8KMJ8_METDI | Q8kmj8 methylobact | 762 | 39 | 41.1 | 832 | 2 | O85996_SPHAR | O85996 sphingomona |
| 690 | 39 | 41.1 | 403 | 2 | P96773_HAEUD | P96773 haemophilus | 763 | 39 | 41.1 | 839 | 1 | Y1369_HAETN | P45182 haemophilus |
| 691 | 39 | 41.1 | 407 | 2 | O65D16_BACLD | O65d16 bacillus li | 764 | 39 | 41.1 | 917 | 2 | Q9BXU6_HUMAN | Q9bxu6 homo sapien |
| 692 | 39 | 41.1 | 417 | 2 | O5B0C8_EMENI | O5b0c8 aspergillus | 765 | 39 | 41.1 | 920 | 2 | Q5QRI1_HUMAN | Q5qri1 homo sapien |
| 693 | 39 | 41.1 | 423 | 2 | O5MP44_MOUSE | O5mp44 mus musculus | 766 | 39 | 41.1 | 924 | 1 | CDC13_YEAST | P32797 saccharomyc |
| 694 | 39 | 41.1 | 426 | 1 | CGED_BACSU | CGed bacillus su | 767 | 39 | 41.1 | 925 | 1 | O8IYF3_HUMAN | O8iyf3 homo sapien |
| 695 | 39 | 41.1 | 433 | 2 | O5AK13_CANAL | O5ak13 candida alb | 768 | 39 | 41.1 | 940 | 2 | Q96LZ4_HUMAN | Q96lza4 homo sapien |
| 696 | 39 | 41.1 | 438 | 2 | O6CR05_KLULA | O6cr05 kluyveromyc | 769 | 39 | 41.1 | 947 | 2 | Q7QVB6_GIALA | Q7qvb6 giardia lam |
| 697 | 39 | 41.1 | 451 | 2 | O5V5W2_HALMA | O5v5w2 haloarcula | 770 | 39 | 41.1 | 1003 | 2 | O8TNK1_METAC | O8tnk1 methanosarc |
| 698 | 39 | 41.1 | 451 | 2 | Q9X2G4_HELVI | Q9x2g4 heliothrix v | 771 | 39 | 41.1 | 1017 | 2 | Q8SQJ6_ENCCU | Q8sqj6 encephalito |
| 699 | 39 | 41.1 | 464 | 2 | O8UF31_AGRF5 | O8uf31 agrobacteri | 772 | 39 | 41.1 | 1030 | 2 | Q6FVW5_CANGA | O6fvw5 candida gla |
| 700 | 39 | 41.1 | 466 | 2 | O5JDQ9_PYROCO | O5jdq9 pyrococcus | 773 | 39 | 41.1 | 1052 | 2 | Q6NGD7_CORDI | O6ngd7 corynebacte |
| 701 | 39 | 41.1 | 470 | 2 | Q7X2L8_SPHEL | Q7x2l8 sphingomona | 774 | 39 | 41.1 | 1090 | 2 | Q4YTE4_PLABE | Q4yte4 plasmodium |
| 702 | 39 | 41.1 | 471 | 2 | O55E11_DICDI | O55e11 dictyosteli | 775 | 39 | 41.1 | 1101 | 2 | O8AB16_BACTN | O8ab16 bacteroides |
| 703 | 39 | 41.1 | 471 | 2 | O97GC7_CLOAB | O97gc7 clostridium | 776 | 39 | 41.1 | 1114 | 2 | O8I352_PLAF7 | O8i352 plasmodium |
| 704 | 39 | 41.1 | 473 | 2 | O82D73_STRAW | O82d73 streptomyc | 777 | 39 | 41.1 | 1121 | 2 | Q4J4R5_AZOVI | Q4j4r5 azobacter |
| 705 | 39 | 41.1 | 479 | 2 | O8S5I4_ORYSA | O8s5i4 oryza sativ | 778 | 39 | 41.1 | 1136 | 2 | Q4XYW5_PLACH | Q4xyw5 plasmodium |
| 706 | 39 | 41.1 | 485 | 2 | O4N9B8_THEPA | O4n9b8 theileria p | 779 | 39 | 41.1 | 1141 | 2 | Q7PT88_ANOGA | Q7pt88 anopheles g |
| 707 | 39 | 41.1 | 485 | 2 | O51AF2_ENTHI | O51af2 entamoeba h | 780 | 39 | 41.1 | 1200 | 2 | Q91O54_HETFR | Q91o54 heterodontu |
| 708 | 39 | 41.1 | 490 | 2 | O5YPP7_NOCFA | O5ypp7 nocardia fa | 781 | 39 | 41.1 | 1202 | 2 | Q7O7F2_ANOGA | Q7o7f2 anopheles g |
| 709 | 39 | 41.1 | 496 | 1 | GLPK_BACSU | P18157 bacillus su | 782 | 39 | 41.1 | 1261 | 2 | O7RKG5_PLAYO | O7rkg5 plasmodium |
| 710 | 39 | 41.1 | 496 | 2 | O6KX8_HUMAN | O6kx8 homo sapien | 783 | 39 | 41.1 | 1276 | 2 | Q8SQ26_PSEPK | Q8sq26 pseudomonas |
| 711 | 39 | 41.1 | 496 | 2 | O8TID4_DICDI | O8tid4 dictyosteli | 784 | 39 | 41.1 | 1285 | 2 | Q6UNF4_ICTPU | Q6unf4 ictaluruss p |
| 712 | 39 | 41.1 | 496 | 2 | O8GN30_BACNA | O8gn30 bacillus su | 785 | 39 | 41.1 | 1321 | 2 | Q6CWE1_KLULA | Q6cwe1 kluyveromyc |
| 713 | 39 | 41.1 | 507 | 2 | O9ATV1_LOLRI | O9atv1 lolium rigi | 786 | 39 | 41.1 | 1361 | 1 | K1199_HUMAN | Q8wu13 homo sapien |
| 714 | 39 | 41.1 | 507 | 2 | O7X7X4_ORYSA | O7x7x4 oryza sativ | 787 | 39 | 41.1 | 1361 | 1 | K1199_MOUSE | O8bi06 mus musculu |
| 715 | 39 | 41.1 | 508 | 1 | GLPK_MYCLE | O9c81 mycobacteri | 788 | 39 | 41.1 | 1361 | 2 | O6L9J5_HUMAN | O6lj95 homo sapien |
| 716 | 39 | 41.1 | 508 | 2 | O6YU8_ORYSA | O6yu8 oryza sativ | 789 | 39 | 41.1 | 1523 | 2 | O4FPJ7_9RICK | Q4fpj7 candidatus |
| 717 | 39 | 41.1 | 509 | 2 | O8TQO4_METAC | O8tqo4 methanosarc | 790 | 39 | 41.1 | 1541 | 2 | Q4P421_USTMA | Q4p421 ustilago ma |
| 718 | 39 | 41.1 | 509 | 2 | O524B9_MAGGR | O524b9 magnaporth | 791 | 39 | 41.1 | 1600 | 2 | Q4XWP5_PLACH | Q4xwp5 plasmodium |
| 719 | 39 | 41.1 | 510 | 2 | O9ATV2_LOLRI | O9atv2 lolium rigi | 792 | 39 | 41.1 | 1645 | 2 | O5S4N3_ICTPU | O5s4n3 ictaluruss p |
| 720 | 39 | 41.1 | 512 | 2 | O60TT6_CAEBR | O60tt6 caenorhabdi | 793 | 39 | 41.1 | 1650 | 2 | O9QVT6_9MURI | O9qvt6 rattus sp. |
| 721 | 39 | 41.1 | 513 | 2 | O4WA77_ARATH | O4wa77 arabidopsis | 794 | 39 | 41.1 | 1661 | 2 | O7QX84_GIALA | O7qx84 giardia lam |
| 722 | 39 | 41.1 | 513 | 2 | O9SOY7_ARATH | O9soy7 arabidopsis | 795 | 39 | 41.1 | 1662 | 2 | Q9F162_ARATH | Q9f162 arabidopsis |
| 723 | 39 | 41.1 | 523 | 2 | O51WZ0_MAGGR | O51wz0 magnaporth | 796 | 39 | 41.1 | 1999 | 2 | Q4YAG7_PLABE | Q4yag7 plasmodium |
| 724 | 39 | 41.1 | 534 | 2 | O7XE29_ORYSA | O7xe29 oryza sativ | 797 | 39 | 41.1 | 2156 | 2 | Q4UUY1_XANCP | Q4uuy1 xanthomonas |
| 725 | 39 | 41.1 | 535 | 2 | O6A1B2_CHITE | O6a1b2 chironomus | 798 | 39 | 41.1 | 2207 | 2 | O88GN0_PSEPK | O88gn0 pseudomonas |
| 726 | 39 | 41.1 | 539 | 2 | O6ZIG7_ORYSA | O6zig7 oryza sativ | 799 | 39 | 41.1 | 2224 | 2 | O8P8Y4_XANCP | O8p8y4 xanthomonas |
| 727 | 39 | 41.1 | 542 | 2 | O7VXQ3_BORPE | O7vxq3 bordetella | 800 | 39 | 41.1 | 2264 | 2 | O7QV56_GIALA | O7qv56 giardia lam |
| 728 | 39 | 41.1 | 542 | 2 | O7W647_BORPA | O7w647 bordetella | 801 | 39 | 41.1 | 2348 | 2 | O5Z1P8_NOCFA | O5z1p8 nocardia fa |
| 729 | 39 | 41.1 | 542 | 2 | O7W113_BORBR | O7w113 bordetella | 802 | 39 | 41.1 | 2474 | 2 | O6ERT4_MOUSE | O6ert4 mus musculu |
| 730 | 39 | 41.1 | 549 | 2 | O7TPX4_MOUSE | O7tpx4 mus musculu | 803 | 39 | 41.1 | 2551 | 2 | O5S9A9_DICDI | O5s9a9 dictyosteli |
| 731 | 39 | 41.1 | 550 | 2 | O4P495_USTMA | O4p495 ustilago ma | 804 | 39 | 41.1 | 2551 | 2 | O86IG0_DICDI | O86igo dictyosteli |
| 732 | 39 | 41.1 | 554 | 2 | Q8RR94_CLOHA | Q8rr94 clostridium | 805 | 39 | 41.1 | 3042 | 2 | O7QZ61_GIALA | O7qz61 giardia lam |
| 733 | 39 | 41.1 | 558 | 2 | O4EE0_DICDI | O4ee0 dictyosteli | 806 | 39 | 41.1 | 4660 | 1 | L8P2_RAT | P98158 rattus norv |
| 734 | 39 | 41.1 | 560 | 1 | INAR1_BOVIN | O04790 bos taurus | 807 | 39 | 41.1 | 4889 | 2 | Q4Z3Z9_PLABE | Q4z3z9 plasmodium |
| 735 | 39 | 41.1 | 571 | 2 | O5P9P2_CANAL | O5p9p2 candida alb | 808 | 39 | 41.1 | 5054 | 2 | Q7RPJ1_PLAYO | Q7rpj1 plasmodium |
| 736 | 39 | 41.1 | 601 | 2 | O5OVH1_ENTHI | O5ovh1 entamoeba h | 809 | 38.5 | 40.5 | 136 | 2 | Q9MDD1_9NEOB | Q9mdd1 limnodynast |
| 737 | 39 | 41.1 | 608 | 2 | O5DY60_VIBF1 | O5dy60 vibrio fies | 810 | 38.5 | 40.5 | 136 | 2 | Q9MDU2_LIMFT | Q9mdu2 limnodynast |
| 738 | 39 | 41.1 | 629 | 2 | O5BBE3_EMENI | O5bbe3 aspergillus | 811 | 38.5 | 40.5 | 180 | 2 | O54FF8_DICDI | O54ff8 dictyosteli |
| 739 | 39 | 41.1 | 631 | 2 | O6DB48_ERWCT | O6db48 erwinia car | 812 | 38.5 | 40.5 | 199 | 2 | O5DA15_SCHJA | O5da15 schistosoma |
| 740 | 39 | 41.1 | 634 | 2 | O22143_ARATH | O22143 arabidopsis | 813 | 38.5 | 40.5 | 202 | 2 | Q9X7H3_9BACT | Q9x7h3 prevotella |
| 741 | 39 | 41.1 | 637 | 1 | PARP2_ARATH | Q11207 arabidopsis | 814 | 38.5 | 40.5 | 215 | 2 | Q8W8U5_9NEOB | Q8w8u5 limnodynast |
| 742 | 39 | 41.1 | 648 | 2 | O61SW6_CAEBR | O61sw6 caenorhabdi | 815 | 38.5 | 40.5 | 215 | 2 | Q8W8X8_9NEOB | Q8w8x8 limnodynast |
| 743 | 39 | 41.1 | 648 | 2 | Q29094_PIG | O29094 sus scrofa | 816 | 38.5 | 40.5 | 215 | 2 | O8WFD6_9NEOB | Q8wfd6 limnodynast |
| 744 | 39 | 41.1 | 655 | 2 | O9PR74_URRPA | O9pr74 ureaplasma | 817 | 38.5 | 40.5 | 241 | 2 | O8DJZ4_SYNEL | O8djz4 synschochoc |
| 745 | 39 | 41.1 | 659 | 2 | O6PSY5_CANGA | O6psy5 candida gla | 818 | 38.5 | 40.5 | 246 | 2 | O7RG28_PLAYO | O7rg28 plasmodium |
| 746 | 39 | 41.1 | 672 | 2 | O851R1_ORYSA | O851r1 oryza sativ | 819 | 38.5 | 40.5 | 306 | 2 | Q5FFH9_EHRRG | Q5ffh9 ehrlichia r |
| 747 | 39 | 41.1 | 680 | 2 | O8AAI4_BACTN | O8aai4 bacteroides | 820 | 38.5 | 40.5 | 306 | 2 | Q5HBU2_EHRRW | Q5hbu2 ehrlichia r |
| 748 | 39 | 41.1 | 712 | 2 | Q21593_CABEL | Q21593 caenorhabdi | 821 | 38.5 | 40.5 | 310 | 1 | VU84_HBV7J | P52534 human herpe |
| 749 | 39 | 41.1 | 727 | 2 | O4HWK8_GIBZE | O4hwk8 gibberella | 822 | 38.5 | 40.5 | 310 | 2 | O56298_9BETA | O56298 human herpe |
| 750 | 39 | 41.1 | 730 | 2 | O6MNJ6_BDEBA | O6mnj6 bdellovibri | 823 | 38.5 | 40.5 | 314 | 2 | O6T2Z8_SOYBN | O6t2z8 glycine max |
| 751 | 39 | 41.1 | 741 | 1 | TKTC_SULTU | O43848 solanum tub | 824 | 38.5 | 40.5 | 339 | 2 | Q7N1P9_PHOLL | Q7n1p9 photorhabdu |
| 752 | 39 | 41.1 | 754 | 2 | O5JOQ6_HUMAN | O5jqo6 homo sapien | 825 | 38.5 | 40.5 | 364 | 2 | Q8GZ94_ARATH | Q8gz94 arabidopsis |
| 753 | 39 | 41.1 | 759 | 2 | O6E3M4_9INFA | O6e3m4 influenza a | 826 | 38.5 | 40.5 | 364 | 2 | Q94CH6_RCMVM | Q94ch6 arabidopsis |
| 754 | 39 | 41.1 | 759 | 2 | O6E3M5_9INFA | O6e3m5 influenza a | 827 | 38.5 | 40.5 | 390 | 2 | Q9DW46_RCMVM | Q9dw46 rat cytomeg |
| 755 | 39 | 41.1 | 765 | 2 | O75CG0_ASHGO | O75cgo ashbya goss | 828 | 38.5 | 40.5 | 407 | 2 | O8BL79_MOUSE | O8bl79 mus musculu |
| 756 | 39 | 41.1 | 779 | 2 | O7RXK0_NEUCR | O7rxk0 neurospora | 829 | 38.5 | 40.5 | 409 | 2 | O51U07_MAGGR | O51u07 magnaporth |
| 757 | 39 | 41.1 | 803 | 2 | O9N691_PYROC | O9n691 pyrodictium | 830 | 38.5 | 40.5 | 419 | 2 | O4MTK5_BACCE | O4mtk5 bacillus ce |
| 758 | 39 | 41.1 | 809 | 2 | O9N3K6_CABEL | O9n3k6 caenorhabdi | 831 | 38.5 | 40.5 | 419 | 2 | Q6HEF3_BACHK | Q6hef3 bacillus th |
| 759 | 39 | 41.1 | 811 | 2 | O8A698_BACTN | O8a698 bacteroides | 832 | 38.5 | 40.5 | 419 | 2 | Q731V1_BACCI | Q731v1 bacillus ce |
| 760 | 39 | 41.1 | 822 | 2 | O41589_GIBZEA | O41589 gibberella | 833 | 38.5 | 40.5 | 419 | 2 | Q635R6_BACCC | Q635r6 bacillus ce |
| 761 | 39 | 41.1 | 831 | 2 | O50076_9CLOT | O50076 clostridium | 834 | 38.5 | 40.5 | 419 | 2 | Q81ML6_BACAN | Q81ml8 bacillus an |

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|-----|------|------|------|---|---------------|---------------------|
| 835 | 38.5 | 40.5 | 438 | 2 | Q1DC7_GIBZE | Q1dc7 gibberella |
| 836 | 38.5 | 40.5 | 447 | 2 | Q7N177 PHOLL | Q7n177 photorhabdu |
| 837 | 38.5 | 40.5 | 448 | 2 | Q5XD23 STRP6 | Q5xd23 streptococc |
| 838 | 38.5 | 40.5 | 448 | 2 | Q9A1J7 STRPY | Q9a1j7 streptococc |
| 839 | 38.5 | 40.5 | 448 | 2 | Q8P2Q2 STRP8 | Q8p2q2 streptococc |
| 840 | 38.5 | 40.5 | 448 | 2 | Q8K8P8 STRP3 | Q8k8p8 streptococc |
| 841 | 38.5 | 40.5 | 480 | 2 | Q5HN22 STAEQ | Q5hn22 staphylococ |
| 842 | 38.5 | 40.5 | 489 | 2 | Q8CR73 STABP | Q8cr73 staphylococ |
| 843 | 38.5 | 40.5 | 508 | 2 | Q8A2F6 BACTN | Q8a2f6 bacteroides |
| 844 | 38.5 | 40.5 | 552 | 2 | Q4WUX7 ASPFU | Q4wux7 aspergillus |
| 845 | 38.5 | 40.5 | 553 | 2 | Q52116 MAGGR | Q52116 magnaporthe |
| 846 | 38.5 | 40.5 | 570 | 2 | Q415H9 GIBZE | Q415h9 gibberella |
| 847 | 38.5 | 40.5 | 613 | 2 | Q8K2N0 MOUSE | Q8k2n0 mus musculu |
| 848 | 38.5 | 40.5 | 666 | 1 | DNAX1 PROMA | Q7vc04 prochloroco |
| 849 | 38.5 | 40.5 | 700 | 2 | Q67RY3 SYMTH | Q67ry3 symbiobacte |
| 850 | 38.5 | 40.5 | 709 | 2 | Q6R5P1 9CREN | Q6r5p1 metallospira |
| 851 | 38.5 | 40.5 | 716 | 2 | Q52314 MAGGR | Q52314 magnaporthe |
| 852 | 38.5 | 40.5 | 730 | 2 | Q9LQ85 ARATH | Q9lq85 arabidopsis |
| 853 | 38.5 | 40.5 | 779 | 2 | Q7RM79 PLAYO | Q7rm79 plasmodium |
| 854 | 38.5 | 40.5 | 807 | 2 | Q7Y2E6 9CAUD | Q7y2e6 bacteriophia |
| 855 | 38.5 | 40.5 | 848 | 2 | Q8BLB3 MOUSE | Q8blb3 mus musculu |
| 856 | 38.5 | 40.5 | 870 | 2 | Q75UG7 BACSH | Q75ug7 bacillus sp |
| 857 | 38.5 | 40.5 | 870 | 2 | Q03988 BACSH | Q03988 bacillus sp |
| 858 | 38.5 | 40.5 | 1050 | 2 | Q8I106 PLA77 | Q8i106 plasmodium |
| 859 | 38.5 | 40.5 | 1121 | 2 | Q8K298 MOUSE | Q8k298 mus musculu |
| 860 | 38.5 | 40.5 | 1316 | 2 | Q4S220 TETNG | Q4s220 tetraodon n |
| 861 | 38 | 40.0 | 43 | 2 | Q45320 BACME | Q45320 bacillus me |
| 862 | 38 | 40.0 | 50 | 2 | Q57G92 SALCH | Q57g92 salmonella |
| 863 | 38 | 40.0 | 50 | 2 | Q57PM44 SALPA | Q57pm44 salmonella |
| 864 | 38 | 40.0 | 50 | 2 | Q8Z0X9 SALTI | Q8z0x9 salmonella |
| 865 | 38 | 40.0 | 54 | 2 | Q5B2U0 SCHJA | Q5b2u0 schistosoma |
| 866 | 38 | 40.0 | 77 | 2 | Q3ULU7 9CAUD | Q3ulu7 lactobacilli |
| 867 | 38 | 40.0 | 86 | 2 | Q854A8 9CAUD | Q854a8 mycobacteri |
| 868 | 38 | 40.0 | 88 | 2 | Q7UL12 RHOBA | Q7ul12 rhodopirell |
| 869 | 38 | 40.0 | 95 | 2 | Q2P912 BACST | Q2p912 bacillus st |
| 870 | 38 | 40.0 | 99 | 2 | Q5L3W3 GEOKA | Q5l3w3 geobacillus |
| 871 | 38 | 40.0 | 100 | 2 | Q8TK59 METAC | Q8tk59 methanosarc |
| 872 | 38 | 40.0 | 107 | 2 | Q8WY21 HUMAN | Q8wy21 homo sapien |
| 873 | 38 | 40.0 | 109 | 2 | Q6B868 9ACAR | Q6b868 ixodes paci |
| 874 | 38 | 40.0 | 109 | 2 | Q4PM75 IXOSC | Q4pm75 ixodes scap |
| 875 | 38 | 40.0 | 109 | 2 | Q4JIM6 DERVA | Q4jim6 dermacentor |
| 876 | 38 | 40.0 | 110 | 2 | Q5AC31 CANAL | Q5ac31 candida alb |
| 877 | 38 | 40.0 | 112 | 2 | Q5FN96 GLUOX | Q5fn96 gluconobact |
| 878 | 38 | 40.0 | 115 | 2 | Q65XS2 ORYSA | Q65xs2 oryza sativ |
| 879 | 38 | 40.0 | 116 | 2 | Q5UEA8 ANOGA | Q5uea8 anopheles g |
| 880 | 38 | 40.0 | 117 | 1 | HV62 MOUSE | P18533 mus musculu |
| 881 | 38 | 40.0 | 129 | 2 | Q4QS36 IPOAL | Q4qs36 ipomoea alb |
| 882 | 38 | 40.0 | 132 | 2 | Q4QS93 9ASTE | Q4qs93 ipomoea lin |
| 883 | 38 | 40.0 | 134 | 2 | Q4QS92 IPOHE | Q4qs92 ipomoea hed |
| 884 | 38 | 40.0 | 134 | 2 | Q4QS94 IPONI | Q4qs94 ipomoea nil |
| 885 | 38 | 40.0 | 142 | 2 | Q4QS91 IPOPU | Q4qs91 ipomoea pur |
| 886 | 38 | 40.0 | 143 | 2 | Q5ESN1 VIBF1 | Q5esn1 vibrio fisc |
| 887 | 38 | 40.0 | 147 | 1 | UBC4 CANAL | P43102 candida alb |
| 888 | 38 | 40.0 | 148 | 2 | Q15B7 FSEAE | Q15b7 pseudomonas |
| 889 | 38 | 40.0 | 154 | 2 | Q7N1X2 PHOLL | Q7n1x2 photorhabdu |
| 890 | 38 | 40.0 | 163 | 2 | Q6YQ94 ONYPE | Q6yq94 onion yello |
| 891 | 38 | 40.0 | 169 | 2 | Q5XM66 ANOGA | Q5xm66 anopheles g |
| 892 | 38 | 40.0 | 175 | 2 | Q5Y199 9ZZZZ | Q5y199 uncultured |
| 893 | 38 | 40.0 | 179 | 2 | Q8N4G4 HUMAN | Q8n4g4 homo sapien |
| 894 | 38 | 40.0 | 185 | 2 | Q4XW11 PLACH | Q4xw11 plasmodium |
| 895 | 38 | 40.0 | 185 | 2 | Q75H10 ORYSA | Q75h10 oryza sativ |
| 896 | 38 | 40.0 | 195 | 2 | Q8L453 ORYSA | Q8l453 oryza sativ |
| 897 | 38 | 40.0 | 201 | 2 | Q5W1X7 BACSK | Q5w1x7 bacillus cl |
| 898 | 38 | 40.0 | 201 | 2 | Q4TGDI TETNG | Q4tgd1 tetraodon n |
| 899 | 38 | 40.0 | 202 | 2 | Q5VKP0 9RHAB | Q5vkp0 west caucas |
| 900 | 38 | 40.0 | 205 | 2 | Q8QNG3 9PHYC | Q8qng3 ectocarpus |
| 901 | 38 | 40.0 | 213 | 2 | Q9CKQ6 PASMU | Q9ckq6 pasteurella |
| 902 | 38 | 40.0 | 215 | 2 | Q4WPH7 ASPFU | Q4wph7 aspergillus |
| 903 | 38 | 40.0 | 216 | 2 | Q57848 PYRHO | Q57848 pyrococcus |
| 904 | 38 | 40.0 | 218 | 2 | Q5AK12 DESPS | Q5ak12 desulfotale |
| 905 | 38 | 40.0 | 219 | 2 | Q5DAC0 SCHJA | Q5dac0 schistosoma |
| 906 | 38 | 40.0 | 219 | 2 | Q9PBR3 XYLFA | Q9pbr3 xylella fas |
| 907 | 38 | 40.0 | 220 | 2 | Q56UG2 LYMAE | Q56ug2 lymanaea sta |

| | | | | | | |
|-----|----|------|-----|---|---------------|--------------------|
| 908 | 38 | 40.0 | 220 | 2 | Q86JW1 DICDI | Q86jw1 dictyosteli |
| 909 | 38 | 40.0 | 227 | 2 | Q9BJC9 BRUMA | Q9bjc9 brugia mala |
| 910 | 38 | 40.0 | 227 | 2 | Q8UG18 AGRT5 | Q8ug18 agrobacteri |
| 911 | 38 | 40.0 | 230 | 2 | Q75EC6 ASHGO | Q75ec6 ashbya goss |
| 912 | 38 | 40.0 | 230 | 2 | Q8NR72 CORGL | Q8nr72 corynebacte |
| 913 | 38 | 40.0 | 233 | 2 | Q83D53 COXBU | Q83d53 coxiella bu |
| 914 | 38 | 40.0 | 237 | 2 | Q8A1F1 BACTN | Q8a1f1 bacteroides |
| 915 | 38 | 40.0 | 240 | 1 | VANR VIBAN | P74946 vibrio angu |
| 916 | 38 | 40.0 | 240 | 2 | Q6WSA1 NOCLA | Q6wsa1 nocardia la |
| 917 | 38 | 40.0 | 243 | 2 | Q6WSA6 NOCLA | Q6wsa6 nocardia la |
| 918 | 38 | 40.0 | 245 | 2 | Q7RKQ3 PLAYO | Q7rkq3 plasmodium |
| 919 | 38 | 40.0 | 247 | 2 | Q7P187 CHRVO | Q7p187 chromobacte |
| 920 | 38 | 40.0 | 258 | 2 | Q64X27 BACFR | Q64x27 bacteroides |
| 921 | 38 | 40.0 | 260 | 2 | Q89YY9 BACTN | Q89yy9 bacteroides |
| 922 | 38 | 40.0 | 265 | 2 | Q7RCF4 PLAYO | Q7rcf4 plasmodium |
| 923 | 38 | 40.0 | 265 | 2 | Q737E7 BACCI | Q737e7 bacillus ce |
| 924 | 38 | 40.0 | 267 | 2 | Q4HU65 GIBZE | Q4hu65 gibberella |
| 925 | 38 | 40.0 | 269 | 2 | Q51H29 ENTHI | Q51h29 entamoeba h |
| 926 | 38 | 40.0 | 270 | 1 | FPG NITEU | Q82812 nitrosomona |
| 927 | 38 | 40.0 | 272 | 2 | Q4QS21 IPOPU | Q4qs21 ipomoea pur |
| 928 | 38 | 40.0 | 276 | 2 | Q937L7 9CYAN | Q937l7 uncultured |
| 929 | 38 | 40.0 | 276 | 2 | Q937L8 9CYAN | Q937l8 uncultured |
| 930 | 38 | 40.0 | 279 | 1 | ATPG MYCGE | P47640 mycoplasma |
| 931 | 38 | 40.0 | 282 | 2 | Q4S1E8 TETNG | Q4s1e8 tetraodon n |
| 932 | 38 | 40.0 | 286 | 2 | Q5CYU8 CRYPV | Q5cyu8 cryptospori |
| 933 | 38 | 40.0 | 286 | 2 | Q5CF61 CRYHO | Q5cf61 cryptospori |
| 934 | 38 | 40.0 | 289 | 2 | Q7NB44 MYCGA | Q7nb44 mycoplasma |
| 935 | 38 | 40.0 | 290 | 2 | Q51169 BORBU | Q51169 borrelia bu |
| 936 | 38 | 40.0 | 291 | 2 | Q13844 SCHPO | Q13844 schizosacch |
| 937 | 38 | 40.0 | 294 | 1 | PET54 SACHA | Q13364 saccharomyc |
| 938 | 38 | 40.0 | 294 | 2 | Q5LGS3 BACFN | Q5lgs3 bacteroides |
| 939 | 38 | 40.0 | 295 | 2 | Q4MQW4 BACCE | Q4mqw4 bacillus ce |
| 940 | 38 | 40.0 | 295 | 2 | Q6HNR5 BACHK | Q6hnr5 bacillus th |
| 941 | 38 | 40.0 | 295 | 2 | Q73DV9 BACCI | Q73dv9 bacillus ce |
| 942 | 38 | 40.0 | 295 | 2 | Q813Z4 BACCR | Q813z4 bacillus ce |
| 943 | 38 | 40.0 | 295 | 2 | Q81YT6 BACAN | Q81yt6 bacillus an |
| 944 | 38 | 40.0 | 295 | 2 | Q63GA1 BACCZ | Q63ga1 bacillus ce |
| 945 | 38 | 40.0 | 296 | 2 | Q7MC52 VIBVU | Q7mc52 vibrio vuln |
| 946 | 38 | 40.0 | 297 | 2 | Q5AUI5 BMENI | Q5aui5 aspergillus |
| 947 | 38 | 40.0 | 297 | 2 | Q9PS44 VITVI | Q9ps44 vitis vinif |
| 948 | 38 | 40.0 | 297 | 2 | Q88H48 FSEPK | Q88h48 pseudomonas |
| 949 | 38 | 40.0 | 298 | 2 | Q8XQS3 RALSO | Q8xqs3 ralstonia s |
| 950 | 38 | 40.0 | 304 | 2 | Q9N120 RABIT | Q9n120 oryctolagus |
| 951 | 38 | 40.0 | 305 | 2 | Q6BG17 PARTE | Q6bg17 paramecium |
| 952 | 38 | 40.0 | 305 | 2 | Q49827 ORYSA | Q49827 oryza sativ |
| 953 | 38 | 40.0 | 305 | 2 | Q04139 ORYSA | Q04139 oryza sativ |
| 954 | 38 | 40.0 | 307 | 2 | Q8KFZ3 CHLTE | Q8kfz3 chlorobium |
| 955 | 38 | 40.0 | 308 | 1 | CAH6 HUMAN | P23280 homo sapien |
| 956 | 38 | 40.0 | 308 | 2 | Q8RP05 PSEYM | Q8rp05 pseudomonas |
| 957 | 38 | 40.0 | 312 | 2 | Q6BL69 DEBHA | Q6bl69 debaryomyce |
| 958 | 38 | 40.0 | 313 | 2 | Q5FC00 HUMAN | Q5fc00 homo sapien |
| 959 | 38 | 40.0 | 315 | 2 | Q4P8M0 USTWA | Q4p8m0 ustilago ma |
| 960 | 38 | 40.0 | 316 | 2 | Q8UD64 AGRT5 | Q8ud64 agrobacteri |
| 961 | 38 | 40.0 | 317 | 2 | Q42353 DASAM | Q42353 dasyatis am |
| 962 | 38 | 40.0 | 319 | 2 | Q7MTY43 PHOLL | Q7my43 photorhabdu |
| 963 | 38 | 40.0 | 321 | 2 | Q6GP37 XENLA | Q6gp37 xenopus lae |
| 964 | 38 | 40.0 | 323 | 2 | Q8DG38 VIBVU | Q8dg38 vibrio vuln |
| 965 | 38 | 40.0 | 330 | 2 | Q4LGP9 BURBK | Q4lgp9 burkholderi |
| 966 | 38 | 40.0 | 333 | 2 | Q60SP5 CAEBR | Q60sp5 caenorhabdi |
| 967 | 38 | 40.0 | 333 | 2 | Q84AQ4 PSEST | Q84aq4 pseudomonas |
| 968 | 38 | 40.0 | 337 | 2 | Q595T1 9ACTO | Q595t1 streptomyce |
| 969 | 38 | 40.0 | 345 | 2 | Q61SD4 CAEBR | Q61sd4 caenorhabdi |
| 970 | 38 | 40.0 | 345 | 2 | Q89VN8 BRAJA | Q89vn8 bradyrhizob |
| 971 | 38 | 40.0 | 350 | 2 | Q5E0J9 VIBF1 | Q5e0j9 vibrio fisc |
| 972 | 38 | 40.0 | 352 | 2 | Q4WL60 ASPFU | Q4wl60 aspergillus |
| 973 | 38 | 40.0 | 362 | 2 | Q652L1 ORYSA | Q652l1 oryza sativ |
| 974 | 38 | 40.0 | 362 | 2 | Q8EGZ6 SHEON | Q8egz6 shewanella |
| 975 | 38 | 40.0 | 363 | 2 | Q5N9P7 ORYSA | Q5n9p7 oryza sativ |
| 976 | 38 | 40.0 | 364 | 2 | Q851D4 ORYSA | Q851d4 oryza sativ |
| 977 | 38 | 40.0 | 367 | 2 | P84129 THETH | P84129 thermus the |
| 978 | 38 | 40.0 | 367 | 2 | Q72GU1 THET2 | Q72gu1 thermus the |
| 979 | 38 | 40.0 | 367 | 2 | Q8RLR1 MYCGA | Q8rlr1 mycoplasma |
| 980 | 38 | 40.0 | 367 | 2 | Q5SLR4 THET8 | Q5slr4 thermus the |

981 38 40.0 375 2 Q876E1_SACBA
 982 38 40.0 376 2 Q5R964_PONPY
 983 38 40.0 376 2 Q56A18_RAT
 984 38 40.0 380 1 Y079_METJA
 985 38 40.0 386 2 Q4Y736_PLACH
 986 38 40.0 386 2 Q5ULR0_9CAUD
 987 38 40.0 387 2 Q86S90_9CILI
 988 38 40.0 388 2 Q7MZ88_PHOLL
 989 38 40.0 388 2 Q504E9_BRARE
 990 38 40.0 389 2 Q93NK1_PSESY
 991 38 40.0 389 2 Q4ZTR0_PSESY
 992 38 40.0 393 2 Q7RUX5_PLAYO
 993 38 40.0 393 2 Q5RDV2_PONPY
 994 38 40.0 395 2 Q6Q947_9GAMM
 995 38 40.0 399 2 Q7ZWC1_BRARE
 996 38 40.0 400 2 Q9P678_PSESY
 997 38 40.0 400 2 Q4SBY0_TETNG
 998 38 40.0 402 2 Q4MSG4_BACCE
 999 38 40.0 402 2 Q6HLK7_BACHK
 1000 38 40.0 402 2 Q73BG3_BACCL

ALIGNMENTS

RESULT 1

Q56LMS_MOUSE
 ID Q56LMS_MOUSE PRELIMINARY; PRT; 485 AA.

DT 10-MAY-2005 (TREMBlrel. 30, Created)
 DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
 DE LOC238447 protein (Fragment).
 GN Name=LOC238447;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Mix FVB/N;
 RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Feingold E.A., Grouse L.H., Detge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

NUCLEOTIDE SEQUENCE.

RP STRAIN=Mix FVB/N;
 RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
 RG NIH MGC Project;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR ENBL; BC093517; AAH93517.1; -; mRNA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 2.
 DR SMART; SM00409; IG; 3.
 DR SMART; SM00407; IGc1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 FT NON_TER 1
 SQ SEQUENCE 485 AA; 52570 MM; E28F4BB70DAF828A CRC64;
 Query Match 100.0%; Score 95; DB 2; Length 485;
 Best Local Similarity 100.0%; Pred. No. 2.4e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HIWDDDKRYNPALKS 16
 DB 69 HIWDDDKRYNPALKS 84

RESULT 2

Q81IUS_MOUSE
 ID Q81IUS_MOUSE PRELIMINARY; PRT; 118 AA.

AC Q81IUS;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Anti-human Fc gamma receptor III 3G8 gamma heavy chain variable region
 DE (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/c;
 RX PubMed=15059139; DOI=10.1111/j.1365-2141.2004.04893.x;
 RA Bruenke J., Fischer B., Barbin K., Schreiter K., Wachter Y., Mahr K.,
 RA Titgemeyer F., Niederweis M., Feipp M., Zunino S.J., Repp R.,
 RA Valerius T., Fey G.H.;
 RT "A recombinant bispecific single-chain Fv antibody against HLA class
 II and Fc gamma receptor III (CD16) triggers effective lysis of lymphoma
 cells";
 RL Br. J. Haematol. 125:167-179(2004).
 DR EMBL; AI173025; AAC18227.1; -; mRNA.
 DR HSSP; P01820; 1A7N.
 DR SNR; Q81IUS; 1-118.
 DR GO; GO:0004872; Fc receptor activity; IEA.
 DR Ensembl; ENSMUSG0000057010; Mus musculus.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 118
 SQ SEQUENCE 118 AA; 12979 MM; F57BB07033742B99 CRC64;
 Query Match 91.6%; Score 87; DB 2; Length 118;
 Best Local Similarity 87.5%; Pred. No. 1e-05;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HIWDDDKRYNPALKS 16

DB 52 HIWDDDKRYNPALKS 67

RESULT 3

Q9UL96_HUMAN
 ID Q9UL96_HUMAN PRELIMINARY; PRT; 121 AA.
 AC Q9UL96;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035018; AAD56254.1; -; mRNA.
DR HSP; P01820; IAN.
DR SMR; Q9UL96; 1-121.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1_1
FT NON_TER 121_121
SQ SEQUENCE 121 AA; 13695 MW; D582D405596BDD35 CRC64;

Query Match 86.3%; Score 82; DB 2; Length 121;
Best Local Similarity 93.3%; Pred. No. 6.3e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IYWDHDKRYNPSLKS 16
Db 53 IYWDHDKRYNPSLKS 67
|||||:|||||
|:|||||:|||||

RESULT 4
Q58E53_MOUSE PRELIMINARY; PRT; 487 AA.
AC Q58E53;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE LOC544903 protein.
GN Name=LOC544903;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC092066; AAH92066.1; -; mRNA.
DR GO; GO:0003823; P:antigen binding; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig CI.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 487 AA; 52616 MW; 839E85363A764CF1 CRC64;

Query Match 82.1%; Score 78; DB 2; Length 487;
Best Local Similarity 75.0%; Pred. No. 0.0012;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HIWDDDKRYNPSLKS 16
Db 71 HIWDDDKRYNPSLKS 86
|||||:|||||
|:|||||:|||||

RESULT 5
HV2E_HUMAN STANDARD; PRT; 121 AA.
AC P01818;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-II region HE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=70114712; PubMed=5264153;
RA Cunningham B.A., Pflumm M.N., Rutishauser U., Edelman G.M.;
RT "Subgroups of amino acid sequences in the variable regions of
RT immunoglobulin heavy chains";
RL Proc. Natl. Acad. Sci. U.S.A. 64:997-1003 (1969).
CC -!- MISCELLANEOUS: This gamma-1 chain was isolated from a myeloma
CC protein.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A02093; GIHHE.
DR HSP; P01820; IAN.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;

KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
 FT DOMAIN 1 120 IG-like.
 FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
 FT NON_TER 121 121
 SQ SEQUENCE 121 AA; 13483 MW; 88AS082273753B4 CRC64;

Query Match 80.0%; Score 76; DB 1; Length 121;
 Best Local Similarity 80.0%; Pred. No. 0.00056;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 IYWDDDKRYNPISLKS 16
 Db 54 LYWDDDKRYNPISLKS 68
 :|||||:|||||

RESULT 6

Q569B3_RAT PRELIMINARY; PRT; 617 AA.
 AC Q569B3;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DE LOC314521 protein.
 GN Name=LOC314521;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RG NIH MGC Project;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC092586; AAH92586.1; -, mRNA.
 DR GO; GO:0003823; F:antigen binding; IEA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 4.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IG1; 4.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 SQ SEQUENCE 617 AA; 68362 MW; 5943B1AFDD14C460 CRC64;

Query Match 76.8%; Score 73; DB 2; Length 617;
 Best Local Similarity 75.0%; Pred. No. 0.0092;
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 HIWDDDKRYNPISLKS 16
 Db 71 NIWDDDKRYNPISLKN 86
 :|||||:|||||

RESULT 7

Q569J1_HUMAN PRELIMINARY; PRT; 493 AA.
 AC Q569J1;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE IGHAI protein.
 GN Name=IGHAI;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Glandular pool- thyroid;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Glandular pool- thyroid;
 RG NIH MGC Project;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC092449; AAH92449.1; -, mRNA.
 DR GO; GO:0003823; F:antigen binding; IEA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 4.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IG1; 4.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 SQ SEQUENCE 493 AA; 53157 MW; 5B037BEE5B5B2ADF CRC64;

Query Match 74.7%; Score 71; DB 2; Length 493;
 Best Local Similarity 80.0%; Pred. No. 0.015;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 IYWDDDKRYNPISLKS 16
 Db 72 IYWDDDKRHRPSLKS 86
 :|||||:|||||

RESULT 8

Q5VLR6_RAT PRELIMINARY; PRT; 482 AA.
 AC Q5VLR6;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE BWK3.
 OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=DONRYU;
 RA Koami K., Yamakita S., Irino T., Osaka M.;
 RT "Cloning of a novel leukemia-related gene."
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY158661; AA017784.1; -, mRNA.
 DR SMR; QSVLR6; 251-460.
 DR GO; GO:0003823; F:antigen binding; IEA.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; IG; 3.
 DR SMART; SM00407; IGcl; 3.
 DR PROSITE; PS0835; IG LIKE; 4.
 DR PROSITE; PS0290; IG MHC; UNKNOWN 2.
 SQ SEQUENCE 482 AA; 52387 MW; 26BBEPDA7FCE0852 CRC64;
 Query Match 71.6%; Score 68; DB 2; Length 482;
 Best Local Similarity 68.8%; Pred. No. 0.044; Indels 1; Gaps 0;
 Matches 11; Conservative 4; Mismatches 1; Indels 1; Gaps 0;
 Qy 1 HIYDDDKRYNPSLKS 16
 Db 71 NIWDDDKRYNPSLKN 86
 RESULT 9
 HV2D HUMAN STANDARD; PRT; 125 AA.
 ID AC P01817;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE IG heavy chain V-II region MCB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP PROTEIN SEQUENCE.
 RC MEDLINE=81118242; PubMed=6780622;
 RA Gerber-Jenson B., Kazin A., Kehoe J.M., Scheffel C., Erickson B.W.,
 RA Litman G.W.;
 RT "Molecular basis for the temperature-dependent insolubility of
 RT cryoglobulins. X. The amino acid sequence of the heavy chain variable
 RT region of MCB."
 RL J Immunol. 126:1212-1216(1981).
 CC -!- MISCELLANEOUS: This chain was derived from a monoclonal IgM
 CC cryoglobulin.
 CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
 CC -----
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC PIR: A02092; MHDMC.
 DR HSSP; P01820; 1A7N.
 DR SMR; P01817; 1-125.
 DR GO; GO:0005576; C:extracellular region; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; IG-like.
 DR SMART; IPR003596; IG_v.
 DR SMART; SM00406; IGv; 1_
 DR PROSITE; PS0835; IG LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin domain;
 KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
 FT DOMAIN 1 113
 FT MOD RES 1 1 Pyrrolidone carboxylic acid.
 FT NON TER 125 125
 SQ SEQUENCE 125 AA; 13785 MW; 7A1ADF4C40F47BBS CRC64;
 Query Match 68.4%; Score 65; DB 1; Length 125;
 Best Local Similarity 73.3%; Pred. No. 0.031;
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 IYDDDKRYNPSLKS 16
 Db 53 INWDDNRYSPSLKS 67
 RESULT 10
 Q5854 MOUSE PRELIMINARY; PRT; 485 AA.
 ID Q5854_MOUSE PRELIMINARY;
 AC Q5854;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DE LOC544903 protein.
 GN Name=LOC544903;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RG NIH MGC Project;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC092085; AA092085.1; -, mRNA.
 DR GO; GO:0003823; F:antigen binding; IEA.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-set; 2.
 DR SMART; SM00409; IG; 3.
 DR SMART; SM00407; IGcl; 3.

```
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_WHC; UNKNOWN 2.
SQ SEQUENCE 485 AA; 52383 MW; 44087147CE49A50B CRC64;

Query Match 65.3%; Score 62; DB 2; Length 485;
Best Local Similarity 62.5%; Pred. No. 0.39;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 HIWDDDKRYNPSLKS 16
|||:|:|:|:|:|:|
Db 71 HIWDDDKRYNPSLKS 86

RESULT 11
HV2B_HUMAN STANDARD; PRT; 120 AA.
AC P01815;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-II region COR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=70258837; PubMed=5449120;
RA Press E.M., Hogg N.M.;
RT "The amino acid sequences of the Fd fragments of two human gamma-1
RL heavy chains."
RL Biochem. J. 117:641-660(1970).
CC -I- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
CC protein.
CC -I- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A02089; GIHUCO.
DR HSP; P01820; IA7N.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 110
FT MOD_RES 1 1 Ig-like.
FT CARBOHYD 62 62 Pyrrolidone carboxylic acid.
FT DISULFID 22 94 N-linked (GlcNAc..).
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13226 MW; 158AB29AE7EBB98 CRC64;

Query Match 57.9%; Score 55; DB 1; Length 120;
Best Local Similarity 66.7%; Pred. No. 1.1;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYDDDDKRYNPSLKS 16
|||:|:|:|:|:|:|
Db 53 IDWDDDKRYNPSLKS 67

RESULT 12
Q8IEB8_PLAF7
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ID Q8IEB8_PLAF7 PRELIMINARY; PRT; 145 AA.
AC Q8IEB8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Hypothetical protein MAL13P1.106.
GN Name=MAL13P1.106;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=3D7;
RA Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,
RA Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,
RA Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL844509; CAD52342.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 145 AA; 16762 MW; 099740DB29FD5B16 CRC64;

Query Match 53.7%; Score 51; DB 2; Length 145;
Best Local Similarity 66.7%; Pred. No. 5.9;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 YWDDDKRYNPSL 14
|||:|:|:|:|:|:|
Db 25 YLDDDKRYNPTM 36

RESULT 13
Q4XWY4_PLACH
ID Q4XWY4_PLACH PRELIMINARY; PRT; 357 AA.
AC Q4XWY4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Phosphoenolpyruvate carboxykinase, putative (Fragment).
GN ORFName=PC001162.02.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."
RL Science 307:82-86(2005).
CC -I- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAJ01002543; CAH78577.1; -; Genomic_DNA.
KW Kinase; Pyruvate.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 357 AA; 40167 MW; E58913F2A8FAEF0F CRC64;

Query Match 53.7%; Score 51; DB 2; Length 357;
Best Local Similarity 56.2%; Pred. No. 15;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 HIYDDDKRYNPSLKS 16
|||:|:|:|:|:|:|
Db 315 HIGWDDDKRYNPSLKS 330

RESULT 14
Q86SX2_HUMAN PRELIMINARY; PRT; 139 AA.
ID Q86SX2_HUMAN
```

AC Q86SX2;
 DT 01-JUN-2003 (TReMBLrel. 24, Created)
 DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Full-length cDNA clone CS0DL004YM19 of B cells (Ramos cell line) of
 DE Homo sapiens (human) (Fragment).
 OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=B cells;
 RA Li W.B., Gruber C., Jessee J., Polayes D.,
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=B cells;
 RA Genoscope;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX248300; CAD62627.1; -; mRNA.
 DR HSSP; P01820; 1G7J.
 DR SMR; Q86SX2; 33-129.
 DR Ensembl; ENSG00000130076; Homo sapiens.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1
 SQ SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;
 Query Match 52.6%; Score 50; DB 2; Length 139;
 Best Local Similarity 56.2%; Pred. No. 8.1;
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 HIYWDKRRYNPSLKS 16
 Db 82 YIYSGSTNYPNPSLKS 97
 RESULT 15
 Q5G7N6.9CAUD
 ID Q5G7N6.9CAUD PRELIMINARY; PRT; 801 AA.
 AC Q5G7N6;
 DT 10-MAY-2005 (TReMBLrel. 30, Created)
 DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
 DE Putative hemagglutinin protein.
 GN Name=ORF33;
 OS Listonella pelagica phage phiH5IC.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales.
 OX NCBI_TaxID=310539;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Paul J.H., Williamson S.J., Long A., Authement R.N., John D.,
 RA Segall A.M., Rohwer F.L., Androlewicz M., Patterson S.;
 RT "Complete genome sequence of phiH5IC, a pseudotemperature marine phage
 RT of Listonella pelagica."
 RL Appl. Environ. Microbiol. 71:3311-3320(2005).
 DR EMBL; AY772740; AAW67530.1; -; Genomic DNA.
 SQ SEQUENCE 801 AA; 85564 MW; E7C5D844E5941C27 CRC64;
 Query Match 52.6%; Score 50; DB 2; Length 801;
 Best Local Similarity 53.8%; Pred. No. 51;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Qy 4 WDDDKRRYNPSLKS 16
 Db 484 WDDDKRRYNPSLKS 496
 RESULT 16

O43234.HUMAN
 ID O43234.HUMAN PRELIMINARY; PRT; 97 AA.
 AC O43234;
 DT 01-JUN-1998 (TReMBLrel. 06, Created)
 DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Rheumatoid factor RF-ET13 (Fragment).
 OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Borrezen M., Natvig J.B., Thompson K.M.;
 RT "Heterogenous RF structures between and within healthy individuals are
 RT not related to HLA DRB1*0401."
 RL Mol. Immunol. 0:0-0(1997).
 DR EMBL; AF035802; AAB88534.1; -; mRNA.
 DR HSSP; P01820; 1G7I.
 DR SMR; O43234; 1-96.
 DR Ensembl; ENSG00000196662; Homo sapiens.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 97
 SQ SEQUENCE 97 AA; 10748 MW; DDC0BF47B9AA812D CRC64;
 Query Match 51.6%; Score 49; DB 2; Length 97;
 Best Local Similarity 56.2%; Pred. No. 8;
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 HIYWDKRRYNPSLKS 16
 Db 50 HIFANDEKSYSTSLKS 65
 RESULT 17
 HV2H.HUMAN
 ID HV2H.HUMAN STANDARD; PRT; 147 AA.
 AC P04438;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig heavy chain V-II region SESS precursor.
 OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=84298107; PubMed=6089186;
 RA Takahashi N., Noma T., Honjo T.;
 RT "Rearranged immunoglobulin heavy chain variable region (VH) pseudogene
 RT that deletes the second complementarity-determining region."
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5194-5198(1984).
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR PIR; A02090; G2HUCC.
 DR HSSP; P01820; 1G7I.
 DR GO; GO:0005576; C:extracellular region; NAS.
 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.

DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG LIKE; 1.
 KW Immunoglobulin domain; Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 147 Ig heavy chain V-II region SESS.
 FT REGION 20 118 V segment.
 FT REGION 119 132 D segment.
 FT REGION 133 147 J segment.
 FT NON_TER 147 147
 SQ SEQUENCE 147 AA; 16323 MW; FCBCDB3D00FB6666 CRC64;
 Query Match 51.6%; Score 49; DB 1; Length 147;
 Best Local Similarity 60.0%; Pred. No. 12;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 2 IYWDKKRYNPSLKS 16
 Db 72 IDWDDKKYGTSLT 86
 |||||
 RESULT 18
 OSXNU6_ANOGA
 ID OSXNU6_ANOGA PRELIMINARY; PRT; 167 AA.
 AC OSXNU6;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DE Cytochrome P450 (Fragment).
 GN Name=CYP307A1;
 OS Anopheles gambiae (African malaria mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
 OC Anophelinae; Anophelinae.
 OC NCBI_TaxID=7165;
 RN [1]
 RA Ranson H., Nikou D.,
 RP "Cytochrome P450s from the malaria vector, *Anopheles gambiae*.";
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
 DR EMBL; AY745209; AAU93476.1; -; mRNA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0004497; F:monooxygenase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR001128; Cytochrome_P450.
 DR InterPro; IPR002401; EP4501.
 DR Pfam; PF00067; P450; 1.
 DR PRINTS; PR00463; EP4501.
 DR PRINTS; PR00385; P450.
 DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
 KW Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase.
 FT NON_TER 1 1
 FT NON_TER 167 167
 SQ SEQUENCE 167 AA; 19140 MW; 3E415B7AD793A4A7 CRC64;
 Query Match 51.6%; Score 49; DB 2; Length 167;
 Best Local Similarity 63.6%; Pred. No. 14;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 3 YWDDKKRYNPS 13
 Db 73 YWSEPKRFNPS 83
 |||
 RESULT 19
 OSJEL9_PYRKO
 ID OSJEL9_PYRKO PRELIMINARY; PRT; 383 AA.
 AC OSJEL9;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DE ABC-type phosphate transport system, periplasmic component.
 GN OrderedLocusNames=TK1864;

OS Pyrococcus kodakaraensis (Thermococcus kodakaraensis).
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Thermococcus.
 OX NCBI_TaxID=69014;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=KOD1;
 RC PubMed=15710748; DOI=10.1101/gr.3003105;
 RA Fukui T., Atomi H., Kanai T., Matsumi R., Fujiwara S., Imanaka T.;
 RT "Complete genome sequence of the hyperthermophilic archaeon
 RT Thermococcus kodakaraensis KOD1 and comparison with Pyrococcus
 RT genomes.";
 RL Genome Res. 15:352-363(2005).
 DR EMBL; AP006878; BAD86053.1; -; Genomic DNA.
 DR GO; GO:0005315; P:inorganic phosphate transporter activity; IEA.
 DR GO; GO:0015114; P:phosphate transporter activity; IEA.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0006817; P:phosphate transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR005673; Peri-phosph.
 DR InterPro; IPR006059; SBP_bac_1.
 DR Pfam; PF01547; SBP_bac_1; 1.
 DR TIGRFAMS; TIGR00975; 3a0107s03; 1.
 KW Complete proteome.
 SQ SEQUENCE 383 AA; 41427 MW; 9C1DAA349C7EC179 CRC64;
 Query Match 51.6%; Score 49; DB 2; Length 383;
 Best Local Similarity 69.2%; Pred. No. 34;
 Matches 9; Conservative 1; Mismatches 1; Indels 2; Gaps 1;
 QY 3 YWDD--KRYNPS 13
 Db 162 YWDDDAKAFNPS 174
 |||||
 RESULT 20
 OSQ6CVD3_KLUJLA
 ID Q6CVD3_KLUJLA PRELIMINARY; PRT; 426 AA.
 AC Q6CVD3;
 DT 23-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Similar to sp|P53264|Saccharomyces cerevisiae YGR110w singleton.
 GN OrderedLocusNames=KLUJLA0B12914g;
 OS Kluyveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_TaxID=28985;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140 / WM37;
 RC PubMed=1529592; DOI=10.1038/nature02579;
 RA Dujon B., Sherman D., Fischer G., Durrans P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neugeglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
 RA Boisrame A., Boyer J.J., Cattolico L., Confanioli F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
 RA Swennen D., Tekia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpetti C., Gaillardin C., Weissenbach J.,
 RA Wincker P., Souciet J.-L.;
 RT "Genome evolution in yeasts.";
 RL Nature 430:35-44(2004).
 DR EMBL; CR382122; CAH02499.1; -; Genomic DNA.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR InterPro; IPR000073; A/b hydrolase.
 DR InterPro; IPR000379; Ser_estrs.
 DR Pfam; PF00561; Abhydrolase_1; 1.

| | |
|---|--|
| DE | ENSANGP00000026791 (Fragment). |
| GN | ORFNames=ENSGANG00000004170; |
| OS | Anopheles gambiae str. ENST. |
| OC | Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; |
| OC | Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae; |
| OC | Anophelinae; Anopheles. |
| OX | NCBI_TaxID=180454; |
| RN | [1] |
| RP | NUCLEOTIDE SEQUENCE. |
| RC | STRAIN=PEST; |
| RG | The Anopheles gambiae Sequence Committee; |
| RL | Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases. |
| CC | -!- CAUTION: The sequence shown here is derived from an |
| CC | EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is |
| CC | preliminary data. |
| CC | -!- SIMILARITY: Belongs to the cytochrome P450 family. |
| DR | EMBL; AAB01008811; EAL41693.1; -; Genomic_DNA. |
| DR | GO; GO:0046872; F-metal ion binding; IEA. |
| DR | GO; GO:0004497; F-monooxygenase activity; IEA. |
| DR | GO; GO:0006118; P-electron transport; IEA. |
| DR | InterPro; IPR001128; Cytochrome_P450. |
| DR | InterPro; IPR002401; EP450I. |
| DR | InterPro; IPR002403; EP450IV. |
| DR | Pfam; PF00067; P450; 1. |
| DR | PRINTS; PR00463; EP450I. |
| DR | PRINTS; PR00465; EP450IV. |
| DR | PRINTS; PR00385; P450. |
| DR | PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1. |
| KW | Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase. |
| FT | NON_TER 1 |
| FT | NON_TER 497 497 |
| SQ | SEQUENCE 497 AA; 56973 MW; 64BD7915DB201431 CRC64; |
| | |
| Query Match 51.6%; Score 49; DB 2; Length 497; | |
| Best Local Similarity 63.8%; Pred.No. 44; | |
| Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps | |
| Oy | 3 YWDDDKRNPS 13 : |
| Db | 376 YMSEPKRFNP 386 : |
| | |
| RESULT 23 | |
| G6GMX1_HUMAN | |
| ID | O6GMX1_HUMAN PRELIMINARY; PRT; 476 AA. |
| AC | G6GMX1 |
| DT | 03-JUL-2004 (TrEMBLrel. 27, Created) |
| DT | 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) |
| DT | 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) |
| DE | Hypothetical protein. |
| OS | Homo sapiens (Human). |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; |
| OC | Homo. |
| OX | NCBI_TaxID=9606; |
| RN | [1] |
| RP | NUCLEOTIDE SEQUENCE. |
| RC | TISSUE=Spleen; |
| RX | MDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899; |
| RA | Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., |
| RA | Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., |
| RA | Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., |
| RA | Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., |
| RA | Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., |
| RA | Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., |
| RA | Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., |
| RA | Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah S.J., |


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Db 170 YWDQNTKYNPDI 181
RESULT 26
Q6LZD6.METMP
ID Q6LZD6.METMP PRELIMINARY; PRT; 288 AA.
AC Q6LZD6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Aminoacyl-tRNA synthetase, class II precursor.
GN OrderedLocusNames=MWP0693;
OS Methanococcus maripaludis.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanococcaceae; Methanococcus.
OX NCBI_TaxID=39152;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=S2 / LL;
RX PubMed=15466049; DOI=10.1128/JB.186.20.6956-6969.2004;
RA Hendrickson E.L., Kaul R., Zhou Y., Bovee D., Chapman P., Chung J.,
RA Conway de Macario E., Dodsworth J.A., Gillett W., Graham D.E.,
RA Hackett M., Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J.,
RA Major I.A., Moore B.C., Porat I., Palmeiri A., Rouse G.,
RA Saenphimmachak C., Soell D., Van Dien S., Wang T., Whitman W.B.,
RA Xia Q., Zhang Y., Larimer F.W., Olson M.V., Leigh J.A.;
RT "Complete genome sequence of the genetically tractable
RT hydrogenotrophic methanogen Methanococcus maripaludis.";
RL J. Bacteriol. 186:6956-6969(2004).
DR EMBL; BX957220; CAF30249.1; -; Genomic DNA.
DR GO; GO:0004812; F:RNA ligase activity; IEA.
DR KW Aminoacyl-tRNA synthetase; Complete proteome; Signal.
FT SIGNAL 1 20 Potential.
SQ SEQUENCE 288 AA; 32668 MW; BA093AC26AF60475 CRC64;

Query Match 50.0%; Score 47.5; DB 2; Length 288;
Best Local Similarity 52.9%; Pred. No. 43;
Matches 9; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

QY 1 HIYWDDDK-RYNPSLKS 16
Db 267 HVYWDGPKITYNPKNNS 283
1:|||||
267 HVYWDGPKITYNPKNNS 283

RESULT 27
Q621X9.CAEBR
ID Q621X9.CAEBR PRELIMINARY; PRT; 400 AA.
AC Q621X9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG02301.
GN Name=CBG02301;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C.Briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAC0100012; CAB59024.1; -; Genomic DNA.
DR InterPro; IPR010733; DUF1308.
DR PANTHER; PTHR13379; DUF1308; 1.
DR Pfam; PF07000; DUF1308; 1.
DR KW Hypothetical protein.
SQ SEQUENCE 400 AA; 45670 MW; 9AFD1B91C98A3D2A CRC64;

Query Match 49.5%; Score 47; DB 2; Length 400;
Best Local Similarity 46.2%; Pred. No. 73;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 4 WDDDKRYNPSLKS 16
Db 207 WDDDEDFDPTTS 219
|||||
207 WDDDEDFDPTTS 219

Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 4 WDDDKRYNPSLKS 16
Db 207 WDDDEDFDPTTS 219
|||||
207 WDDDEDFDPTTS 219

RESULT 28
Q7XPL1.ORYSA
ID Q7XPL1.ORYSA PRELIMINARY; PRT; 778 AA.
AC Q7XPL1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE OSJNBa0085110.15 protein.
GN Name=OSJNBa0085110.15;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2237377; PubMed=12447439; DOI=10.1038/nature01183;
RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Wang Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Xu Z., Fan D.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jia J., Wang R., Yin H.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia Z., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL Nature 420:316-320(2002).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AL606684; CA0303570.2; -; Genomic DNA.
DR HSP; P06213; 1144.
DR Gramene; Q7XPL1; -.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; UNKNOWN_1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 778 AA; 84453 MW; 7A76578AAE91338B CRC64;

Query Match 49.5%; Score 47; DB 2; Length 778;
Best Local Similarity 61.5%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 WDDDKRYNPSLKS 16
Db 750 WDDDPQRPSFS 762
|||||
750 WDDDPQRPSFS 762

RESULT 29
Q99JU0.MOUSE
ID Q99JU0.MOUSE PRELIMINARY; PRT; 208 AA.
AC Q99JU0;

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```
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Rps6kb2 protein.
GN Name=Rps6kb2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan E., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buttrickfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RA Strausberg R.;
RL EMBL: BC005694; AAH05694.1; -; mRNA.
DR MGI: MGI:1927343; Rps6kb2.
DR GO: GO:0005524; F-ATP binding; IEA.
DR GO: GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000961; Pkinase C.
DR InterPro: IPR000719; Prot_kinase.
DR Pfam: PF00433; Pkinase_C; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00133; S_TK_X; 1.
KW Nucleotide-binding.
SQ SEQUENCE 208 AA; 22968 MW; 228A8B586D7AE30B CRC64;

Query Match 48.4%; Score 46; DB 2; Length 208;
Best Local Similarity 45.5%; Pred. No. 53;
Matches 10; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

QY 1 HIYWDV-----DKRYNPISLKS 16
Db 53 HINWDDLARRVDPPRPRLQS 74

RESULT 30
KS6B2 MOUSE
ID KS6B2 MOUSE STANDARD; PRT; 485 AA.
AC Q92IM4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Ribosomal protein S6 kinase beta 2 (EC 2.7.1.37) (S6K-beta 2) (70 kDa
DE Ribosomal protein S6 kinase beta 2 (p70-S6KB) (p70 ribosomal S6 kinase
DE beta) (p70_S6KBeta) (S6K2).
GN Names=Rps6kb2;
OS Mus musculus (Mouse).
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KW Serine/threonine-protein kinase; Transferase.
FT DOMAIN 67 328
  NP BIND 73 81 ATP (By similarity).
  COMPBTAS 411 485 Pro-rich.
  ACT SITE 194 194 Proton acceptor (By similarity).
  BINDING 99 99 ATP (By similarity).
SQ SEQUENCE 485 AA; 53538 MW; 396929ADAB0F6CB6 CRC64;

Query Match 48.4%; Score 46; DB 1; Length 485;
Best Local Similarity 45.5%; Pred. No. 1.3e+02;
Matches 10; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

Qy 1 HIYWD-----DKRYNPSLKS 16
  ||||| :|||
Db 330 HINWDDLARVDPPFRPSLQS 351

RESULT 31
Q72374 HUMAN
ID Q72374 HUMAN PRELIMINARY; PRT; 492 AA.
AC Q72374;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686C02218 (Fragment).
GN Name=DKFZp686C02218;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN 1
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human rectum tumor;
RA Bloecher H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
  Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538077; CAD98001.1; -; mRNA.
DR HSP; P01820; 1G7J.
DR SMR; Q72374; 262-470.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;

Query Match 48.4%; Score 46; DB 2; Length 492;
Best Local Similarity 53.3%; Pred. No. 1.3e+02;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IYWDDDKRYNPSLKS 16
  ||||| :|||
Db 84 IYNYNTYSPSLKS 98

RESULT 32
Q5F6L0 NEIG1
ID Q5F6L0 NEIG1 PRELIMINARY; PRT; 492 AA.
AC Q5F6L0;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Putative UDP-N-acetylmuramyl-tripeptide synthetase (EC 6.3.2.13).
GN OrderedLocusNames=NG01541;
OS Neisseria gonorrhoeae (strain ATCC 700825 / FA 1090).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

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OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=242231;
RN 1
RP NUCLEOTIDS SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Lewis L.A., Gillaspay A.F., McLaughlin R.E., Gipson M., Ducey T.F.,
  Onwey T., Hartman K., Nydick C., Carson M.B., Vaughn J., Thomson C.,
  Song L., Lin S., Yuan X., Najjar F., Zhan M., Ren Q., Zhu H., Qi S.,
  Kerton S.M., Lai H., White J.D., Clifton S., Roe B.A., Dyer D.W.;
RA "The complete genome sequence of Neisseria gonorrhoeae.";
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AE004969; AAN90177.1; -; Genomic DNA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008765; F:UDP-N-acetylmuramoylanyl-D-glutamate-2,6-...; IEA.
DR InterPro; IPR005761; MurE.
DR InterPro; IPR004101; Mur_ligase_C.
DR InterPro; IPR000713; Mur_ligase_N.
DR InterPro; IPR012237; UDP-NACM_Align.
DR Pfam; PF01225; Mur_ligase; 1.
DR Pfam; PF02875; Mur_ligase_C; 1.
DR PIRSF; PIRSF001562; UDP-NACM_Align; 1.
DR TIGRPFAMs; TIGR01085; murE; 1.
KW Complete proteome; Ligase.
SQ SEQUENCE 492 AA; 53010 MW; 9ED0CF2865C86A20 CRC64;

Query Match 48.4%; Score 46; DB 2; Length 492;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

Qy 2 IYWDDDKRY--NPSLK 15
  :||| :|||
Db 64 VFWDGGRFAWNPWK 79

RESULT 33
Q7T6H2_9LUTE
ID Q7T6H2_9LUTE PRELIMINARY; PRT; 524 AA.
AC Q7T6H2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
OS Sugarcane yellow leaf virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
OC Polerovirus.
OX NCBI_TaxID=94290;
RN 1
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20318675; PubMed=10859394;
RA Smith G.R., Borg Z., Lockhart B.E.L., Braithwaite K.S., Gibbs M.J.;
RT "Sugarcane yellow leaf virus: a novel member of the Luteoviridae that
  probably arose by inter-species recombination.";
RL J. Gen. Virol. 81:1865-1869(2000).
RN 2
RP NUCLEOTIDE SEQUENCE.
RA Borg Z., Braithwaite K.S., Smith G.R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ491131; CAD36539.1; -; mRNA.
DR MEROPS; S39.002; -.
DR InterPro; IPR000382; Peptidase_S39B.
DR Pfam; PF02122; Luteo_ORF2; 1.
DR PRINTS; PR00913; LVIRUSORF2.
KW Hypothetical protein.
FT NON TER 524
SQ SEQUENCE 524 AA; 58837 MW; 89372CE19C0DB394 CRC64;

Query Match 48.4%; Score 46; DB 2; Length 524;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HIYWDGGRYNN 11
  :||| :|||
Db 382 HVGDDSKNYN 392

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RESULT 34
Q704G6_9LUTE
ID Q704G6_9LUTE PRELIMINARY; PRT; 525 AA.
AC Q704G6_9LUTE PRELIMINARY; PRT; 525 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Sugarcane yellow leaf virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
OC Polerovirus.
OX NCBI_TaxID=94290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaf.
RA Rassaby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X.,
RA Smith G., Rott P.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ621182; CAF18410.1; -; Genomic_DNA.
DR InterPro; IPR000382; Peptidase_S39B.
DR Pfam; PF02122; Luteo_ORF2; 1.
DR PRINTS; PR00913; LVIRUSORF2.
KW Hypothetical protein.
FT NON TER 1
FT NON TER 525
SQ SEQUENCE 525 AA; 58860 MW; D4AEC9C9A2F086E7 CRC64;

Query Match 48.4%; Score 46; DB 2; Length 525;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HIYWDGDKRYN 11
|:|:|:|:|:|
Db 374 HVYGDGSKRYN 384

RESULT 35
Q704G9_9LUTE
ID Q704G9_9LUTE PRELIMINARY; PRT; 525 AA.
AC Q704G9_9LUTE PRELIMINARY; PRT; 525 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Sugarcane yellow leaf virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
OC Polerovirus.
OX NCBI_TaxID=94290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaf.
RA Rassaby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X.,
RA Smith G., Rott P.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ621181; CAF18407.1; -; Genomic_DNA.
DR InterPro; IPR000382; Peptidase_S39B.
DR Pfam; PF02122; Luteo_ORF2; 1.
DR PRINTS; PR00913; LVIRUSORF2.
KW Hypothetical protein.
FT NON TER 1
FT NON TER 525
SQ SEQUENCE 525 AA; 58860 MW; D4AEC9C9A2F086E7 CRC64;

Query Match 48.4%; Score 46; DB 2; Length 525;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HIYWDGDKRYN 11
|:|:|:|:|:|
Db 374 HVYGDGSKRYN 384

RESULT 36
Q70417_9LUTE
ID Q70417_9LUTE PRELIMINARY; PRT; 525 AA.
AC Q70417_9LUTE PRELIMINARY; PRT; 525 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Sugarcane yellow leaf virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
OC Polerovirus.
OX NCBI_TaxID=94290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaf.
RA Rassaby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X.,
RA Smith G., Rott P.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ621175; CAF18386.1; -; Genomic_DNA.
DR InterPro; IPR000382; Peptidase_S39B.
DR Pfam; PF02122; Luteo_ORF2; 1.
DR PRINTS; PR00913; LVIRUSORF2.
KW Hypothetical protein.
FT NON TER 1
FT NON TER 525
SQ SEQUENCE 525 AA; 58746 MW; DC638C04B08714B3 CRC64;

Query Match 48.4%; Score 46; DB 2; Length 525;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HIYWDGDKRYN 11
|:|:|:|:|:|
Db 374 HVYGDGSKRYN 384

RESULT 37
Q704K5_9LUTE
ID Q704K5_9LUTE PRELIMINARY; PRT; 525 AA.
AC Q704K5_9LUTE PRELIMINARY; PRT; 525 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Sugarcane yellow leaf virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
OC Polerovirus.
OX NCBI_TaxID=94290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaf.
RA Rassaby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X.,
RA Smith G., Rott P.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ621169; CAF18368.1; -; Genomic_DNA.
DR InterPro; IPR000382; Peptidase_S39B.
DR Pfam; PF02122; Luteo_ORF2; 1.
DR PRINTS; PR00913; LVIRUSORF2.
KW Hypothetical protein.
FT NON TER 1
FT NON TER 525
SQ SEQUENCE 525 AA; 58642 MW; OD8933C444B23F3D CRC64;

Query Match 48.4%; Score 46; DB 2; Length 525;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HIYWDGDKRYN 11
|:~|:~|:~|:~|
Db 374 HVYGDGSKRYN 384

RESULT 38
Q704G6_9LUTE
ID Q704G6_9LUTE PRELIMINARY; PRT; 525 AA.
AC Q704G6_9LUTE PRELIMINARY; PRT; 525 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Sugarcane yellow leaf virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
OC Polerovirus.
OX NCBI_TaxID=94290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaf.
RA Rassaby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X.,
RA Smith G., Rott P.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ621182; CAF18410.1; -; Genomic_DNA.
DR InterPro; IPR000382; Peptidase_S39B.
DR Pfam; PF02122; Luteo_ORF2; 1.
DR PRINTS; PR00913; LVIRUSORF2.
KW Hypothetical protein.
FT NON TER 1
FT NON TER 525
SQ SEQUENCE 525 AA; 58860 MW; D4AEC9C9A2F086E7 CRC64;

Query Match 48.4%; Score 46; DB 2; Length 525;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HIYWDGDKRYN 11
|:~|:~|:~|:~|
Db 374 HVYGDGSKRYN 384
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Q704N5_9LUTE
ID Q704N5_9LUTE PRELIMINARY; PRT; 525 AA.
AC Q704N5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Sugarcane yellow leaf virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
OC Polerovirus.
OX NCBI_TaxID=94290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaf;
RA Rassaby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X.,
RL Smith G., Rott P.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ621159; CAF18329.1; -; Genomic_DNA.
DR InterPro; IPR000382; Peptidase_S39B.
DR Pfam; PF02122; Luteo_ORF2; 1.
DR PRINTS; PR00913; LVIRUSORF2.
KW Capsid protein; Hypothetical protein; Structural protein.
FT NON_TER 1
FT NON_TER 525
SQ SEQUENCE 525 AA; 59015 MW; E3B3E6BA686152B6 CRC64;

Query Match 48.4%; Score 46; DB 2; Length 525;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HIYWDDDKRYN 11
|:|:|:|:|
Db 374 HVYGDGSKNYN 384

RESULT 39
Q704N2_9LUTE
ID Q704N2_9LUTE PRELIMINARY; PRT; 525 AA.
AC Q704N2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Sugarcane yellow leaf virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
OC Polerovirus.
OX NCBI_TaxID=94290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaf;
RA Rassaby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X.,
RL Smith G., Rott P.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ621160; CAF18341.1; -; Genomic_DNA.
DR InterPro; IPR000382; Peptidase_S39B.
DR Pfam; PF02122; Luteo_ORF2; 1.
DR PRINTS; PR00913; LVIRUSORF2.
KW Capsid protein; Hypothetical protein; Structural protein.
FT NON_TER 1
FT NON_TER 525
SQ SEQUENCE 525 AA; 58976 MW; E8F8A0237D2522DB CRC64;

Query Match 48.4%; Score 46; DB 2; Length 525;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HIYWDDDKRYN 11
|:|:|:|:|
Db 374 HVYGDGSKNYN 384

Q704M9_9LUTE
ID Q704M9_9LUTE PRELIMINARY; PRT; 525 AA.
AC Q704M9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Sugarcane yellow leaf virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
OC Polerovirus.
OX NCBI_TaxID=94290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaf;
RA Rassaby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X.,
RL Smith G., Rott P.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ621161; CAF18344.1; -; Genomic_DNA.
DR InterPro; IPR000382; Peptidase_S39B.
DR Pfam; PF02122; Luteo_ORF2; 1.
DR PRINTS; PR00913; LVIRUSORF2.
KW Capsid protein; Hypothetical protein; Structural protein.
FT NON_TER 1
FT NON_TER 525
SQ SEQUENCE 525 AA; 58854 MW; FF906A158C80A8A2 CRC64;

Query Match 48.4%; Score 46; DB 2; Length 525;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HIYWDDDKRYN 11
|:|:|:|:|
Db 374 HVYGDGSKNYN 384

RESULT 41
Q704M6_9LUTE
ID Q704M6_9LUTE PRELIMINARY; PRT; 525 AA.
AC Q704M6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Sugarcane yellow leaf virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
OC Polerovirus.
OX NCBI_TaxID=94290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaf;
RA Rassaby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X.,
RL Smith G., Rott P.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ621162; CAF18347.1; -; Genomic_DNA.
DR InterPro; IPR000382; Peptidase_S39B.
DR Pfam; PF02122; Luteo_ORF2; 1.
DR PRINTS; PR00913; LVIRUSORF2.
KW Capsid protein; Hypothetical protein; Structural protein.
FT NON_TER 1
FT NON_TER 525
SQ SEQUENCE 525 AA; 58828 MW; 3C5EB2618752331C CRC64;

Query Match 48.4%; Score 46; DB 2; Length 525;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HIYWDDDKRYN 11
|:|:~|:|:|
Db 374 HVYGDGSKNYN 384

RESULT 42
Q704M3_9LUTE
ID Q704M3_9LUTE PRELIMINARY; PRT; 525 AA.

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AC Q704M3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Sugarcane yellow leaf virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
OC Polerovirus.
OX NCBI_TaxID=94290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaf;
RA Rassaby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X.,
RA Smith G., Rott P.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ621163; CAF18350.1; -; Genomic_DNA.
DR InterPro: IPR000382; Peptidase_S39B.
DR Pfam: PF02122; Luteo_ORF2; 1.
DR PRINTS; PR00913; LVIRUSORF2.
KW Capsid protein; Hypothetical protein; Structural protein.
FT NON_TER 1 1
FT NON_TER 525 525
SQ SEQUENCE 525 AA; 58789 MW; E12E4FADE48A1A34 CRC64;

Query Match 48.4%; Score 46; DB 2; Length 525;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HIYWDGDKRYN 11
Db 374 HVYGDGSKNYN 384

RESULT 43
Q704M0_9LUTE
ID Q704M0_9LUTE PRELIMINARY; PRT; 525 AA.
AC Q704M0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Sugarcane yellow leaf virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
OC Polerovirus.
OX NCBI_TaxID=94290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaf;
RA Rassaby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X.,
RA Smith G., Rott P.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ621164; CAF18353.1; -; Genomic_DNA.
DR InterPro: IPR000382; Peptidase_S39B.
DR Pfam: PF02122; Luteo_ORF2; 1.
DR PRINTS; PR00913; LVIRUSORF2.
KW Capsid protein; Hypothetical protein; Structural protein.
FT NON_TER 1 1
FT NON_TER 525 525
SQ SEQUENCE 525 AA; 58872 MW; 170BFA700BCA511 CRC64;

Query Match 48.4%; Score 46; DB 2; Length 525;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HIYWDGDKRYN 11
Db 374 HVYGDGSKNYN 384

RESULT 44
Q704L7_9LUTE
ID Q704L7_9LUTE PRELIMINARY; PRT; 525 AA.
AC Q704L7;
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DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Sugarcane yellow leaf virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
OC Polerovirus.
OX NCBI_TaxID=94290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaf;
RA Rassaby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X.,
RA Smith G., Rott P.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ621165; CAF18356.1; -; Genomic_DNA.
DR InterPro: IPR000382; Peptidase_S39B.
DR Pfam: PF02122; Luteo_ORF2; 1.
DR PRINTS; PR00913; LVIRUSORF2.
KW Capsid protein; Hypothetical protein; Structural protein.
FT NON_TER 1 1
FT NON_TER 525 525
SQ SEQUENCE 525 AA; 58820 MW; 1F51DC03A8DB2F40 CRC64;

Query Match 48.4%; Score 46; DB 2; Length 525;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HIYWDGDKRYN 11
Db 374 HVYGDGSKNYN 384

RESULT 45
Q704L4_9LUTE
ID Q704L4_9LUTE PRELIMINARY; PRT; 525 AA.
AC Q704L4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Sugarcane yellow leaf virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
OC Polerovirus.
OX NCBI_TaxID=94290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaf;
RA Rassaby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X.,
RA Smith G., Rott P.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ621166; CAF18359.1; -; Genomic_DNA.
DR InterPro: IPR000382; Peptidase_S39B.
DR Pfam: PF02122; Luteo_ORF2; 1.
DR PRINTS; PR00913; LVIRUSORF2.
KW Capsid protein; Hypothetical protein; Structural protein.
FT NON_TER 1 1
FT NON_TER 525 525
SQ SEQUENCE 525 AA; 58848 MW; C3BAC1B90BA2F0E3 CRC64;

Query Match 48.4%; Score 46; DB 2; Length 525;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HIYWDGDKRYN 11
Db 374 HVYGDGSKNYN 384

RESULT 46
Q704L1_9LUTE
ID Q704L1_9LUTE PRELIMINARY; PRT; 525 AA.
AC Q704L1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
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DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein (Fragment)
OS Sugarcane yellow leaf virus
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
OC Polerovirus.
OX NCBI_TaxID=94290;
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Leaf;
RA Rassaby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X.,
RA Smith G., Rott P.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ621167; CAF18362.1; -; Genomic_DNA.
DR InterPro; IPR000382; Peptidase_S39B.
DR Pfam; PF02122; Luteo_ORF2; 1.
DR PRINTS; PR00913; LVIRUSORF2.
KW Capsid protein; Hypothetical protein; Structural protein.
FT NON_TER 1
FT NON_TER 525
SQ SEQUENCE 525 AA; 58823 MW; EB9CB74C9FA4B6AC CRC64;

Query Match 48.4%; Score 46; DB 2; Length 525;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HIYWDDDKRYN 11
Db 374 HVGDDSKNYN 384

RESULT 47
Q704K8_9LUTE
ID Q704K8_9LUTE PRELIMINARY; PRT; 525 AA.
AC Q704K8_
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein (Fragment)
OS Sugarcane yellow leaf virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
OC Polerovirus.
OX NCBI_TaxID=94290;
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Leaf;
RA Rassaby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X.,
RA Smith G., Rott P.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ621168; CAF18365.1; -; Genomic_DNA.
DR InterPro; IPR000382; Peptidase_S39B.
DR Pfam; PF02122; Luteo_ORF2; 1.
DR PRINTS; PR00913; LVIRUSORF2.
KW Capsid protein; Hypothetical protein; Structural protein.
FT NON_TER 1
FT NON_TER 525
SQ SEQUENCE 525 AA; 58817 MW; E612C70F75A29AA9 CRC64;

Query Match 48.4%; Score 46; DB 2; Length 525;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HIYWDDDKRYN 11
Db 374 HVGDDSKNYN 384

RESULT 48
Q704K2_9LUTE
ID Q704K2_9LUTE PRELIMINARY; PRT; 525 AA.
AC Q704K2_
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment)
OS Sugarcane yellow leaf virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
OC Polerovirus.
OX NCBI_TaxID=94290;
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Leaf;
RA Rassaby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X.,
RA Smith G., Rott P.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ621170; CAF18371.1; -; Genomic_DNA.
DR InterPro; IPR000382; Peptidase_S39B.
DR Pfam; PF02122; Luteo_ORF2; 1.
DR PRINTS; PR00913; LVIRUSORF2.
KW Capsid protein; Hypothetical protein; Structural protein.
FT NON_TER 1
FT NON_TER 525
SQ SEQUENCE 525 AA; 58846 MW; E774B1B7C83B4699 CRC64;

Query Match 48.4%; Score 46; DB 2; Length 525;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HIYWDDDKRYN 11
Db 374 HVGDDSKNYN 384

RESULT 49
Q704J9_9LUTE
ID Q704J9_9LUTE PRELIMINARY; PRT; 525 AA.
AC Q704J9_
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein (Fragment)
OS Sugarcane yellow leaf virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
OC Polerovirus.
OX NCBI_TaxID=94290;
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Leaf;
RA Rassaby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X.,
RA Smith G., Rott P.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ621171; CAF18374.1; -; Genomic_DNA.
DR InterPro; IPR000382; Peptidase_S39B.
DR Pfam; PF02122; Luteo_ORF2; 1.
DR PRINTS; PR00913; LVIRUSORF2.
KW Capsid protein; Hypothetical protein; Structural protein.
FT NON_TER 1
FT NON_TER 525
SQ SEQUENCE 525 AA; 58889 MW; 46231937027492A6 CRC64;

Query Match 48.4%; Score 46; DB 2; Length 525;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HIYWDDDKRYN 11
Db 374 HVGDDSKNYN 384

RESULT 50
Q704J6_9LUTE
ID Q704J6_9LUTE PRELIMINARY; PRT; 525 AA.
AC Q704J6_
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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DE Hypothetical protein (Fragment).
OS Sugarcane yellow leaf virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
OC Polerovirus
OX NCBI_TaxID=94290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaf;
RA Raseaby L., Royer M., Borg Z., Braithwaite K., Mirkov E., Perrier X.,
RA Smith G., Rott P.;
RL Submitted (Nov-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ621172; CAF18377.1; -; Genomic_DNA.
DR InterPro; IPR000382; Peptidase_S39B.
DR Pfam; PF02122; Luteo_ORF2; 1.
DR PRINTS; PR00913; LVIRUSORE2.
KW Capsid protein; Hypothetical protein; Structural protein.
FT NON_TER 1
FT NON_TER 525
SQ SEQUENCE 525 AA; 58721 MW; 70943818E8BD7875 CRC64;

Query Match 48.4%; Score 46; DB 2; Length 525;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HIYDDDKRYN 11
|:| | | | |
Db 374 HVYDDSKNYN 384

Search completed: February 23, 2006, 09:51:54
Job time : 171.846 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2006, 09:29:34 ; Search time 94.7692 Seconds
(without alignments)
50.999 Million cell updates/sec

Title: US-10-723-872-26
Perfect score: 66
Sequence: 1 RETVFWYFDV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|---------------------|
| 1 | 66 | 100.0 | 11 | 2 | Aar70200 MAB 3B9 h |
| 2 | 66 | 100.0 | 11 | 2 | Aay23777 CDR of th |
| 3 | 66 | 100.0 | 11 | 2 | Aay18113 Heavy cha |
| 4 | 66 | 100.0 | 121 | 2 | Aay23780 Heavy cha |
| 5 | 66 | 100.0 | 121 | 2 | Aay18122 Heavy cha |
| 6 | 66 | 100.0 | 140 | 2 | Aar70190 Mouse Mab |
| 7 | 66 | 100.0 | 140 | 2 | Aay23768 Heavy cha |
| 8 | 66 | 100.0 | 140 | 2 | Aay18125 Heavy cha |
| 9 | 66 | 100.0 | 141 | 2 | Aar70192 Humanized |
| 10 | 66 | 100.0 | 141 | 2 | Aar70191 Chimeric |
| 11 | 66 | 100.0 | 141 | 2 | Aay23770 Heavy cha |
| 12 | 66 | 100.0 | 141 | 2 | Aay23769 Heavy cha |
| 13 | 66 | 100.0 | 141 | 2 | Aay18125 Chimeric |
| 14 | 66 | 100.0 | 141 | 2 | Aay18117 Heavy cha |
| 15 | 52 | 78.8 | 13 | 8 | Adp47150 Human pho |
| 16 | 52 | 78.8 | 13 | 8 | Adp47171 Human pho |
| 17 | 49 | 74.2 | 137 | 2 | Aar99470 Monoclonal |
| 18 | 47 | 71.2 | 120 | 5 | Abp66387 Human RSV |
| 19 | 47 | 71.2 | 120 | 5 | Abp66421 Human RSV |
| 20 | 47 | 71.2 | 120 | 5 | Abp66405 Human RSV |
| 21 | 47 | 71.2 | 120 | 5 | Abp66382 Human RSV |
| 22 | 47 | 71.2 | 120 | 5 | Abp66409 Human RSV |
| 23 | 47 | 71.2 | 120 | 5 | Aae28076 Human mod |
| 24 | 47 | 71.2 | 120 | 5 | Aae28042 Human mod |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|----------|---------------------|-----|----|------|-----|---|----------|--------------------|
| 98 | 46 | 69.7 | 57 | 3 | AAy68013 | AAy68013 Kunitz pr | 171 | 43 | 65.2 | 240 | 8 | ADN14294 | Adn14294 Mouse pro |
| 99 | 46 | 69.7 | 61 | 2 | AAW18404 | Aaw18404 KPI(-4 to | 172 | 43 | 65.2 | 244 | 8 | ADH00896 | Adh00896 Kidney di |
| 100 | 46 | 69.7 | 61 | 2 | AAW18401 | Aaw18401 KPI(-4 to | 173 | 42 | 63.6 | 10 | 4 | AAE10504 | Aae10504 Humanised |
| 101 | 46 | 69.7 | 61 | 2 | AAW18403 | Aaw18403 KPI(-4 to | 174 | 42 | 63.6 | 10 | 5 | ABP66383 | Abp66383 Human RSV |
| 102 | 46 | 69.7 | 61 | 3 | AAy68058 | AAy68058 Kunitz pr | 175 | 42 | 63.6 | 10 | 5 | AAE28038 | Aae28038 Human mod |
| 103 | 46 | 69.7 | 61 | 3 | AAy68050 | AAy68050 Kunitz pr | 176 | 42 | 63.6 | 10 | 6 | ABU69246 | Abu69246 Respirato |
| 104 | 46 | 69.7 | 61 | 3 | AAy68169 | AAy68169 Kunitz pr | 177 | 42 | 63.6 | 10 | 7 | ADe35741 | Ad35741 SYNAGIS a |
| 105 | 46 | 69.7 | 61 | 3 | AAy68052 | AAy68052 Kunitz pr | 178 | 42 | 63.6 | 10 | 8 | ADi56903 | Adi56903 RSV antib |
| 106 | 46 | 69.7 | 61 | 3 | AAy68182 | AAy68182 KPI-P48 p | 179 | 42 | 63.6 | 10 | 8 | ADT89226 | Adt89226 Humanised |
| 107 | 46 | 69.7 | 61 | 3 | AAy68159 | AAy68159 Kunitz pr | 180 | 42 | 63.6 | 10 | 9 | ADW19883 | Adw19883 RSV anti |
| 108 | 46 | 69.7 | 61 | 3 | AAy68056 | AAy68056 Kunitz pr | 181 | 42 | 63.6 | 10 | 9 | AEb06865 | Aeb06865 RSV-speci |
| 109 | 46 | 69.7 | 61 | 3 | AAy68168 | AAy68168 Kunitz pr | 182 | 42 | 63.6 | 17 | 3 | AAb06402 | Aab06402 Randomise |
| 110 | 46 | 69.7 | 61 | 4 | AAU09329 | AAU09329 Human KPI | 183 | 42 | 63.6 | 17 | 3 | AAb06356 | Aab06356 Randomise |
| 111 | 46 | 69.7 | 61 | 4 | AAU09319 | AAU09319 Human KPI | 184 | 42 | 63.6 | 17 | 3 | AAb06404 | Aab06404 Randomise |
| 112 | 46 | 69.7 | 61 | 4 | AAU09328 | AAU09328 Human KPI | 185 | 42 | 63.6 | 17 | 3 | AAb07767 | Aab07767 Non-nativ |
| 113 | 46 | 69.7 | 146 | 3 | AAy68055 | AAy68055 Yeast mat | 186 | 42 | 63.6 | 58 | 2 | AAW07763 | Aaw07763 Non-nativ |
| 114 | 46 | 69.7 | 146 | 3 | AAy68049 | AAy68049 Yeast mat | 187 | 42 | 63.6 | 58 | 2 | AAW64139 | Aaw64139 Human Kun |
| 115 | 46 | 69.7 | 146 | 3 | AAy68051 | AAy68051 Yeast mat | 188 | 42 | 63.6 | 58 | 2 | AAW64135 | Aaw64135 Human Kun |
| 116 | 46 | 69.7 | 146 | 3 | AAy68057 | AAy68057 Yeast mat | 189 | 42 | 63.6 | 61 | 2 | AAW18427 | Aaw18427 KPI(-4 to |
| 117 | 46 | 69.7 | 146 | 3 | AAy68181 | AAy68181 Yeast mat | 190 | 42 | 63.6 | 61 | 2 | AAy68124 | Aay68124 Kunitz pr |
| 118 | 46 | 69.7 | 233 | 3 | AAy68180 | AAy68180 PhOA sign | 191 | 42 | 63.6 | 61 | 3 | AAy68036 | Aay68036 Kunitz pr |
| 119 | 45 | 68.2 | 61 | 2 | AAW18405 | Aaw18405 KPI(-4 to | 192 | 42 | 63.6 | 61 | 3 | AAU09216 | Aau09216 Human KPI |
| 120 | 45 | 68.2 | 61 | 2 | AAW18402 | Aaw18402 KPI(-4 to | 193 | 42 | 63.6 | 142 | 8 | ADF72584 | Adf72584 Mouse mon |
| 121 | 45 | 68.2 | 61 | 2 | AAW18426 | Aaw18426 KPI(-4 to | 194 | 42 | 63.6 | 146 | 2 | AAW18448 | Aaw18448 Alpha mat |
| 122 | 45 | 68.2 | 61 | 2 | AAW18406 | Aaw18406 KPI(-4 to | 195 | 42 | 63.6 | 146 | 2 | AAy68027 | Aay68027 Yeast mat |
| 123 | 45 | 68.2 | 61 | 3 | AAy68163 | AAy68163 Kunitz pr | 196 | 42 | 63.6 | 146 | 4 | AAU09207 | Aau09207 Yeast alp |
| 124 | 45 | 68.2 | 61 | 3 | AAy68166 | AAy68166 Kunitz pr | 197 | 41 | 62.1 | 10 | 5 | ABP66448 | Abp66448 Human RSV |
| 125 | 45 | 68.2 | 61 | 3 | AAy68175 | AAy68175 Kunitz pr | 198 | 41 | 62.1 | 10 | 6 | ABU69311 | Abu69311 Respirato |
| 126 | 45 | 68.2 | 61 | 3 | AAy68167 | AAy68167 Kunitz pr | 199 | 41 | 62.1 | 10 | 7 | ADe35806 | Ade35806 SYNAGIS a |
| 127 | 45 | 68.2 | 61 | 3 | AAy68164 | AAy68164 Kunitz pr | 200 | 41 | 62.1 | 10 | 8 | ADi56968 | Adi56968 RSV antib |
| 128 | 45 | 68.2 | 61 | 3 | AAy68122 | AAy68122 Kunitz pr | 201 | 41 | 62.1 | 10 | 8 | ADU87704 | Adu87704 Mouse Luc |
| 129 | 45 | 68.2 | 61 | 3 | AAy68157 | AAy68157 Kunitz pr | 202 | 41 | 62.1 | 10 | 8 | ADU87718 | Adu87718 Anti-CS1 |
| 130 | 45 | 68.2 | 61 | 3 | AAy68170 | AAy68170 Kunitz pr | 203 | 41 | 62.1 | 10 | 9 | ADW19948 | Adw19948 RSV anti |
| 131 | 45 | 68.2 | 61 | 3 | AAy68042 | AAy68042 Kunitz pr | 204 | 41 | 62.1 | 10 | 9 | AEb06930 | Aeb06930 RSV-speci |
| 132 | 45 | 68.2 | 61 | 4 | AAU09330 | AAU09330 Human KPI | 205 | 41 | 62.1 | 12 | 7 | ABR61519 | Abr61519 Humanised |
| 133 | 45 | 68.2 | 61 | 4 | AAU09327 | AAU09327 Human KPI | 206 | 41 | 62.1 | 12 | 9 | ADW95714 | Adw95714 Anti-HIL- |
| 134 | 45 | 68.2 | 61 | 4 | AAU09335 | AAU09335 Human KPI | 207 | 41 | 62.1 | 12 | 9 | ADX15719 | Adx15719 Mouse ant |
| 135 | 45 | 68.2 | 61 | 4 | AAU09317 | AAU09317 Human KPI | 208 | 41 | 62.1 | 13 | 7 | ADJ94579 | Adj94579 Humanised |
| 136 | 45 | 68.2 | 61 | 4 | AAU09324 | AAU09324 Human KPI | 209 | 41 | 62.1 | 13 | 8 | ADL73178 | Adl73178 CDK3 of t |
| 137 | 45 | 68.2 | 61 | 4 | AAU09323 | AAU09323 Human KPI | 210 | 41 | 62.1 | 13 | 8 | ADP79605 | Adp79605 Murine 2H |
| 138 | 45 | 68.2 | 61 | 4 | AAU09326 | AAU09326 Human KPI | 211 | 41 | 62.1 | 13 | 9 | ADW21314 | Adw21314 Mouse ant |
| 139 | 45 | 68.2 | 61 | 4 | AAU09222 | AAU09222 Human KPI | 212 | 41 | 62.1 | 16 | 9 | AEb08081 | Aeb08081 Chimeric |
| 140 | 45 | 68.2 | 146 | 2 | AAW19809 | Aaw19809 Alpha mat | 213 | 41 | 62.1 | 18 | 3 | AAb06400 | Aab06400 Randomise |
| 141 | 45 | 68.2 | 146 | 3 | AAy68048 | AAy68048 Yeast mat | 214 | 41 | 62.1 | 19 | 5 | Aau70381 | Aau70381 Mouse hea |
| 142 | 45 | 68.2 | 146 | 4 | AAU09228 | AAU09228 Yeast alp | 215 | 41 | 62.1 | 24 | 9 | ADW95711 | Adw95711 Anti-HIL- |
| 143 | 45 | 68.2 | 233 | 2 | AAW19808 | Aaw19808 phOA-KIP(- | 216 | 41 | 62.1 | 24 | 9 | ADW95711 | Adw95711 Mouse ant |
| 144 | 45 | 68.2 | 233 | 3 | AAy68047 | AAy68047 PhOA-KPI | 217 | 41 | 62.1 | 61 | 2 | AAW18419 | Aaw18419 KPI(-4 to |
| 145 | 45 | 68.2 | 233 | 3 | AAU09227 | AAU09227 Bacterial | 218 | 41 | 62.1 | 61 | 3 | AAy68038 | Aay68038 Kunitz pr |
| 146 | 44 | 66.7 | 9 | 8 | ADM41731 | Adm41731 Peptide t | 219 | 41 | 62.1 | 61 | 3 | AAy68125 | Aay68125 Kunitz pr |
| 147 | 44 | 66.7 | 10 | 2 | AAW18418 | Aaw18418 Murine an | 220 | 41 | 62.1 | 61 | 3 | AAy68082 | Aay68082 Kunitz pr |
| 148 | 44 | 66.7 | 61 | 2 | AAW18418 | Aaw18418 KPI(-4 to | 221 | 41 | 62.1 | 61 | 3 | AAy68142 | Aay68142 Kunitz pr |
| 149 | 44 | 66.7 | 61 | 3 | AAy68156 | AAy68156 Kunitz pr | 222 | 41 | 62.1 | 61 | 3 | AAy68161 | Aay68161 Kunitz pr |
| 150 | 44 | 66.7 | 61 | 3 | AAy68128 | AAy68128 Kunitz pr | 223 | 41 | 62.1 | 61 | 4 | AAU09321 | Aau09321 Human KPI |
| 151 | 44 | 66.7 | 61 | 3 | AAy68037 | AAy68037 Kunitz pr | 224 | 41 | 62.1 | 61 | 4 | AAU09302 | Aau09302 Human KPI |
| 152 | 44 | 66.7 | 61 | 3 | AAy68174 | AAy68174 Kunitz pr | 225 | 41 | 62.1 | 61 | 4 | AAU09252 | Aau09252 Human KPI |
| 153 | 44 | 66.7 | 61 | 3 | AAy68081 | AAy68081 Kunitz pr | 226 | 41 | 62.1 | 61 | 4 | AAU09218 | Aau09218 Human KPI |
| 154 | 44 | 66.7 | 61 | 3 | AAy68141 | AAy68141 Kunitz pr | 227 | 41 | 62.1 | 106 | 2 | AAU0937 | Aau0937 Sequence |
| 155 | 44 | 66.7 | 61 | 4 | AAU09316 | AAU09316 Human KPI | 228 | 41 | 62.1 | 115 | 2 | AAW34018 | Aaw34018 BW 835 VH |
| 156 | 44 | 66.7 | 61 | 4 | AAU09301 | AAU09301 Human KPI | 229 | 41 | 62.1 | 116 | 2 | AAW00827 | Aaw00827 Variant v |
| 157 | 44 | 66.7 | 61 | 4 | AAU09334 | AAU09334 Human KPI | 230 | 41 | 62.1 | 116 | 2 | AAW19014 | Aaw19014 Anti-huma |
| 158 | 44 | 66.7 | 61 | 4 | AAU09217 | AAU09217 Human KPI | 231 | 41 | 62.1 | 117 | 2 | AAW00837 | Aaw00837 Variable |
| 159 | 44 | 66.7 | 61 | 4 | AAU09251 | AAU09251 Human KPI | 232 | 41 | 62.1 | 118 | 9 | ADW50592 | Adw50592 Protein o |
| 160 | 44 | 66.7 | 116 | 2 | AAW38609 | Aaw38609 MCPC heav | 233 | 41 | 62.1 | 119 | 8 | ADW44272 | Adw44272 Primer in |
| 161 | 44 | 66.7 | 126 | 2 | AAW62879 | Aaw62879 Murine an | 234 | 41 | 62.1 | 119 | 8 | ADU87733 | Adu87733 Heavy cha |
| 162 | 44 | 66.7 | 126 | 2 | AAW62880 | Aaw62880 Murine an | 235 | 41 | 62.1 | 119 | 8 | ADU87692 | Adu87692 Mouse Luc |
| 163 | 44 | 66.7 | 146 | 2 | AAW18449 | Aaw18449 Alpha mat | 236 | 41 | 62.1 | 119 | 8 | ADU87724 | Adu87724 Heavy cha |
| 164 | 44 | 66.7 | 146 | 3 | AAy68028 | AAy68028 Yeast mat | 237 | 41 | 62.1 | 119 | 8 | ADU87727 | Adu87727 Humanized |
| 165 | 44 | 66.7 | 146 | 4 | AAU09208 | AAU09208 Yeast alp | 238 | 41 | 62.1 | 119 | 8 | ADU87731 | Adu87731 VH region |
| 166 | 44 | 66.7 | 624 | 8 | ADN19874 | Adn19874 Bacterial | 239 | 41 | 62.1 | 120 | 7 | ABR61521 | Abr61521 Murine RS |
| 167 | 43 | 65.2 | 61 | 3 | AAy68155 | AAy68155 Kunitz pr | 240 | 41 | 62.1 | 120 | 8 | ADW44280 | Adw44280 Humanised |
| 168 | 43 | 65.2 | 61 | 3 | AAy68149 | AAy68149 Kunitz pr | 241 | 41 | 62.1 | 120 | 8 | ADW44274 | Adw44274 Consensus |
| 169 | 43 | 65.2 | 61 | 4 | AAU09315 | AAU09315 Human KPI | 242 | 41 | 62.1 | 120 | 8 | ADW44271 | Adw44271 Sequence |
| 170 | 43 | 65.2 | 61 | 4 | AAU09309 | AAU09309 Human KPI | 243 | 41 | 62.1 | 121 | 2 | AAW88846 | Aaw88846 Murine an |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|-----------|---------------------|-----|----|------|-----|---|-----------|---------------------|
| 244 | 41 | 62.1 | 121 | 6 | ABP59986 | Abp59986 Antibody | 317 | 41 | 62.1 | 422 | 7 | ADD25591 | Add25591 Binding d |
| 245 | 41 | 62.1 | 121 | 7 | ABR61525 | Abf61525 Humanised | 318 | 41 | 62.1 | 422 | 7 | ADD25473 | Add25473 Binding d |
| 246 | 41 | 62.1 | 121 | 7 | ADP69650 | Adf69650 Humanised | 319 | 41 | 62.1 | 422 | 7 | ADM42748 | Adm42748 2H7scFv-C |
| 247 | 41 | 62.1 | 121 | 8 | ADO26409 | Ado26409 Murine an | 320 | 41 | 62.1 | 422 | 9 | ABE95416 | Aeb95416 Mouse 2H7 |
| 248 | 41 | 62.1 | 121 | 9 | ADW03412 | Adw03412 Murine an | 321 | 41 | 62.1 | 422 | 9 | ABE94450 | Aeb94450 Mouse ant |
| 249 | 41 | 62.1 | 121 | 9 | ADM955708 | Adm955708 Mouse ant | 322 | 41 | 62.1 | 423 | 4 | AAB30695 | Aab30695 A fusion |
| 250 | 41 | 62.1 | 121 | 9 | ADX15713 | Adx15713 Mouse ant | 323 | 41 | 62.1 | 423 | 6 | ABJ39010 | Abj39010 B9E9 scFv |
| 251 | 41 | 62.1 | 121 | 9 | ABE03869 | Aeb03869 B-CDL pha | 324 | 41 | 62.1 | 426 | 9 | ADY22144 | Ady22144 Antibody |
| 252 | 41 | 62.1 | 122 | 1 | AAP91382 | Aap91382 Antibody | 325 | 41 | 62.1 | 426 | 9 | ABE95423 | Aeb95423 Mouse 2H7 |
| 253 | 41 | 62.1 | 122 | 2 | AAR79878 | Aar79878 Anti-EGFR | 326 | 41 | 62.1 | 426 | 9 | ABE94457 | Aeb94457 Mouse ant |
| 254 | 41 | 62.1 | 122 | 2 | AAW02201 | Aaw02201 CDR swtcc | 327 | 41 | 62.1 | 426 | 9 | ABE94457 | Aeb94457 Mouse ant |
| 255 | 41 | 62.1 | 122 | 8 | ADP79573 | Adp79573 Murine 2H | 328 | 41 | 62.1 | 452 | 8 | ADS33304 | Ads33304 Anti-CD20 |
| 256 | 41 | 62.1 | 122 | 8 | ADP79574 | Adp79574 Humanised | 329 | 41 | 62.1 | 452 | 9 | ADM03410 | Adm03410 Humanized |
| 257 | 41 | 62.1 | 122 | 8 | ADS33302 | Ads33302 Anti-CD20 | 330 | 41 | 62.1 | 452 | 9 | ADM03411 | Adm03411 Humanized |
| 258 | 41 | 62.1 | 122 | 8 | ADM03408 | Adm03408 Humanized | 331 | 41 | 62.1 | 452 | 9 | ABE21728 | Aeb21728 Humanized |
| 259 | 41 | 62.1 | 122 | 9 | ADW211310 | Adw211310 Mouse ant | 332 | 41 | 62.1 | 452 | 9 | ABE17638 | Aeb17638 Heavy cha |
| 260 | 41 | 62.1 | 122 | 9 | ADM211309 | Adm211309 Mouse ant | 333 | 41 | 62.1 | 468 | 9 | ABE08072 | Aeb08072 Murine/hu |
| 261 | 41 | 62.1 | 122 | 9 | ADX00803 | Adx00803 Humanized | 334 | 41 | 62.1 | 469 | 7 | ABR61529 | Abf61529 Humanised |
| 262 | 41 | 62.1 | 122 | 9 | ADY21867 | Ady21867 Human ant | 335 | 41 | 62.1 | 469 | 7 | ABR61527 | Abf61527 Humanised |
| 263 | 41 | 62.1 | 122 | 9 | ADY62623 | Ady62623 Humanized | 336 | 41 | 62.1 | 471 | 8 | ADP79584 | Adp79584 2H7.v31 H |
| 264 | 41 | 62.1 | 122 | 9 | ABE27726 | Aeb27726 Humanized | 337 | 41 | 62.1 | 471 | 8 | ADP79585 | Adp79585 2H7.v31 L |
| 265 | 41 | 62.1 | 122 | 9 | ABE17636 | Aeb17636 Variable | 338 | 41 | 62.1 | 471 | 9 | ADM03399 | Adm03399 Human ant |
| 266 | 41 | 62.1 | 123 | 2 | AAR79877 | Aar79877 Anti-EGFR | 339 | 41 | 62.1 | 471 | 9 | ADM03406 | Adm03406 Human ant |
| 267 | 41 | 62.1 | 123 | 5 | AG688244 | Ag688244 Mouse mon | 340 | 41 | 62.1 | 471 | 9 | ADM211319 | Adm211319 Mouse ant |
| 268 | 41 | 62.1 | 123 | 8 | ADR38656 | Adr38656 Mouse hea | 341 | 41 | 62.1 | 471 | 9 | ADM211320 | Adm211320 Mouse ant |
| 269 | 41 | 62.1 | 137 | 8 | ADL73173 | Adl73173 Anti-idio | 342 | 41 | 62.1 | 471 | 9 | ADX00805 | Adx00805 Humanized |
| 270 | 41 | 62.1 | 137 | 8 | ADU87714 | Adu87714 Anti-CS1 | 343 | 41 | 62.1 | 471 | 9 | ADY62625 | Ady62625 Humanized |
| 271 | 41 | 62.1 | 140 | 1 | AAP70627 | Aap70627 Sequence | 344 | 41 | 62.1 | 482 | 5 | ABG31031 | Abg31031 Synthetic |
| 272 | 41 | 62.1 | 140 | 1 | AAP94780 | Aap94780 2 H7 VH 9 | 345 | 41 | 62.1 | 482 | 7 | ADD25472 | Add25472 Binding d |
| 273 | 41 | 62.1 | 140 | 2 | AAW10242 | Aaw10242 Heavy cha | 346 | 41 | 62.1 | 482 | 7 | ADD25589 | Add25589 Binding d |
| 274 | 41 | 62.1 | 140 | 2 | AAW10588 | Aaw10588 2H7 antib | 347 | 41 | 62.1 | 482 | 7 | ADM42747 | Adm42747 2H7-CD154 |
| 275 | 41 | 62.1 | 140 | 2 | AAW16343 | Aaw16343 2H7 heavy | 348 | 41 | 62.1 | 482 | 9 | ABE95415 | Aeb95415 Mouse 2H7 |
| 276 | 41 | 62.1 | 140 | 2 | AAW41070 | Aaw41070 Mouse 2H7 | 349 | 41 | 62.1 | 482 | 9 | ABE94449 | Aeb94449 Mouse ant |
| 277 | 41 | 62.1 | 140 | 2 | AAW47513 | Aaw47513 Mouse 2H7 | 350 | 41 | 62.1 | 486 | 9 | ADY22142 | Ady22142 Antibody |
| 278 | 41 | 62.1 | 140 | 2 | AAW47520 | Aaw47520 Mouse 2H7 | 351 | 41 | 62.1 | 486 | 9 | ABE95425 | Aeb95425 Mouse 2H7 |
| 279 | 41 | 62.1 | 140 | 2 | AAW89540 | Aaw89540 Mouse ant | 352 | 41 | 62.1 | 486 | 9 | ABE94456 | Aeb94456 Mouse ant |
| 280 | 41 | 62.1 | 140 | 4 | AAW98092 | Aaw98092 2H7 heavy | 353 | 41 | 62.1 | 498 | 7 | ADD25674 | Add25674 Binding d |
| 281 | 41 | 62.1 | 140 | 7 | ABC65027 | Abc65027 Immunoglo | 354 | 41 | 62.1 | 498 | 5 | ABG31026 | Abg31026 Synthetic |
| 282 | 41 | 62.1 | 142 | 9 | ABE08073 | Aeb08073 HLA-DR sp | 355 | 41 | 62.1 | 499 | 5 | ABG31027 | Abg31027 Synthetic |
| 283 | 41 | 62.1 | 146 | 2 | AAW18450 | Aaw18450 Alpha mat | 356 | 41 | 62.1 | 499 | 5 | ABG31025 | Abg31025 Synthetic |
| 284 | 41 | 62.1 | 146 | 3 | AAW68029 | Aaw68029 Yeast mat | 357 | 41 | 62.1 | 499 | 7 | ADD25587 | Add25587 Binding d |
| 285 | 41 | 62.1 | 146 | 3 | AAW09209 | Aaw09209 Yeast alp | 358 | 41 | 62.1 | 499 | 7 | ADD25454 | Add25454 Binding d |
| 286 | 41 | 62.1 | 147 | 2 | AAR98411 | Aar98411 3H1 heavy | 359 | 41 | 62.1 | 499 | 7 | ADD25456 | Add25456 Binding d |
| 287 | 41 | 62.1 | 147 | 2 | AAR99687 | Aar99687 Monoclonal | 360 | 41 | 62.1 | 499 | 7 | ADD25455 | Add25455 Binding d |
| 288 | 41 | 62.1 | 147 | 2 | AAE04728 | Aae04728 Mouse ant | 361 | 41 | 62.1 | 499 | 7 | ADM42731 | Adm42731 2H7scFv-I |
| 289 | 41 | 62.1 | 147 | 2 | AAW26729 | Aaw26729 Anti-idio | 362 | 41 | 62.1 | 499 | 7 | ADM42729 | Adm42729 2H7scFv-I |
| 290 | 41 | 62.1 | 147 | 3 | AAW49962 | Aaw49962 Murine MA | 363 | 41 | 62.1 | 499 | 7 | ADM42730 | Adm42730 2H7scFv-I |
| 291 | 41 | 62.1 | 147 | 5 | AAO14017 | Aao14017 Mouse 3H1 | 364 | 41 | 62.1 | 499 | 9 | ABE95397 | Aeb95397 Mouse hum |
| 292 | 41 | 62.1 | 147 | 5 | ABO08120 | Abb08120 Antibody | 365 | 41 | 62.1 | 499 | 9 | ABE95398 | Aeb95398 Mouse hum |
| 293 | 41 | 62.1 | 147 | 6 | AAO16295 | Aao16295 Mouse 3H1 | 366 | 41 | 62.1 | 499 | 9 | ABE95399 | Aeb95399 Mouse hum |
| 294 | 41 | 62.1 | 147 | 7 | ADC16717 | Adc16717 Heavy cha | 367 | 41 | 62.1 | 499 | 9 | ABE94431 | Aeb94431 Mouse ant |
| 295 | 41 | 62.1 | 147 | 9 | ADV86079 | Adv86079 3H1 heavy | 368 | 41 | 62.1 | 499 | 9 | ABE94433 | Aeb94433 Mouse ant |
| 296 | 41 | 62.1 | 151 | 1 | AAP30252 | Aap30252 Sequence | 369 | 41 | 62.1 | 499 | 9 | ABE94432 | Aeb94432 Mouse ant |
| 297 | 41 | 62.1 | 222 | 9 | ADW50595 | Adw50595 Protein o | 370 | 41 | 62.1 | 500 | 7 | ADD25826 | Add25826 Binding d |
| 298 | 41 | 62.1 | 239 | 2 | AAR64812 | Aar64812 ScFv anti | 371 | 41 | 62.1 | 500 | 7 | ADD25837 | Add25837 Binding d |
| 299 | 41 | 62.1 | 244 | 8 | ADG28554 | Adg28554 Paramyxov | 372 | 41 | 62.1 | 500 | 7 | ADD25713 | Add25713 Binding d |
| 300 | 41 | 62.1 | 246 | 9 | ADW50596 | Adw50596 Protein o | 373 | 41 | 62.1 | 500 | 7 | ADD25836 | Add25836 Binding d |
| 301 | 41 | 62.1 | 253 | 8 | ADP79580 | Adp79580 Chimeric | 374 | 41 | 62.1 | 500 | 7 | ADD25824 | Add25824 Binding d |
| 302 | 41 | 62.1 | 266 | 5 | ABG31021 | Abg31021 Mouse sin | 375 | 41 | 62.1 | 500 | 7 | ADD25827 | Add25827 Binding d |
| 303 | 41 | 62.1 | 266 | 7 | ADD25450 | Add25450 Binding d | 376 | 41 | 62.1 | 500 | 7 | ADD25827 | Add25827 Binding d |
| 304 | 41 | 62.1 | 266 | 7 | ADM42725 | Adm42725 Synthetic | 377 | 41 | 62.1 | 500 | 7 | ADD25835 | Add25835 Binding d |
| 305 | 41 | 62.1 | 266 | 9 | ABE95393 | Aeb95393 Mouse 2H7 | 378 | 41 | 62.1 | 500 | 7 | ADD25828 | Add25828 Binding d |
| 306 | 41 | 62.1 | 266 | 9 | ABE94427 | Aeb94427 Mouse ant | 379 | 41 | 62.1 | 500 | 7 | ADD25825 | Add25825 Binding d |
| 307 | 41 | 62.1 | 267 | 9 | ADY21839 | Ady21839 Human ant | 380 | 41 | 62.1 | 500 | 7 | ADD25791 | Add25791 Binding d |
| 308 | 41 | 62.1 | 268 | 9 | ADY21859 | Ady21859 Human ant | 381 | 41 | 62.1 | 500 | 9 | ADY21783 | Ady21783 Antibody |
| 309 | 41 | 62.1 | 268 | 9 | ADY21861 | Ady21861 Human ant | 382 | 41 | 62.1 | 500 | 9 | ADY21891 | Ady21891 Antibody |
| 310 | 41 | 62.1 | 268 | 9 | ADY21869 | Ady21869 Human ant | 383 | 41 | 62.1 | 500 | 9 | ADY21764 | Ady21764 Antibody |
| 311 | 41 | 62.1 | 268 | 9 | ADY21837 | Ady21837 Human ant | 384 | 41 | 62.1 | 500 | 9 | ADY21793 | Ady21793 Antibody |
| 312 | 41 | 62.1 | 305 | 9 | ABE39435 | Aeb39435 L. pneumo | 385 | 41 | 62.1 | 500 | 9 | ADY21915 | Ady21915 Antibody |
| 313 | 41 | 62.1 | 305 | 9 | ABE36006 | Aeb36006 L. pneumo | 386 | 41 | 62.1 | 500 | 9 | ADY21997 | Ady21997 Antibody |
| 314 | 41 | 62.1 | 402 | 4 | AAB30694 | Aab30694 A fusion | 387 | 41 | 62.1 | 500 | 9 | ADY21787 | Ady21787 Antibody |
| 315 | 41 | 62.1 | 412 | 6 | ABJ39009 | Abj39009 B9E9 scFv | 388 | 41 | 62.1 | 500 | 9 | ADY21931 | Ady21931 Antibody |
| 316 | 41 | 62.1 | 422 | 5 | ABG31032 | Abg31032 Synthetic | 389 | 41 | 62.1 | 500 | 9 | ADY21993 | Ady21993 Antibody |

| | | | | | | | | | | | | | |
|-----|------|------|-----|---|-----------|---------------------|-----|----|------|-----|---|-----------|---------------------|
| 390 | 41 | 62.1 | 500 | 9 | ADY21683 | Ady21683 Antibody | 463 | 40 | 60.6 | 122 | 8 | ADW931270 | Adw931270 VEGF mono |
| 391 | 41 | 62.1 | 500 | 9 | ADY21785 | Ady21785 Antibody | 464 | 40 | 60.6 | 138 | 4 | AAG66455 | Aag66455 VEGF ScPv |
| 392 | 41 | 62.1 | 500 | 9 | ADY21789 | Ady21789 Antibody | 465 | 40 | 60.6 | 146 | 4 | AAW18447 | Aaw18447 Alpha mat |
| 393 | 41 | 62.1 | 500 | 9 | ADY21653 | Ady21653 Antibody | 466 | 40 | 60.6 | 146 | 3 | AAy68026 | Aay68026 Yeast mat |
| 394 | 41 | 62.1 | 500 | 9 | ADY21933 | Ady21933 Antibody | 467 | 40 | 60.6 | 146 | 4 | AAU09206 | Aau09206 Yeast alp |
| 395 | 41 | 62.1 | 500 | 9 | ADY21760 | Ady21760 Antibody | 468 | 40 | 60.6 | 155 | 5 | ABB72375 | Abb72375 Murine pr |
| 396 | 41 | 62.1 | 500 | 9 | ADY21781 | Ady21781 Antibody | 469 | 40 | 60.6 | 171 | 4 | AAE05363 | Aae05363 Mouse hep |
| 397 | 41 | 62.1 | 500 | 9 | ADY21791 | Ady21791 Antibody | 470 | 40 | 60.6 | 306 | 9 | Adx58064 | Adx58064 A single |
| 398 | 41 | 62.1 | 500 | 9 | ADY21871 | Ady21871 Antibody | 471 | 40 | 60.6 | 406 | 8 | Adx23619 | Adx23619 Bacterial |
| 399 | 41 | 62.1 | 500 | 9 | ADY21889 | Ady21889 Antibody | 472 | 40 | 60.6 | 441 | 7 | ABO83560 | AbO83560 Pseudomon |
| 400 | 41 | 62.1 | 500 | 9 | ADY21909 | Ady21909 Antibody | 473 | 40 | 60.6 | 481 | 5 | ABR338845 | ABr338845 A. niger |
| 401 | 41 | 62.1 | 500 | 9 | ADY21917 | Ady21917 Antibody | 474 | 39 | 59.1 | 17 | 3 | AABo6394 | AABo6394 Randomise |
| 402 | 41 | 62.1 | 500 | 9 | ADY21925 | Ady21925 Antibody | 475 | 39 | 59.1 | 57 | 3 | AAy68014 | Aay68014 Kunitz pr |
| 403 | 41 | 62.1 | 500 | 9 | ADY21901 | Ady21901 Antibody | 476 | 39 | 59.1 | 58 | 2 | AAW07746 | Aaw07746 Non-nativ |
| 404 | 41 | 62.1 | 500 | 9 | ADY21995 | Ady21995 Antibody | 477 | 39 | 59.1 | 58 | 2 | AAW07768 | Aaw07768 Non-nativ |
| 405 | 41 | 62.1 | 500 | 9 | ADY21893 | Ady21893 Antibody | 478 | 39 | 59.1 | 58 | 2 | AAW64082 | Aaw64082 Human Kun |
| 406 | 41 | 62.1 | 500 | 9 | ADY21899 | Ady21899 Antibody | 479 | 39 | 59.1 | 58 | 2 | AAW64140 | Aaw64140 Human Kun |
| 407 | 41 | 62.1 | 500 | 9 | ADY21762 | Ady21762 Antibody | 480 | 39 | 59.1 | 61 | 2 | AAW18420 | Aaw18420 KPI (-4 to |
| 408 | 41 | 62.1 | 500 | 9 | ADY21756 | Ady21756 Antibody | 481 | 39 | 59.1 | 61 | 3 | AAy68143 | Aay68143 Kunitz pr |
| 409 | 41 | 62.1 | 500 | 9 | ADY21923 | Ady21923 Antibody | 482 | 39 | 59.1 | 61 | 3 | AAy68172 | Aay68172 Kunitz pr |
| 410 | 41 | 62.1 | 500 | 9 | ADY21779 | Ady21779 Antibody | 483 | 39 | 59.1 | 61 | 3 | AAy68083 | Aay68083 Kunitz pr |
| 411 | 41 | 62.1 | 500 | 9 | ADY21907 | Ady21907 Antibody | 484 | 39 | 59.1 | 61 | 3 | AAy68147 | Aay68147 Kunitz pr |
| 412 | 41 | 62.1 | 501 | 9 | ADY21855 | Ady21855 Antibody | 485 | 39 | 59.1 | 61 | 3 | AAy68160 | Aay68160 Kunitz pr |
| 413 | 41 | 62.1 | 501 | 9 | ADY21853 | Ady21853 Antibody | 486 | 39 | 59.1 | 61 | 3 | AAy68171 | Aay68171 Kunitz pr |
| 414 | 41 | 62.1 | 502 | 7 | ADD25744 | Add25744 Binding d | 487 | 39 | 59.1 | 61 | 4 | AAU09320 | Aau09320 Human KPI |
| 415 | 41 | 62.1 | 502 | 9 | ADY21701 | Ady21701 Antibody | 488 | 39 | 59.1 | 61 | 4 | AAU09331 | Aau09331 Human KPI |
| 416 | 41 | 62.1 | 502 | 9 | ADY22140 | Ady22140 Human ant | 489 | 39 | 59.1 | 61 | 4 | AAU09303 | Aau09303 Human KPI |
| 417 | 41 | 62.1 | 502 | 9 | ABE95424 | Aeb95424 Mouse hum | 490 | 39 | 59.1 | 61 | 4 | AAU09253 | Aau09253 Human KPI |
| 418 | 41 | 62.1 | 502 | 9 | ABE94458 | Aeb94458 Mouse ant | 491 | 39 | 59.1 | 61 | 4 | AAU09332 | Aau09332 Human KPI |
| 419 | 41 | 62.1 | 503 | 7 | ADD25676 | Add25676 Binding d | 492 | 39 | 59.1 | 61 | 4 | AAU09307 | Aau09307 Human KPI |
| 420 | 41 | 62.1 | 503 | 9 | ADY21651 | Ady21651 Antibody | 493 | 39 | 59.1 | 117 | 2 | AAU07318 | Aau07318 VH domain |
| 421 | 41 | 62.1 | 505 | 5 | ABG31028 | Abg31028 Synthetic | 494 | 39 | 59.1 | 117 | 2 | AAW14486 | Aaw14486 Monoclonal |
| 422 | 41 | 62.1 | 505 | 7 | ADD25723 | Add25723 Binding d | 495 | 39 | 59.1 | 117 | 2 | AAU99875 | Aau99875 Monoclonal |
| 423 | 41 | 62.1 | 505 | 7 | ADD25457 | Add25457 Binding d | 496 | 39 | 59.1 | 118 | 2 | AAU99875 | Aau99875 Monoclonal |
| 424 | 41 | 62.1 | 505 | 7 | ADMA42732 | Adm42732 2H7scFv-1 | 497 | 39 | 59.1 | 120 | 7 | ADP03974 | Adp03974 Murine-ex |
| 425 | 41 | 62.1 | 505 | 9 | ADY21685 | Ady21685 Antibody | 498 | 39 | 59.1 | 120 | 7 | ADP03873 | Adp03873 Murine-ex |
| 426 | 41 | 62.1 | 505 | 9 | ABE95400 | Aeb95400 Mouse hum | 499 | 39 | 59.1 | 126 | 4 | AAE62268 | Aae62268 Heavy cha |
| 427 | 41 | 62.1 | 505 | 9 | ABE94434 | Aeb94434 Mouse ant | 500 | 39 | 59.1 | 126 | 4 | AAE62274 | Aae62274 Mutant he |
| 428 | 41 | 62.1 | 507 | 9 | ADY21879 | Ady21879 Antibody | 501 | 39 | 59.1 | 533 | 5 | ABE54368 | ABe54368 Lactococc |
| 429 | 41 | 62.1 | 514 | 7 | ADD25675 | Add25675 Binding d | 502 | 39 | 59.1 | 616 | 8 | ADY24775 | Ady24775 Plant ful |
| 430 | 41 | 62.1 | 514 | 7 | ADY21649 | Ady21649 Antibody | 503 | 39 | 59.1 | 832 | 2 | AAW04302 | Aaw04302 Antibody/ |
| 431 | 41 | 62.1 | 516 | 7 | ADD25738 | Add25738 Binding d | 504 | 39 | 59.1 | 909 | 2 | AAU50092 | Aau50092 Humanised |
| 432 | 41 | 62.1 | 516 | 9 | ADY21877 | Ady21877 Antibody | 505 | 38 | 58.3 | 121 | 7 | ADJ94609 | Adj94609 Humanised |
| 433 | 41 | 62.1 | 516 | 9 | ADY21696 | Ady21696 Antibody | 506 | 38 | 58.3 | 121 | 7 | ADJ94608 | Adj94608 Humanised |
| 434 | 41 | 62.1 | 520 | 7 | ADD25725 | Add25725 Binding d | 507 | 38 | 58.3 | 140 | 7 | ADJ94616 | Adj94616 Human ant |
| 435 | 41 | 62.1 | 520 | 9 | ADY21687 | Ady21687 Antibody | 508 | 38 | 58.3 | 140 | 7 | ADJ94618 | Adj94618 Human ant |
| 436 | 41 | 62.1 | 551 | 9 | ADY22067 | Ady22067 2H7 scFv | 509 | 38 | 57.6 | 8 | 8 | ADJ94618 | Adj94618 Human ant |
| 437 | 41 | 62.1 | 592 | 7 | ADD25773 | Add25773 Binding d | 510 | 38 | 57.6 | 8 | 8 | ADJ94618 | Adj94618 Human ant |
| 438 | 41 | 62.1 | 592 | 9 | ADY21754 | Ady21754 Antibody | 511 | 38 | 57.6 | 10 | 7 | ADD69225 | Add69225 Human hea |
| 439 | 41 | 62.1 | 593 | 9 | ADY21873 | Ady21873 Antibody | 512 | 38 | 57.6 | 10 | 7 | ADD69228 | Add69228 Human hea |
| 440 | 41 | 62.1 | 599 | 9 | ADY21875 | Ady21875 Antibody | 513 | 38 | 57.6 | 15 | 8 | ADG31813 | Adg31813 Experimen |
| 441 | 41 | 62.1 | 619 | 4 | ABB70767 | Abb70767 Drosophil | 514 | 38 | 57.6 | 16 | 5 | ABP46939 | ABp46939 Human Bly |
| 442 | 41 | 62.1 | 619 | 8 | ADS96522 | Ads96522 Drosophil | 515 | 38 | 57.6 | 16 | 5 | ABP47012 | ABp47012 Human Bly |
| 443 | 41 | 62.1 | 768 | 7 | ADD25789 | Add25789 Binding d | 516 | 38 | 57.6 | 16 | 5 | ABP46155 | ABp46155 Human Bly |
| 444 | 41 | 62.1 | 768 | 9 | ADY21740 | Ady21740 Antibody | 517 | 38 | 57.6 | 16 | 7 | ADG97839 | Adg97839 scFV VHCD |
| 445 | 40.5 | 61.4 | 117 | 2 | AAR53929 | Aar53929 Heavy cha | 518 | 38 | 57.6 | 16 | 7 | ADG97766 | Adg97766 scFV VHCD |
| 446 | 40.5 | 61.4 | 286 | 5 | ABB09485 | Abb09485 AaEPV tri | 519 | 38 | 57.6 | 16 | 7 | ADG96982 | Adg96982 scFV VHCD |
| 447 | 40 | 60.6 | 58 | 2 | AAW07747 | Aaw07747 Non-nativ | 520 | 38 | 57.6 | 17 | 3 | AABo6373 | AABo6373 Randomise |
| 448 | 40 | 60.6 | 58 | 2 | AAW64110 | Aaw64110 Human Kun | 521 | 38 | 57.6 | 17 | 3 | AABo5891 | AABo5891 Randomise |
| 449 | 40 | 60.6 | 61 | 2 | AAW18430 | Aaw18430 KPI (-4 to | 522 | 38 | 57.6 | 17 | 3 | AABo6355 | AABo6355 Randomise |
| 450 | 40 | 60.6 | 61 | 2 | AAW18428 | Aaw18428 KPI (-4 to | 523 | 38 | 57.6 | 17 | 3 | AABo6403 | AABo6403 Randomise |
| 451 | 40 | 60.6 | 61 | 3 | AAy68090 | Aay68090 Kunitz pr | 524 | 38 | 57.6 | 17 | 3 | AABo5885 | AABo5885 Randomise |
| 452 | 40 | 60.6 | 61 | 3 | AAy68035 | Aay68035 Kunitz pr | 525 | 38 | 57.6 | 17 | 3 | AABo6357 | AABo6357 Randomise |
| 453 | 40 | 60.6 | 61 | 3 | AAy68123 | Aay68123 Kunitz pr | 526 | 38 | 57.6 | 17 | 3 | AABo6361 | AABo6361 Randomise |
| 454 | 40 | 60.6 | 61 | 3 | AAy68173 | Aay68173 Kunitz pr | 527 | 38 | 57.6 | 17 | 3 | AAJ80380 | AAj80380 JH gene 1 |
| 455 | 40 | 60.6 | 61 | 3 | AAy68129 | Aay68129 Kunitz pr | 528 | 38 | 57.6 | 17 | 9 | ADJ75410 | Adj75410 Human ger |
| 456 | 40 | 60.6 | 61 | 3 | AAy68162 | Aay68162 Kunitz pr | 529 | 38 | 57.6 | 17 | 9 | AEA54006 | Aea54006 Novel hum |
| 457 | 40 | 60.6 | 61 | 4 | AAU09322 | Aau09322 Human KPI | 530 | 38 | 57.6 | 17 | 9 | AEA13665 | Aea13665 IGG heavy |
| 458 | 40 | 60.6 | 61 | 4 | AAU09260 | Aau09260 Human KPI | 531 | 38 | 57.6 | 19 | 8 | ADG31815 | Adg31815 Anti-VEGF |
| 459 | 40 | 60.6 | 61 | 4 | AAU09333 | Aau09333 Human KPI | 532 | 38 | 57.6 | 19 | 8 | ADG31817 | Adg31817 Anti-VEGF |
| 460 | 40 | 60.6 | 61 | 4 | AAU09292 | Aau09292 Human KPI | 533 | 38 | 57.6 | 19 | 8 | ADG31822 | Adg31822 Anti-VEGF |
| 461 | 40 | 60.6 | 61 | 4 | AAU09215 | Aau09215 Human KPI | 534 | 38 | 57.6 | 19 | 8 | ADG31825 | Adg31825 Variant p |
| 462 | 40 | 60.6 | 101 | 3 | AAy95711 | Aay95711 Cosmid cH | 535 | 38 | 57.6 | 19 | 8 | ADG31819 | Adg31819 Anti-VEGF |

| | | | | | | | | | | | | | |
|-----|----|------|----|---|----------|---------------------|-----|----|------|-----|---|----------|-----------|
| 536 | 38 | 57.6 | 19 | 8 | ADG31820 | Adg31820 Anti-VRGF | 609 | 38 | 57.6 | 61 | 3 | AAy68144 | Kunitz pr |
| 537 | 38 | 57.6 | 19 | 8 | ADG31816 | Adg31816 Anti-VRGF | 610 | 38 | 57.6 | 61 | 3 | AAy68158 | Kunitz pr |
| 538 | 38 | 57.6 | 19 | 8 | ADG31818 | Adg31818 Anti-VRGF | 611 | 38 | 57.6 | 61 | 3 | AAy68039 | Kunitz pr |
| 539 | 38 | 57.6 | 19 | 8 | ADG31823 | Adg31823 Anti-VRGF | 612 | 38 | 57.6 | 61 | 3 | AAy68084 | Kunitz pr |
| 540 | 38 | 57.6 | 19 | 8 | ADG31824 | Adg31824 Anti-VRGF | 613 | 38 | 57.6 | 61 | 3 | AAy68126 | Kunitz pr |
| 541 | 38 | 57.6 | 20 | 5 | ADP47138 | Human Bly | 614 | 38 | 57.6 | 61 | 3 | AAy68136 | Kunitz pr |
| 542 | 38 | 57.6 | 20 | 7 | ADG97965 | Adg97965 scFV VHCD | 615 | 38 | 57.6 | 61 | 3 | AAy68148 | Kunitz pr |
| 543 | 38 | 57.6 | 20 | 9 | ADY70246 | Ady70246 Human Mab | 616 | 38 | 57.6 | 61 | 3 | AAy68071 | Kunitz pr |
| 544 | 38 | 57.6 | 26 | 8 | ADG31857 | Adg31857 Anti-VRGF | 617 | 38 | 57.6 | 61 | 3 | AAy68130 | Kunitz pr |
| 545 | 38 | 57.6 | 26 | 8 | ADG31840 | Adg31840 Anti-VRGF | 618 | 38 | 57.6 | 61 | 3 | AAy68072 | Kunitz pr |
| 546 | 38 | 57.6 | 26 | 8 | ADG31843 | Adg31843 Anti-VRGF | 619 | 38 | 57.6 | 61 | 4 | AAU09293 | Human KPI |
| 547 | 38 | 57.6 | 26 | 8 | ADG31842 | Adg31842 Anti-VRGF | 620 | 38 | 57.6 | 61 | 4 | AAU09241 | Human KPI |
| 548 | 38 | 57.6 | 26 | 8 | ADG31853 | Adg31853 Anti-VRGF | 621 | 38 | 57.6 | 61 | 4 | AAU09318 | Human KPI |
| 549 | 38 | 57.6 | 26 | 8 | ADG31852 | Adg31852 Anti-VRGF | 622 | 38 | 57.6 | 61 | 4 | AAU09254 | Human KPI |
| 550 | 38 | 57.6 | 26 | 8 | ADG31891 | Adg31891 Anti-VRGF | 623 | 38 | 57.6 | 61 | 4 | AAU09304 | Human KPI |
| 551 | 38 | 57.6 | 53 | 6 | ABU56846 | Abu56846 BoNT/A Hc | 624 | 38 | 57.6 | 61 | 4 | AAU09219 | Human KPI |
| 552 | 38 | 57.6 | 57 | 2 | AAW18395 | Aaw18395 KPI (1-57) | 625 | 38 | 57.6 | 61 | 4 | AAU09219 | Human KPI |
| 553 | 38 | 57.6 | 57 | 2 | AAW18410 | Aaw18410 KPI (1-57) | 626 | 38 | 57.6 | 61 | 4 | AAU09308 | Human KPI |
| 554 | 38 | 57.6 | 57 | 3 | AAy68079 | Aay68079 Kunitz pr | 627 | 38 | 57.6 | 61 | 4 | AAU09290 | Human KPI |
| 555 | 38 | 57.6 | 57 | 4 | AAU09249 | Aau09249 Human KPI | 628 | 38 | 57.6 | 98 | 6 | ABU01118 | S. pneumo |
| 556 | 38 | 57.6 | 57 | 4 | AAU32803 | Aau32803 Novel hum | 629 | 38 | 57.6 | 109 | 8 | ADK46294 | Streptoco |
| 557 | 38 | 57.6 | 57 | 4 | AAU32802 | Aau32802 Novel hum | 630 | 38 | 57.6 | 109 | 8 | ADR95909 | Novel S. |
| 558 | 38 | 57.6 | 58 | 2 | AAr88955 | Aar88955 Mutant se | 631 | 38 | 57.6 | 113 | 7 | ADD69210 | Human ant |
| 559 | 38 | 57.6 | 58 | 2 | AAr88956 | Aar88956 Mutant se | 632 | 38 | 57.6 | 117 | 8 | ADP22112 | Human ant |
| 560 | 38 | 57.6 | 58 | 2 | AAr88966 | Aar88966 Mutant se | 633 | 38 | 57.6 | 117 | 8 | ADS87917 | Anti-IFN- |
| 561 | 38 | 57.6 | 58 | 2 | AAr88983 | Aar88983 Mutant se | 634 | 38 | 57.6 | 117 | 8 | ADS87921 | Anti-IFN- |
| 562 | 38 | 57.6 | 58 | 2 | AAr88965 | Aar88965 Mutant se | 635 | 38 | 57.6 | 117 | 8 | ADS87937 | Anti-IFN- |
| 563 | 38 | 57.6 | 58 | 2 | AAr88958 | Aar88958 Mutant se | 636 | 38 | 57.6 | 117 | 8 | ADS94914 | Anti-IFN- |
| 564 | 38 | 57.6 | 58 | 2 | AAr88957 | Aar88957 Mutant se | 637 | 38 | 57.6 | 117 | 8 | ADS94934 | Anti-IFN- |
| 565 | 38 | 57.6 | 58 | 2 | AAr88984 | Aar88984 Mutant se | 638 | 38 | 57.6 | 117 | 8 | ADS94918 | Anti-IFN- |
| 566 | 38 | 57.6 | 58 | 2 | AAr88967 | Aar88967 Mutant se | 639 | 38 | 57.6 | 119 | 7 | ADD69209 | Human ant |
| 567 | 38 | 57.6 | 58 | 2 | AAr88964 | Aar88964 Mutant se | 640 | 38 | 57.6 | 119 | 8 | ADR38669 | Mouse hea |
| 568 | 38 | 57.6 | 58 | 2 | AAW18527 | Aaw18527 Kunitz ty | 641 | 38 | 57.6 | 119 | 8 | ADR38668 | Mouse hea |
| 569 | 38 | 57.6 | 58 | 2 | AAW18533 | Aaw18533 Kunitz ty | 642 | 38 | 57.6 | 124 | 7 | ADKL7415 | Anti-huma |
| 570 | 38 | 57.6 | 58 | 2 | AAW18535 | Aaw18535 Kunitz ty | 643 | 38 | 57.6 | 124 | 8 | ADG42837 | scFv AB12 |
| 571 | 38 | 57.6 | 58 | 2 | AAW18552 | Aaw18552 Kunitz ty | 644 | 38 | 57.6 | 124 | 9 | ADZ83527 | Human BpC |
| 572 | 38 | 57.6 | 58 | 2 | AAW18526 | Aaw18526 Kunitz ty | 645 | 38 | 57.6 | 124 | 9 | ADZ83527 | AntiEpCam |
| 573 | 38 | 57.6 | 58 | 2 | AAW18536 | Aaw18536 Kunitz ty | 646 | 38 | 57.6 | 125 | 8 | ADO36377 | Intracell |
| 574 | 38 | 57.6 | 58 | 2 | AAW18525 | Aaw18525 Kunitz ty | 647 | 38 | 57.6 | 127 | 6 | ADA89170 | Human ant |
| 575 | 38 | 57.6 | 58 | 2 | AAW18524 | Aaw18524 Kunitz ty | 648 | 38 | 57.6 | 129 | 9 | ADY70208 | Human mon |
| 576 | 38 | 57.6 | 58 | 2 | AAW18553 | Aaw18553 Kunitz ty | 649 | 38 | 57.6 | 136 | 3 | AAy64677 | Human 5' |
| 577 | 38 | 57.6 | 58 | 2 | AAW72798 | Aaw72798 Mutant in | 650 | 38 | 57.6 | 136 | 8 | ADU72241 | Signal pe |
| 578 | 38 | 57.6 | 58 | 2 | AAW72818 | Aaw72818 Mutant in | 651 | 38 | 57.6 | 136 | 9 | ADZ73232 | Human inc |
| 579 | 38 | 57.6 | 58 | 2 | AAW72789 | Aaw72789 Mutant in | 652 | 38 | 57.6 | 136 | 9 | ADZ73232 | Human inc |
| 580 | 38 | 57.6 | 58 | 2 | AAW72800 | Aaw72800 Mutant in | 653 | 38 | 57.6 | 143 | 5 | ABP51943 | Silenced |
| 581 | 38 | 57.6 | 58 | 2 | AAW72817 | Aaw72817 Mutant in | 654 | 38 | 57.6 | 146 | 2 | AAW19801 | Alpha mat |
| 582 | 38 | 57.6 | 58 | 2 | AAW72790 | Aaw72790 Mutant in | 655 | 38 | 57.6 | 146 | 3 | AAy68030 | Yeast mat |
| 583 | 38 | 57.6 | 58 | 2 | AAW72788 | Aaw72788 Kunitz do | 656 | 38 | 57.6 | 146 | 4 | AAU09210 | Yeast alp |
| 584 | 38 | 57.6 | 58 | 2 | AAW72791 | Aaw72791 Mutant in | 657 | 38 | 57.6 | 188 | 4 | ABG11932 | Novel hum |
| 585 | 38 | 57.6 | 58 | 2 | AAW72792 | Aaw72792 Mutant in | 658 | 38 | 57.6 | 245 | 9 | ABE31466 | ScFv IG64 |
| 586 | 38 | 57.6 | 58 | 2 | AAW72801 | Aaw72801 Mutant in | 659 | 38 | 57.6 | 248 | 5 | ABP45312 | Human Bly |
| 587 | 38 | 57.6 | 58 | 2 | AAW94223 | Aaw94223 Serine pr | 660 | 38 | 57.6 | 248 | 5 | ABP44824 | Human Bly |
| 588 | 38 | 57.6 | 58 | 2 | AAW94240 | Aaw94240 Serine pr | 661 | 38 | 57.6 | 248 | 5 | ABP44905 | Human Bly |
| 589 | 38 | 57.6 | 58 | 2 | AAW94214 | Aaw94214 Serine pr | 662 | 38 | 57.6 | 248 | 5 | ABP44903 | Human Bly |
| 590 | 38 | 57.6 | 58 | 2 | AAW94212 | Aaw94212 Serine pr | 663 | 38 | 57.6 | 248 | 7 | ADG95736 | Single ch |
| 591 | 38 | 57.6 | 58 | 2 | AAW94213 | Aaw94213 Serine pr | 664 | 38 | 57.6 | 248 | 7 | ADG95730 | Single ch |
| 592 | 38 | 57.6 | 58 | 2 | AAW94215 | Aaw94215 Serine pr | 665 | 38 | 57.6 | 248 | 7 | ADG95651 | Single ch |
| 593 | 38 | 57.6 | 58 | 2 | AAW94224 | Aaw94224 Serine pr | 666 | 38 | 57.6 | 248 | 7 | ADG95732 | Single ch |
| 594 | 38 | 57.6 | 58 | 2 | AAW94211 | Aaw94211 Tissue fa | 667 | 38 | 57.6 | 248 | 7 | ADG96139 | Single ch |
| 595 | 38 | 57.6 | 58 | 2 | AAW94221 | Aaw94221 Serine pr | 668 | 38 | 57.6 | 249 | 5 | ABP44901 | Human Bly |
| 596 | 38 | 57.6 | 58 | 2 | AAW94241 | Aaw94241 Serine pr | 669 | 38 | 57.6 | 249 | 5 | ADG95728 | Single ch |
| 597 | 38 | 57.6 | 58 | 2 | AAW92870 | Aaw92870 US5880256 | 670 | 38 | 57.6 | 251 | 2 | AAy17962 | Mouse scF |
| 598 | 38 | 57.6 | 58 | 2 | AAW92895 | Aaw92895 US5880256 | 671 | 38 | 57.6 | 251 | 5 | ABP45798 | Human Bly |
| 599 | 38 | 57.6 | 58 | 2 | AAW92857 | Aaw92857 US5880256 | 672 | 38 | 57.6 | 251 | 5 | ABP45298 | Human Bly |
| 600 | 38 | 57.6 | 58 | 2 | AAW92879 | Aaw92879 US5880256 | 673 | 38 | 57.6 | 251 | 5 | ABP44944 | Human Bly |
| 601 | 38 | 57.6 | 58 | 2 | AAW92896 | Aaw92896 US5880256 | 674 | 38 | 57.6 | 251 | 5 | ABP45103 | Human Bly |
| 602 | 38 | 57.6 | 58 | 2 | AAW92869 | Aaw92869 US5880256 | 675 | 38 | 57.6 | 251 | 5 | ABP45306 | Human Bly |
| 603 | 38 | 57.6 | 58 | 2 | AAW92867 | Aaw92867 US5880256 | 676 | 38 | 57.6 | 251 | 5 | ABP45321 | Human Bly |
| 604 | 38 | 57.6 | 58 | 2 | AAW92868 | Aaw92868 US5880256 | 677 | 38 | 57.6 | 251 | 7 | ADG95771 | Single ch |
| 605 | 38 | 57.6 | 58 | 2 | AAW92876 | Aaw92876 US5880256 | 678 | 38 | 57.6 | 251 | 7 | ADG96125 | Single ch |
| 606 | 38 | 57.6 | 58 | 2 | AAW92878 | Aaw92878 US5880256 | 679 | 38 | 57.6 | 251 | 7 | ADG95930 | Single ch |
| 607 | 38 | 57.6 | 61 | 2 | AAW18422 | KPI (-4 to | 680 | 38 | 57.6 | 251 | 7 | ADG96148 | Single ch |
| 608 | 38 | 57.6 | 61 | 2 | AAW18416 | KPI (-4 to | 681 | 38 | 57.6 | 251 | 7 | ADG96133 | Single ch |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|----------|--------------------|-----|----|------|-----|---|----------|--------------------|
| 682 | 38 | 57.6 | 251 | 7 | ADG96625 | Adg96625 Single ch | 755 | 37 | 56.1 | 16 | 7 | ADG97562 | Adg97562 scFV VRCD |
| 683 | 38 | 57.6 | 252 | 5 | ABP44977 | Abp44977 Human Bly | 756 | 37 | 56.1 | 18 | 3 | ABP06399 | Abp06399 Randomise |
| 684 | 38 | 57.6 | 252 | 7 | ADG95804 | Adg95804 Single ch | 757 | 37 | 56.1 | 43 | 6 | ABP54221 | Abp54221 Human lun |
| 685 | 38 | 57.6 | 256 | 5 | ABP46108 | Abp46108 Human Bly | 758 | 37 | 56.1 | 50 | 1 | AAp70039 | AAp70039 Secretary |
| 686 | 38 | 57.6 | 256 | 5 | ADG96935 | Adg96935 Single ch | 759 | 37 | 56.1 | 54 | 6 | ABU56894 | Abu56894 BONT/A HC |
| 687 | 38 | 57.6 | 282 | 2 | AAW18558 | Aw18558 Novel fus | 760 | 37 | 56.1 | 55 | 6 | ABU56893 | Abu56893 BONT/A HC |
| 688 | 38 | 57.6 | 282 | 2 | AAW18557 | Aw18557 Novel fus | 761 | 37 | 56.1 | 56 | 2 | AAW25278 | Aw25278 Anti-tryp |
| 689 | 38 | 57.6 | 287 | 2 | AAW18559 | Aw18559 Novel fus | 762 | 37 | 56.1 | 58 | 2 | AAW07764 | Aw07764 Non-nativ |
| 690 | 38 | 57.6 | 292 | 2 | AAW18560 | Aw18560 Novel fus | 763 | 37 | 56.1 | 58 | 2 | AAW64136 | Aw64136 Human Kun |
| 691 | 38 | 57.6 | 297 | 2 | AAW18561 | Aw18561 Novel fus | 764 | 37 | 56.1 | 61 | 2 | AAW18424 | Aw18424 KPI (-4 to |
| 692 | 38 | 57.6 | 302 | 2 | AAW18562 | Aw18562 Novel fus | 765 | 37 | 56.1 | 61 | 3 | AAW68092 | Aw68092 Kunitz pr |
| 693 | 38 | 57.6 | 307 | 2 | AAW18563 | Aw18563 Novel fus | 766 | 37 | 56.1 | 61 | 3 | AAW68135 | Aw68135 Kunitz pr |
| 694 | 38 | 57.6 | 312 | 2 | AAW18564 | Aw18564 Novel fus | 767 | 37 | 56.1 | 61 | 3 | AAW68068 | Aw68068 Kunitz pr |
| 695 | 38 | 57.6 | 323 | 3 | AEb37793 | Aeb37793 L. pneumo | 768 | 37 | 56.1 | 61 | 3 | AAW68073 | Aw68073 Kunitz pr |
| 696 | 38 | 57.6 | 384 | 4 | AAU14462 | Aau14462 Human nov | 769 | 37 | 56.1 | 61 | 3 | AAW68134 | Aw68134 Kunitz pr |
| 697 | 38 | 57.6 | 384 | 4 | AAU14463 | Aau14463 Human nov | 770 | 37 | 56.1 | 61 | 3 | AAW68085 | Aw68085 Kunitz pr |
| 698 | 38 | 57.6 | 384 | 4 | AAU14461 | Aau14461 Human nov | 771 | 37 | 56.1 | 61 | 3 | AAW68132 | Aw68132 Kunitz pr |
| 699 | 38 | 57.6 | 384 | 4 | AAU14464 | Aau14464 Human nov | 772 | 37 | 56.1 | 61 | 4 | AAU09242 | Aau09242 Human KPI |
| 700 | 38 | 57.6 | 384 | 8 | ADH80782 | Adh80782 Human pol | 773 | 37 | 56.1 | 61 | 4 | AAU09238 | Aau09238 Human KPI |
| 701 | 38 | 57.6 | 384 | 8 | ADH80779 | Adh80779 Human pol | 774 | 37 | 56.1 | 61 | 4 | AAU09354 | Aau09354 Protease |
| 702 | 38 | 57.6 | 384 | 8 | ADH80781 | Adh80781 Human pol | 775 | 37 | 56.1 | 61 | 4 | AAU09262 | Aau09262 Human KPI |
| 703 | 38 | 57.6 | 385 | 8 | ADH80780 | Adh80780 Human pol | 776 | 37 | 56.1 | 61 | 4 | AAU09298 | Aau09298 Human KPI |
| 704 | 38 | 57.6 | 447 | 8 | ADS87928 | Ads87928 Anti-IFN- | 777 | 37 | 56.1 | 61 | 4 | AAU09297 | Aau09297 Human KPI |
| 705 | 38 | 57.6 | 447 | 8 | ADS87926 | Ads87926 Anti-IFN- | 778 | 37 | 56.1 | 61 | 4 | AAU09255 | Aau09255 Human KPI |
| 706 | 38 | 57.6 | 447 | 8 | ADS87939 | Ads87939 Anti-IFN- | 779 | 37 | 56.1 | 61 | 4 | AAU09295 | Aau09295 Human KPI |
| 707 | 38 | 57.6 | 447 | 8 | ADS94936 | Ads94936 Anti-IFN- | 780 | 37 | 56.1 | 76 | 4 | AAW87658 | Aw87658 Human imm |
| 708 | 38 | 57.6 | 447 | 8 | ADS94923 | Ads94923 Anti-IFN- | 781 | 37 | 56.1 | 97 | 6 | ABU70514 | Abu70514 Human adi |
| 709 | 38 | 57.6 | 447 | 8 | ADS94925 | Ads94925 Anti-IFN- | 782 | 37 | 56.1 | 112 | 8 | ADT89241 | Adt89241 Humanised |
| 710 | 38 | 57.6 | 477 | 8 | ADS44647 | Ads44647 Bacterial | 783 | 37 | 56.1 | 119 | 1 | AAW60335 | AAw60335 Immunoglo |
| 711 | 38 | 57.6 | 499 | 9 | ADZ83669 | Adz83669 CD3 speci | 784 | 37 | 56.1 | 119 | 1 | AAW60335 | AAw60335 Immunoglo |
| 712 | 38 | 57.6 | 499 | 9 | ADZ83697 | Adz83697 CD3 speci | 785 | 37 | 56.1 | 119 | 1 | AAW60335 | AAw60335 Immunoglo |
| 713 | 38 | 57.6 | 499 | 9 | ADZ83661 | Adz83661 CD3 speci | 790 | 37 | 56.1 | 120 | 4 | AAE10474 | AAe10474 Humanised |
| 714 | 38 | 57.6 | 499 | 9 | ADZ83665 | Adz83665 CD3 speci | 791 | 37 | 56.1 | 120 | 4 | AAE10474 | AAe10474 Humanised |
| 715 | 38 | 57.6 | 499 | 9 | ADZ83665 | Adz83665 CD3 speci | 792 | 37 | 56.1 | 120 | 5 | ABP66378 | Abp66378 Human RSV |
| 716 | 38 | 57.6 | 499 | 9 | ADZ83685 | Adz83685 CD3 speci | 793 | 37 | 56.1 | 120 | 5 | ABP66361 | Abp66361 Human RSV |
| 717 | 38 | 57.6 | 499 | 9 | ADZ83701 | Adz83701 CD3 speci | 794 | 37 | 56.1 | 120 | 5 | ABP66394 | Abp66394 Human RSV |
| 718 | 38 | 57.6 | 499 | 9 | ADZ83681 | Adz83681 CD3 speci | 795 | 37 | 56.1 | 120 | 5 | ABP66394 | Abp66394 Human RSV |
| 719 | 38 | 57.6 | 499 | 9 | ADZ83693 | Adz83693 CD3 speci | 796 | 37 | 56.1 | 120 | 5 | ABP66390 | Abp66390 Human RSV |
| 720 | 38 | 57.6 | 499 | 9 | ADZ83689 | Adz83689 CD3 speci | 797 | 37 | 56.1 | 120 | 5 | ABP66398 | Abp66398 Human RSV |
| 721 | 38 | 57.6 | 499 | 9 | ADZ83673 | Adz83673 CD3 speci | 798 | 37 | 56.1 | 120 | 5 | ABP66371 | Abp66371 Human RSV |
| 722 | 38 | 57.6 | 499 | 9 | ADZ83677 | Adz83677 CD3 speci | 799 | 37 | 56.1 | 120 | 5 | ABG31432 | Abg31432 Humanised |
| 723 | 38 | 57.6 | 500 | 9 | ADZ83703 | Adz83703 CD3 speci | 800 | 37 | 56.1 | 120 | 5 | ABG31433 | Abg31433 Amino aci |
| 724 | 38 | 57.6 | 500 | 9 | ADZ83675 | Adz83675 CD3 speci | 801 | 37 | 56.1 | 120 | 5 | AAE28016 | AAe28016 Human mod |
| 725 | 38 | 57.6 | 500 | 9 | ADZ83687 | Adz83687 CD3 speci | 802 | 37 | 56.1 | 120 | 5 | AAE28049 | AAe28049 Human mod |
| 726 | 38 | 57.6 | 500 | 9 | ADZ83413 | Adz83413 C-termina | 803 | 37 | 56.1 | 120 | 5 | AAE28045 | AAe28045 Human mod |
| 727 | 38 | 57.6 | 500 | 9 | ADZ83667 | Adz83667 CD3 speci | 804 | 37 | 56.1 | 120 | 5 | AAE28057 | AAe28057 Human mod |
| 728 | 38 | 57.6 | 500 | 9 | ADZ83679 | Adz83679 CD3 speci | 805 | 37 | 56.1 | 120 | 5 | AAE28026 | AAe28026 Human mod |
| 729 | 38 | 57.6 | 500 | 9 | ADZ83699 | Adz83699 CD3 speci | 806 | 37 | 56.1 | 120 | 5 | AAE28033 | AAe28033 Human mod |
| 730 | 38 | 57.6 | 500 | 9 | ADZ83411 | Adz83411 C-termina | 807 | 37 | 56.1 | 120 | 5 | AAE28053 | AAe28053 Human mod |
| 731 | 38 | 57.6 | 500 | 9 | ADZ83695 | Adz83695 CD3 speci | 808 | 37 | 56.1 | 120 | 6 | ABU69234 | Abu69234 Respirato |
| 732 | 38 | 57.6 | 500 | 9 | ADZ83663 | Adz83663 CD3 speci | 809 | 37 | 56.1 | 120 | 6 | ABU69241 | Abu69241 Respirato |
| 733 | 38 | 57.6 | 500 | 9 | ADZ83691 | Adz83691 CD3 speci | 810 | 37 | 56.1 | 120 | 6 | ABU69261 | Abu69261 Respirato |
| 734 | 38 | 57.6 | 503 | 9 | ADV66093 | Adv66093 Anti-CD3- | 811 | 37 | 56.1 | 120 | 6 | ABU69253 | Abu69253 Respirato |
| 735 | 38 | 57.6 | 503 | 9 | ADV66091 | Adv66091 Anti-CD3- | 812 | 37 | 56.1 | 120 | 6 | ABU69257 | Abu69257 Respirato |
| 736 | 38 | 57.6 | 506 | 9 | ADV66097 | Adv66097 Anti-CD3- | 813 | 37 | 56.1 | 120 | 6 | ABU69224 | Abu69224 Respirato |
| 737 | 38 | 57.6 | 506 | 9 | ADV66099 | Adv66099 Anti-CD3- | 814 | 37 | 56.1 | 120 | 6 | ABU69265 | Abu69265 Respirato |
| 738 | 38 | 57.6 | 506 | 9 | ADV66085 | Adv66085 Anti-CD3- | 815 | 37 | 56.1 | 120 | 6 | ABR55858 | ABr55858 Anti-RSV- |
| 739 | 38 | 57.6 | 507 | 5 | AAU72858 | Aau72858 8G7C10x4- | 816 | 37 | 56.1 | 120 | 7 | ADR35736 | Adr35736 SYNAGIS a |
| 740 | 38 | 57.6 | 510 | 5 | AAU72859 | Aau72859 6B5AVx4-7 | 817 | 37 | 56.1 | 120 | 7 | ADR35756 | Adr35756 SYNAGIS a |
| 741 | 38 | 57.6 | 510 | 5 | AAU72860 | Aau72860 Human p53 | 818 | 37 | 56.1 | 120 | 7 | ADR35729 | Adr35729 SYNAGIS a |
| 742 | 38 | 57.6 | 520 | 9 | AAU72860 | Aau72860 Human p53 | 819 | 37 | 56.1 | 120 | 7 | ADR35719 | Adr35719 SYNAGIS a |
| 743 | 38 | 57.6 | 520 | 9 | ADZ83439 | Adz83439 Deimmuniz | 820 | 37 | 56.1 | 120 | 7 | ADR35752 | Adr35752 SYNAGIS a |
| 744 | 38 | 57.6 | 526 | 9 | ADV66119 | Adv66119 Anti-CD3- | 821 | 37 | 56.1 | 120 | 7 | ADR35748 | Adr35748 SYNAGIS a |
| 745 | 38 | 57.6 | 532 | 3 | AAV78328 | Aav78328 B1specifi | 822 | 37 | 56.1 | 120 | 7 | ADR35760 | Adr35760 SYNAGIS a |
| 746 | 38 | 57.6 | 588 | 5 | AAO17251 | Aao17251 A thalian | 823 | 37 | 56.1 | 120 | 8 | ADI56910 | Adi56910 RSV antib |
| 747 | 38 | 57.6 | 597 | 5 | AAO17259 | Aao17259 A thalian | 824 | 37 | 56.1 | 120 | 8 | ADI56898 | Adi56898 RSV antib |
| 748 | 38 | 57.6 | 631 | 8 | ADG74904 | Adg74904 A thalian | 825 | 37 | 56.1 | 120 | 8 | ADI56918 | Adi56918 RSV antib |
| 749 | 38 | 57.6 | 632 | 5 | ABR91401 | ABr91401 Herbicida | 826 | 37 | 56.1 | 120 | 8 | ADI56891 | Adi56891 RSV antib |
| 750 | 38 | 57.6 | 632 | 5 | ADZ83435 | Adz83435 B7.1-scFv | 827 | 37 | 56.1 | 120 | 8 | ADI56922 | Adi56922 RSV antib |
| 751 | 38 | 57.6 | 697 | 8 | ADN19789 | Adn19789 Bacterial | 828 | 37 | 56.1 | 120 | 8 | ADI56922 | Adi56922 RSV antib |
| 752 | 38 | 57.6 | 709 | 8 | ADN19789 | Adn19789 Bacterial | 829 | 37 | 56.1 | 120 | 8 | ADI56922 | Adi56922 RSV antib |
| 753 | 38 | 57.6 | 738 | 8 | ADN19789 | Adn19789 Bacterial | 830 | 37 | 56.1 | 120 | 8 | ADI56922 | Adi56922 RSV antib |
| 754 | 37 | 56.1 | 16 | 5 | ABP46735 | Abp46735 Human Bly | 831 | 37 | 56.1 | 120 | 8 | ADI56922 | Adi56922 RSV antib |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|----------|--------------------|-----|----|------|-----|---|----------|-----------|
| 828 | 37 | 56.1 | 120 | 8 | ADI56914 | Adi56914 RSV antib | 901 | 37 | 56.1 | 450 | 5 | ABP66580 | Human RSV |
| 829 | 37 | 56.1 | 120 | 8 | ADI56881 | Adi56881 RSV antib | 902 | 37 | 56.1 | 450 | 5 | ABP66574 | Human RSV |
| 830 | 37 | 56.1 | 120 | 8 | ADJ97212 | Adj97212 Human pro | 903 | 37 | 56.1 | 450 | 5 | ABP66562 | Human RSV |
| 831 | 37 | 56.1 | 120 | 8 | ADN49709 | Adn49709 Light Cha | 904 | 37 | 56.1 | 450 | 5 | ABP66568 | Human RSV |
| 832 | 37 | 56.1 | 120 | 8 | ADR38650 | Adr38650 Mouse hea | 905 | 37 | 56.1 | 450 | 6 | ABU69443 | Respirato |
| 833 | 37 | 56.1 | 120 | 8 | ADT89237 | Adt89237 Humanised | 906 | 37 | 56.1 | 450 | 6 | ABU69437 | Respirato |
| 834 | 37 | 56.1 | 120 | 8 | ADT89204 | Adt89204 Humanised | 907 | 37 | 56.1 | 450 | 6 | ABU69471 | Respirato |
| 835 | 37 | 56.1 | 120 | 8 | ADT89221 | Adt89221 Humanised | 908 | 37 | 56.1 | 450 | 6 | ABU69429 | Respirato |
| 836 | 37 | 56.1 | 120 | 8 | ADT89245 | Adt89245 Humanised | 909 | 37 | 56.1 | 450 | 6 | ABU69439 | Respirato |
| 837 | 37 | 56.1 | 120 | 8 | ADT89214 | Adt89214 Humanised | 910 | 37 | 56.1 | 450 | 6 | ABU69473 | Respirato |
| 838 | 37 | 56.1 | 120 | 8 | ADT89233 | Adt89233 Humanised | 911 | 37 | 56.1 | 450 | 6 | ABU69425 | Respirato |
| 839 | 37 | 56.1 | 120 | 8 | ADU74385 | Adu74385 Synagis 1 | 912 | 37 | 56.1 | 450 | 6 | ABU69441 | Respirato |
| 840 | 37 | 56.1 | 120 | 9 | ADM19871 | Adm19871 RSV antib | 913 | 37 | 56.1 | 450 | 6 | ABU69465 | Respirato |
| 841 | 37 | 56.1 | 120 | 9 | ADM19894 | Adm19894 RSV antib | 914 | 37 | 56.1 | 450 | 6 | ABU69431 | Respirato |
| 842 | 37 | 56.1 | 120 | 9 | ADM19890 | Adm19890 RSV antib | 915 | 37 | 56.1 | 450 | 6 | ABU69469 | Respirato |
| 843 | 37 | 56.1 | 120 | 9 | ADM19898 | Adm19898 RSV antib | 916 | 37 | 56.1 | 450 | 6 | ABG75662 | Synagis h |
| 844 | 37 | 56.1 | 120 | 9 | ADM19861 | Adm19861 RSV antib | 917 | 37 | 56.1 | 450 | 7 | ADG75662 | Synagis h |
| 845 | 37 | 56.1 | 120 | 9 | ADM19878 | Adm19878 RSV antib | 918 | 37 | 56.1 | 450 | 7 | ADG75662 | Synagis h |
| 846 | 37 | 56.1 | 120 | 9 | ADM19902 | Adm19902 RSV antib | 919 | 37 | 56.1 | 450 | 7 | ADG75662 | Synagis h |
| 847 | 37 | 56.1 | 120 | 9 | ABE06872 | Abe06872 RSV-speci | 920 | 37 | 56.1 | 450 | 7 | ADG75662 | Synagis h |
| 848 | 37 | 56.1 | 120 | 9 | ABE06853 | Abe06853 RSV-speci | 921 | 37 | 56.1 | 450 | 7 | ADG75662 | Synagis h |
| 849 | 37 | 56.1 | 120 | 9 | ABE07115 | Abe07115 RSV-speci | 922 | 37 | 56.1 | 450 | 7 | ADG75662 | Synagis h |
| 850 | 37 | 56.1 | 120 | 9 | ABE06880 | Abe06880 RSV-speci | 923 | 37 | 56.1 | 450 | 7 | ADG75662 | Synagis h |
| 851 | 37 | 56.1 | 120 | 9 | ABE06860 | Abe06860 RSV-speci | 924 | 37 | 56.1 | 450 | 7 | ADG75662 | Synagis h |
| 852 | 37 | 56.1 | 120 | 9 | ABE06876 | Abe06876 RSV-speci | 925 | 37 | 56.1 | 450 | 7 | ADG75662 | Synagis h |
| 853 | 37 | 56.1 | 120 | 9 | ABE07117 | Abe07117 RSV-speci | 926 | 37 | 56.1 | 450 | 7 | ADG75662 | Synagis h |
| 854 | 37 | 56.1 | 120 | 9 | ABE06843 | Abe06843 RSV-speci | 927 | 37 | 56.1 | 450 | 7 | ADG75662 | Synagis h |
| 855 | 37 | 56.1 | 120 | 9 | ABE06884 | Abe06884 RSV-speci | 928 | 37 | 56.1 | 450 | 7 | ADG75662 | Synagis h |
| 856 | 37 | 56.1 | 121 | 7 | ADB78580 | Adb78580 Rat F997- | 929 | 37 | 56.1 | 450 | 9 | ADM20068 | RSV antib |
| 857 | 37 | 56.1 | 121 | 8 | ADR38649 | Adr38649 Mouse hea | 930 | 37 | 56.1 | 450 | 9 | ADM20068 | RSV antib |
| 858 | 37 | 56.1 | 122 | 7 | ABR82777 | AbR82777 Hybridoma | 931 | 37 | 56.1 | 450 | 9 | ADM20062 | RSV antib |
| 859 | 37 | 56.1 | 122 | 7 | ABR82887 | AbR82887 Hybridoma | 932 | 37 | 56.1 | 450 | 9 | ADM20102 | RSV antib |
| 860 | 37 | 56.1 | 122 | 9 | ADK16331 | Adk16331 Modified | 933 | 37 | 56.1 | 450 | 9 | ADM20106 | RSV antib |
| 861 | 37 | 56.1 | 122 | 9 | ADK16294 | Adk16294 Lue16 ant | 934 | 37 | 56.1 | 450 | 9 | ADM20108 | RSV antib |
| 862 | 37 | 56.1 | 122 | 9 | ADK16295 | Adk16295 Vny light | 935 | 37 | 56.1 | 450 | 9 | ADM20076 | RSV antib |
| 863 | 37 | 56.1 | 134 | 5 | ABP64505 | Abp64505 Human ORF | 936 | 37 | 56.1 | 450 | 9 | ADM20078 | RSV antib |
| 864 | 37 | 56.1 | 139 | 2 | AAU36269 | Aau36269 Pseudom | 937 | 37 | 56.1 | 450 | 9 | ADM20074 | RSV antib |
| 865 | 37 | 56.1 | 139 | 2 | AAU36369 | Aau36369 Pseudom | 938 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 866 | 37 | 56.1 | 139 | 2 | AAU36369 | Aau36369 Pseudom | 939 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 867 | 37 | 56.1 | 139 | 2 | AAU36369 | Aau36369 Pseudom | 940 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 868 | 37 | 56.1 | 139 | 2 | AAU36369 | Aau36369 Pseudom | 941 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 869 | 37 | 56.1 | 139 | 3 | AAU36369 | Aau36369 Pseudom | 942 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 870 | 37 | 56.1 | 139 | 3 | AAU36369 | Aau36369 Pseudom | 943 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 871 | 37 | 56.1 | 139 | 8 | ADU72247 | Adu72247 Signal pe | 944 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 872 | 37 | 56.1 | 139 | 8 | ADU72247 | Adu72247 Signal pe | 945 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 873 | 37 | 56.1 | 140 | 2 | AAW06205 | Aaw06205 Xenograft | 946 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 874 | 37 | 56.1 | 145 | 5 | ABP32070 | Abp32070 Human RNA | 947 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 875 | 37 | 56.1 | 227 | 6 | ABG75663 | Abg75663 Synagis h | 948 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 876 | 37 | 56.1 | 238 | 6 | ABU36269 | Abu36269 Pseudom | 949 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 877 | 37 | 56.1 | 238 | 6 | ABU36269 | Abu36269 Pseudom | 950 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 878 | 37 | 56.1 | 239 | 7 | ADC79231 | Adc79231 Anti-CA12 | 951 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 879 | 37 | 56.1 | 239 | 7 | ADC79232 | Adc79232 Control s | 952 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 880 | 37 | 56.1 | 249 | 5 | ABP44930 | Abp44930 Human Bly | 953 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 881 | 37 | 56.1 | 249 | 7 | ADG95757 | Adg95757 Single ch | 954 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 882 | 37 | 56.1 | 250 | 7 | ABO75868 | AbO75868 Pseudom | 955 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 883 | 37 | 56.1 | 333 | 8 | ADR05370 | Adr05370 Mouse ana | 956 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 884 | 37 | 56.1 | 347 | 8 | ADO28206 | Ado28206 Mouse GPC | 957 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 885 | 37 | 56.1 | 426 | 2 | AAU05501 | Aau05501 Bacillus | 958 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 886 | 37 | 56.1 | 432 | 4 | AAU05501 | Aau05501 Escherich | 959 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 887 | 37 | 56.1 | 434 | 7 | ADG35960 | Adg35960 Synagis a | 960 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 888 | 37 | 56.1 | 434 | 7 | ADG35960 | Adg35960 Synagis a | 961 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 889 | 37 | 56.1 | 450 | 4 | AAE10525 | Aae10525 Humanised | 962 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 890 | 37 | 56.1 | 450 | 4 | AAE10513 | Aae10513 Humanised | 963 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 891 | 37 | 56.1 | 450 | 4 | AAE10517 | Aae10517 Humanised | 964 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 892 | 37 | 56.1 | 450 | 4 | AAE10523 | Aae10523 Humanised | 965 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 893 | 37 | 56.1 | 450 | 4 | AAE10511 | Aae10511 Humanised | 966 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 894 | 37 | 56.1 | 450 | 5 | ABP66578 | Abp66578 Human RSV | 967 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 895 | 37 | 56.1 | 450 | 5 | ABP66576 | Abp66576 Human RSV | 968 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 896 | 37 | 56.1 | 450 | 5 | ABP66608 | Abp66608 Human RSV | 969 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 897 | 37 | 56.1 | 450 | 5 | ABP66610 | Abp66610 Human RSV | 970 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 898 | 37 | 56.1 | 450 | 5 | ABP66602 | Abp66602 Human RSV | 971 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 899 | 37 | 56.1 | 450 | 5 | ABP66606 | Abp66606 Human RSV | 972 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |
| 900 | 37 | 56.1 | 450 | 5 | ABP66566 | Abp66566 Human RSV | 973 | 37 | 56.1 | 450 | 9 | ADM20066 | RSV antib |

774 36.5 55.3 1011 8 ADO43987
775 36 54.5 8 7 ADL17583
776 36 54.5 11 9 ADW10893
777 36 54.5 14 2 RAAW70699
778 36 54.5 14 2 RAAW70701
779 36 54.5 14 2 RAAW70613
780 36 54.5 14 2 RAAW70691
781 36 54.5 14 2 RAAW70691
782 36 54.5 14 5 ABP61260
783 36 54.5 14 5 ABP61270
784 36 54.5 14 5 ABP61268
785 36 54.5 15 8 ADG31814
786 36 54.5 15 9 AEA40801
787 36 54.5 16 3 AAB06382
788 36 54.5 17 3 AAB06368
789 36 54.5 17 3 AAB06396
790 36 54.5 17 3 AAB06398
791 36 54.5 17 3 AAB05886
792 36 54.5 17 3 AAB06393
793 36 54.5 17 3 AAB05893
794 36 54.5 17 3 AAB06369
795 36 54.5 17 3 AAB06376
796 36 54.5 17 3 AAB06406
797 36 54.5 17 3 AAB05883
798 36 54.5 17 3 AAB06359
799 36 54.5 17 3 AAB06374
1000 36 54.5 17 3 AAB06388

ALIGNMENTS

RESULT 1
AAR70200
ID AAR70200 standard; protein; 11 AA.
XX AC AAR70200;
DT 25-MAR-2003 (revised)
DT 20-SEP-1995 (first entry)
XX MA3 3B9 heavy chain CDR.
DE Chimeric antibody; humanized antibody; antibody engineering;
XX monoclonal antibody; Mab; interleukin-4; IL-4; allergy; CDR;
KW complementarity determining region.
XX Mus sp.
XX WO9507301-A1.
XX 16-MAR-1995.
XX 07-SEP-1994; 94WO-US010308.
XX 07-SEP-1993; 93US-00117366.
XX 14-OCT-1993; 93US-00136783.
XX (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX Holmes S, Gross MS, Sylvestre DR;
XX WPI; 1995-123387/16.
XX Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from
PT high affinity mAbs - useful in treatment of IL-4-mediated and IgE-
PT mediated allergic conditions.
XX Disclosure; Page 58; 97pp; English.
XX Spleen cells from mice immunized with human IL-4 were used to prepare
CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only clone

CC 3B9 was positive. cDNA clones of the 3B9 light and heavy chains were
CC cloned into pGEM7f+ and transformed into E. coli DH5-alpha. A heavy chain
CC cDNA clone was sequenced (AAQ83491) that encoded the protein given in
CC AAR70190. 3 CDRs (AAR70198-200) were identified. (Updated on 25-MAR-2003
CC to correct FN field.)
XX SQ Sequence 11 AA;
Query Match 100.0%; Score 66; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RETVFWYFVDV 11
Db 1 RETVFWYFVDV 11
|||||
RESULT 2
AAY23777
ID AAY23777 standard; peptide; 11 AA.
XX AC AAY23777;
XX DT 13-SEP-1999 (first entry)
XX DE CDR of the heavy chain variable region of antibody 3B9.
XX KW Heavy chain variable region; interleukin-4; IL-4; antibody 3B9;
KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
KW Immunoglobulin E-mediated allergic reaction; allergic rhinitis;
KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy;
KW complementarity determining region.
XX OS Mus sp.
XX US5928904-A.
XX 27-JUL-1999.
XX 07-JUN-1995; 95US-00483632.
XX 07-SEP-1993; 93US-00117366.
PR 14-OCT-1993; 93US-00136783.
PR 07-SEP-1994; 94WO-US010308.
XX (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX Holmes SD, Sylvestre DR, Gross MS;
XX WPI; 1999-429500/36.
DR N-PSDB; AAX85894.
XX New DNA molecules encoding recombinant antibodies useful for treating IL4
-mediated conditions.
XX Example 3; Col 47; 50pp; English.
XX The present sequence represents a complementarity determining region
CC (CDR) of the heavy chain variable region of murine interleukin-4 (IL-4)
CC antibody 3B9. The specification describes chimeric and humanised IL-4
CC monoclonal antibodies. The antibodies of the invention are used in
CC therapeutic and pharmaceutical compositions for treating IL-4 mediated
CC and immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis,
CC conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock,
CC rheumatoid arthritis, host-versus-graft disease and renal disease. They
CC are also useful in the diagnosis of an allergy or condition associated
CC with excess IL-4 production through the measurement e.g. by ELISA of
CC circulating endogenous IL-4 levels in humans
XX SQ Sequence 11 AA;


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Query Match      100.0%; Score 66; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RETVFWYFDV 11
DB 1 RETVFWYFDV 11

RESULT 3
AA18113
ID AAY18113 standard; peptide; 11 AA.
XX AC AAY18113;
XX DT 11-AUG-1999 (first entry)
XX DE Heavy chain CDR for hIL-4 specific antibody.
XX KW Antibody; interleukin-4; IL4; immunoglobulin E; IGE mediated disease;
XX KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
XX KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
XX KW autoimmune disease; graft versus host disease;
XX KW complementarity determining region; CDR.
XX OS Synthetic.
XX PN US5914110-A.
XX PD 22-JUN-1999.
XX PF 07-JUN-1995; 95US-00483636.
XX PR 07-SEP-1993; 93US-00117366.
XX PR 14-OCT-1993; 93US-00136783.
XX PR 07-SEP-1994; 94WO-US010308.
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX PI Sylvester DR, Holmes SD, Gross MS;
XX WPI; 1999-370482/31.
XX DR N-PSDB; AAX79512.
XX PT Recombinant IL4 antibodies useful for treatment of allergic rhinitis,
XX PT atopic asthma and anaphylactic shock.
XX PS Claim 7; Col 47; 50pp; English.
XX CC This sequence represents a heavy chain complementarity determining region
XX CC (CDR) from an antibody of the invention. The antibody is a chimeric or
XX CC humanised interleukin-4 (IL4) monoclonal antibody for the treatment of
XX CC immunoglobulin E (Ige) mediated diseases. The antibodies are useful for
XX CC the treatment of allergic disorders such as allergic rhinitis,
XX CC conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.
XX CC The antibodies are also useful for regulating B and T cell proliferation
XX CC and as such are useful in the treatment of autoimmune diseases and graft
XX CC versus host disease
XX SQ Sequence 11 AA;

Query Match      100.0%; Score 66; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RETVFWYFDV 11
DB 1 RETVFWYFDV 11

RESULT 4
AAY23780
ID AAY23780 standard; protein; 121 AA.
XX AC AAY23780;
XX DT 13-SEP-1999 (first entry)
XX DE Heavy chain variable region of Ig NEW.
XX KW Light chain variable region; interleukin-4; IL-4; antibody 3B9;
XX KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
XX KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;
XX KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
XX KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy;
XX KW Ig NEW.
XX OS Synthetic.
XX PN US5928904-A.
XX PD 27-JUL-1999.
XX PF 07-JUN-1995; 95US-00483632.
XX PR 07-SEP-1993; 93US-00117366.
XX PR 14-OCT-1993; 93US-00136783.
XX PR 07-SEP-1994; 94WO-US010308.
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX PI Holmes SD, Sylvester DR, Gross MS;
XX WPI; 1999-429500/36.
XX DR N-PSDB; AAX85929.
XX PT New DNA molecules encoding recombinant antibodies useful for treating IL4
XX PT -mediated conditions.
XX PS Disclosure; Col 65-66; 50pp; English.
XX CC The specification describes chimeric and humanised IL-4 monoclonal
XX CC antibodies. The antibodies of the invention are used in therapeutic and
XX CC pharmaceutical compositions for treating IL-4 mediated and immunoglobulin
XX CC E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis,
XX CC atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid
XX CC arthritis, host-versus-graft disease and renal disease. They are also
XX CC useful in the diagnosis of an allergy or condition associated with excess
XX CC IL-4 production through the measurement e.g. by ELISA of circulating
XX CC endogenous IL-4 levels in humans. The present sequence represents the
XX CC heavy chain variable region of Ig NEW, and is used in the course of the
XX CC invention
XX SQ Sequence 121 AA;

Query Match      100.0%; Score 66; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RETVFWYFDV 11
DB 100 RETVFWYFDV 110

RESULT 5
AAY18122
ID AAY18122 standard; protein; 121 AA.
XX AC AAY18122;
XX DT 11-AUG-1999 (first entry)
XX DE Heavy chain sequence for humanised 3B9 antibody.
XX

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KW Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;
 KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
 KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
 KW autoimmune disease; graft versus host disease.
 XX Synthetic.
 XX US5914110-A.
 XX 22-JUN-1999.
 XX 07-JUN-1995; 95US-00483636.
 XX 07-SEP-1993; 93US-00117366.
 XX 14-OCT-1993; 93US-00136783.
 XX 07-SEP-1994; 94WO-US010308.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX Sylvester DR, Holmes SD, Gross MS;
 XX WPI; 1999-370482/31.
 DR N-PSDB; AAX79527.
 XX Recombinant IL4 antibodies useful for treatment of allergic rhinitis,
 XX atopic asthma and anaphylactic shock.
 XX Example 3; Col 65-66; 50pp; English.
 XX This sequence represents the heavy chain of the humanised 3B9 antibody of
 CC the invention. The antibody is a chimeric or humanised interleukin-4
 CC (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE)
 CC mediated diseases. The antibodies are useful for the treatment of
 CC allergic disorders such as allergic rhinitis, conjunctivitis, atopic
 CC dermatitis, atopic asthma and anaphylactic shock. The antibodies are also
 CC useful for regulating B and T cell proliferation and as such are useful
 CC in the treatment of autoimmune diseases and graft versus host disease
 XX Sequence 121 AA;
 SQ Query Match 100.0%; Score 66; DB 2; Length 121;
 Best Local Similarity 100.0%; Pred. No. 0.0031;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RETVFYWFYFDV 11
 Db |||||
 100 RETVFYWFYFDV 110
 RESULT 6
 AAR70190
 ID AAR70190 standard; protein; 140 AA.
 XX AC AAR70190;
 XX AC
 XX 25-MAR-2003 (revised)
 DT 20-SEP-1995 (first entry)
 XX Mouse MAb 3B9 heavy chain.
 DE Chimeric antibody; humanized antibody; antibody engineering;
 XX monoclonal antibody; MAb; interleukin-4; IL-4; allergy.
 KW Mus sp.
 XX US5928904-A.
 XX 27-JUL-1999.
 PD 07-JUN-1995; 95US-00483632.
 XX 07-SEP-1993; 93US-00117366.
 PR 14-OCT-1993; 93US-00136783.

FT /label= CDR
 FT /note= "complementarity determining region"
 FT 119..129
 FT /label= CDR
 FT /note= "complementarity determining region"
 XX MO9507301-A1.
 PN 16-MAR-1995.
 PD 07-SEP-1994; 94WO-US010308.
 XX 07-SEP-1993; 93US-00117366.
 PR 14-OCT-1993; 93US-00136783.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX Holmes S, Gross MS, Sylvester DR;
 XX WPI; 1995-123387/16.
 DR N-PSDB; AAQ83491.
 XX Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from
 PT high affinity mAbs - useful in treatment of IL-4-mediated and IgE-
 PT mediated allergic conditions.
 XX Disclosure; Fig 2; 97pp; English.
 PS Spleen cells from mice immunized with human IL-4 were used to prepare
 CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only clone
 CC 3B9 was positive. cDNA clones of the 3B9 light and heavy chains were
 CC cloned into pGEM7f+ and transformed into E. coli DH5-alpha. The clones
 CC were sequenced (AAQ83490-91), and used for antibody engineering. (Updated
 CC on 25-MAR-2003 to correct PN field.)
 XX Sequence 140 AA;
 SQ Query Match 100.0%; Score 66; DB 2; Length 140;
 Best Local Similarity 100.0%; Pred. No. 0.0036;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RETVFYWFYFDV 11
 Db |||||
 119 RETVFYWFYFDV 129
 RESULT 7
 AAY23768
 ID AAY23768 standard; protein; 140 AA.
 XX AC AAY23768;
 XX AC
 XX 13-SEP-1999 (first entry)
 DT Heavy chain variable region of murine IL-4 antibody 3B9.
 DE Heavy chain variable region; interleukin-4; IL-4; antibody 3B9;
 XX chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
 KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.
 XX Mus sp.
 OS US5928904-A.
 XX 27-JUL-1999.
 PD 07-JUN-1995; 95US-00483632.
 XX 07-SEP-1993; 93US-00117366.
 PR 14-OCT-1993; 93US-00136783.

```

PR 07-SEP-1994; 94WO-US010308.
XX (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Holmes SD, Sylvester DR, Gross MS;
XX
XX WPI; 1999-429500/36.
XX N-PSDB; AAX85885.
XX
XX New DNA molecules encoding recombinant antibodies useful for treating IL4
XX -mediated conditions.
XX
XX Example 3; Fig 2; 50pp; English.
XX
XX The present sequence represents the heavy chain variable region of murine
XX interleukin-4 (IL-4) antibody 3B9. The sequences are used in the
XX production chimeric and humanised IL-4 monoclonal antibodies. The
XX antibodies of the invention are used in therapeutic and pharmaceutical
XX compositions for treating IL-4 mediated and immunoglobulin E-mediated
XX allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic
XX dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host
XX -versus-graft disease and renal disease. They are also useful in the
XX diagnosis of an allergy or condition associated with excess IL-4
XX production through the measurement e.g. by ELISA of circulating
XX endogenous IL-4 levels in humans
XX
XX Sequence 140 AA;
SQ
Query Match 100.0%; Score 66; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RETVFWYFDV 11
Db 119 RETVFWYFDV 129
RESULT 8
AAV18121
ID AAV18121 standard; protein; 140 AA.
XX
XX AAV18121;
XX
XX 11-AUG-1999 (first entry)
XX
XX Heavy chain sequence for murine 3B9 antibody.
XX
XX Antibody; interleukin-4; IL4; immunoglobulin E; IGE mediated disease;
XX allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
XX atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
XX autoimmune disease; graft versus host disease.
XX
XX Mus sp.
XX
XX US5914110-A.
XX
XX 22-JUN-1999.
XX
XX 07-JUN-1995; 95US-00483636.
XX
XX 07-SEP-1993; 93US-00117366.
XX
XX 14-OCT-1993; 93US-00136783.
XX
XX 07-SEP-1994; 94WO-US010308.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX Sylvester DR, Holmes SD, Gross MS;
XX
XX WPI; 1999-370482/31.
XX N-PSDB; AAX79520.
XX

```

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PT Recombinant IL4 antibodies useful for treatment of allergic rhinitis,
XX atopic asthma and anaphylactic shock.
XX
XX Claim 24; Fig 2; 50pp; English.
XX
XX This sequence represents the heavy chain of the murine 3B9 antibody of
XX the invention. The antibody is a chimeric or humanised interleukin-4
XX (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE)
XX mediated diseases. The antibodies are useful for the treatment of
XX allergic disorders such as allergic rhinitis, conjunctivitis, atopic
XX dermatitis, atopic asthma and anaphylactic shock. The antibodies are also
XX useful for regulating B and T cell proliferation and as such are useful
XX in the treatment of autoimmune diseases and graft versus host disease
XX
XX Sequence 140 AA;
SQ
Query Match 100.0%; Score 66; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RETVFWYFDV 11
Db 119 RETVFWYFDV 129
RESULT 9
AAR70192
ID AAR70192 standard; protein; 141 AA.
XX
XX AAR70192;
XX
XX 25-MAR-2003 (revised)
XX 20-SEP-1995 (first entry)
XX
XX Humanized antibody 3B9 heavy chain.
XX
XX Humanized antibody; antibody engineering; monoclonal antibody; MAb;
XX interleukin-4; IL-4; allergy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..19
XX /label= Sig_peptide
XX Region 51..57
XX /label= CDR
XX Region 72..87
XX /label= CDR
XX /note= "complementarity determining region"
XX Region 120..130
XX /label= CDR
XX /note= "complementarity determining region"
XX Region 120..130
XX /label= CDR
XX /note= "complementarity determining region"
XX
XX WO9507301-A1.
XX
XX 16-MAR-1995.
XX
XX 07-SEP-1994; 94WO-US010308.
XX
XX 07-SEP-1993; 93US-00117366.
XX
XX 14-OCT-1993; 93US-00136783.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Holmes S, Gross MS, Sylvester DR;
XX
XX WPI; 1995-123387/16.
XX N-PSDB; AAX83493.
XX
XX Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from
XX high affinity mAbs - useful in treatment of IL-4-mediated and IgE-
XX

```

PT mediated allergic conditions.
XX
PS Disclosure; Fig 4; 97pp; English.
XX
CC A humanized antibody heavy chain variable region and signal sequence is
CC given in AAR70192. The signal sequence is also provided in AAR70193. The
CC CDR sequences of the construct are identical to the native CDRs of mouse
CC anti-human IL-4 Mab 3B9 (AAR70198-200). (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 141 AA;

Query Match 100.0%; Score 66; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RETVFYWFYFDV 11
Db 120 RETVFYWFYFDV 130
|||||

RESULT 10
AAR70191
ID AAR70191 standard; protein; 141 AA.
XX
AC AAR70191;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 20-SEP-1995 (first entry)
XX
XX Chimeric antibody 3B9 heavy chain.
XX Chimeric antibody; antibody engineering; monoclonal antibody; Mab;
KW Interleukin-4; IL-4; allergy.
XX
OS Homo sapiens.
OS Mus sp.
XX
PH Key Location/Qualifiers
FT Peptide 1..19 /label= Sig_peptide
FT Region 51..57 /label= CDR
FT /note= "complementarity determining region"
FT Region 72..87 /label= CDR
FT /note= "complementarity determining region"
FT Peptide 120..130 /label= CDR
FT /note= "complementarity determining region"
XX
PN W09507301-A1.
XX
PD 16-MAR-1995.
XX
PF 07-SEP-1994; 94WO-US010308.
XX
PR 07-SEP-1993; 93US-00117366.
PR 14-OCT-1993; 93US-00136783.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Holmes S, Gross MS, Sylvester DR;
XX
DR WPI; 1995-123387/16.
DR N-PSDB; AAQ83492.
XX
XX Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from
PT high affinity mAbs - useful in treatment of IL-4-mediated and Ige-
PT mediated allergic conditions.
XX

PS Disclosure; Fig 3; 97pp; English.
XX
CC A human/mouse chimeric antibody heavy chain variable region was
CC constructed (given in AAR70191) that contained the mouse anti-human IL-4
CC Mab 3B9 variable region including 3 CDRs (AAR70198-200) and a human
CC antibody signal peptide (AAR70193). The construct was used for humanized
CC antibody production. (Updated on 25-MAR-2003 to correct PN field.)
CC (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 141 AA;

Query Match 100.0%; Score 66; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RETVFYWFYFDV 11
Db 120 RETVFYWFYFDV 130
|||||

RESULT 11
AAY23770
ID AAY23770 standard; protein; 141 AA.
XX
AC AAY23770;
XX
DT 13-SEP-1999 (first entry)
XX
DE Heavy chain variable region of humanised murine IL-4 antibody 3B9.
XX
KW Heavy chain variable region; interleukin-4; IL-4; antibody 3B9;
KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
KW Immunoglobulin E-mediated allergic reaction; allergic rhinitis;
KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.
XX
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
PN US5928904-A.
XX
PD 27-JUL-1999.
XX
PF 07-JUN-1995; 95US-00483632.
XX
PR 07-SEP-1993; 93US-00117366.
PR 14-OCT-1993; 93US-00136783.
PR 07-SEP-1994; 94WO-US010308.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Holmes SD, Sylvester DR, Gross MS;
XX
DR WPI; 1999-429500/36.
DR N-PSDB; AAX85887.
XX
PT New DNA molecules encoding recombinant antibodies useful for treating IL4
PT -mediated conditions.
XX
PS Example 3; Fig 4; 50pp; English.
XX
CC The present sequence represents the heavy chain variable region of a
CC humanised murine interleukin-4 (IL-4) antibody 3B9. The specification
CC describes chimeric and humanised IL-4 monoclonal antibodies. The
CC antibodies of the invention are used in therapeutic and pharmaceutical
CC compositions for treating IL-4 mediated and immunoglobulin E-mediated
CC allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic
CC dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host
CC -versus-graft disease and renal disease. They are also useful in the
CC diagnosis of an allergy or condition associated with excess IL-4
CC production through the measurement e.g. by ELISA of circulating

CC endogenous IL-4 levels in humans

XX Sequence 141 AA;

Query Match 100.0%; Score 66; DB 2; Length 141;

Best Local Similarity 100.0%; Pred. No. 0.0036;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RETVFWYFDV 11

|||||

120 RETVFWYFDV 130

RESULT 12

AAV23769

ID AAV23769 standard; protein; 141 AA.

XX AAV23769;

DT 17-OCT-2003 (revised)

DT 13-SEP-1999 (first entry)

XX Heavy chain variable region of murine/human chimeric antibody 3B9.

XX Heavy chain variable region; interleukin-4; IL-4; antibody 3B9;
 KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
 KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KW rheumatoid arthritis; host-versus-graft disease; renal disease; allergy.

XX Mus sp.

OS Homo sapiens.

OS Chimeric.

XX US5928904-A.

XX 27-JUL-1999.

XX 07-JUN-1995; 95US-00483632.

XX 07-SEP-1993; 93US-00117366.

XX 14-OCT-1993; 93US-00136783.

XX 07-SEP-1994; 94WO-US010308.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Holmes SD, Sylvester DR, Gross MS;

XX WPI; 1999-429500/36.

XX N-PSDB; AAX85886.

XX New DNA molecules encoding recombinant antibodies useful for treating IL4

XX -mediated conditions.

XX Example 3; Fig 3; 50pp; English.

XX The present sequence represents the heavy chain variable region of

XX murine/human interleukin-4 (IL-4) chimeric antibody 3B9. The

XX specification describes chimeric and humanised IL-4 monoclonal

XX antibodies. The antibodies of the invention are used in therapeutic and

XX pharmaceutical compositions for treating IL-4 mediated and immunoglobulin

XX E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis,

XX atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid

XX arthritis, host-versus-graft disease and renal disease. They are also

XX useful in the diagnosis of an allergy or condition associated with excess

XX IL-4 production through the measurement e.g. by ELISA of circulating

XX endogenous IL-4 levels in humans. (Updated on 17-OCT-2003 to standardise

XX OS field)

XX Sequence 141 AA;

XX Query Match 100.0%; Score 66; DB 2; Length 141;

Best Local Similarity 100.0%; Pred. No. 0.0036;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RETVFWYFDV 11

|||||

120 RETVFWYFDV 130

RESULT 13

AAV18125

ID AAV18125 standard; protein; 141 AA.

XX AAV18125;

XX 11-AUG-1999 (first entry)

XX Chimeric 3B9 monoclonal antibody heavy chain.

XX Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;

XX allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;

XX atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;

XX autoimmune disease; graft versus host disease.

XX Synthetic.

XX US5914110-A.

XX 22-JUN-1999.

XX 07-JUN-1995; 95US-00483636.

XX 07-SEP-1993; 93US-00117366.

XX 14-OCT-1993; 93US-00136783.

XX 07-SEP-1994; 94WO-US010308.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Sylvester DR, Holmes SD, Gross MS;

XX WPI; 1999-370482/31.

XX N-PSDB; AAX79542.

XX Recombinant IL4 antibodies useful for treatment of allergic rhinitis,

XX atopic asthma and anaphylactic shock.

XX Example 5; Fig 3; 50pp; English.

XX This sequence represents the light chain of the chimeric 3B9 antibody of

XX the invention. The antibody is a chimeric or humanised interleukin-4

XX (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE)

XX mediated diseases. The antibodies are useful for the treatment of

XX allergic disorders such as allergic rhinitis, conjunctivitis, atopic

XX dermatitis, atopic asthma and anaphylactic shock. The antibodies are also

XX useful for regulating B and T cell proliferation and as such are useful

XX in the treatment of autoimmune diseases and graft versus host disease

XX Sequence 141 AA;

XX Query Match 100.0%; Score 66; DB 2; Length 141;

XX Best Local Similarity 100.0%; Pred. No. 0.0036;

XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Qy 1 RETVFWYFDV 11

|||||

120 RETVFWYFDV 130

RESULT 14

AAV18117

ID AAV18117 standard; protein; 141 AA.

XX AAV18117;

XX 11-AUG-1999 (first entry)
 XX Heavy chain sequence for humanised 3B9 antibody.
 DE
 XX
 XX Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;
 KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
 KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
 KW autoimmune disease; graft versus host disease.
 XX
 OS Synthetic.
 XX
 XX US5914110-A.
 XX
 XX 22-JUN-1999.
 PD
 XX
 XX 07-JUN-1995; 95US-00483636.
 PF
 XX 07-SEP-1993; 93US-00117366.
 PR
 PR 14-OCT-1993; 93US-00136783.
 PR
 XX 07-SEP-1994; 94WO-US010308.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 XX Sylvester DR, Holmes SD, Gross MS;
 XX
 XX WPI; 1999-370482/31.
 DR
 DR N-PSDB; AAX79516.
 XX
 XX Recombinant IL4 antibodies useful for treatment of allergic rhinitis,
 PT atopic asthma and anaphylactic shock.
 PT
 XX Claim 15; Fig 4; 50pp; English.
 PS
 XX This sequence represents the heavy chain of the humanised 3B9 antibody of
 CC the invention. The antibody is a chimeric or humanised interleukin-4
 CC (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE)
 CC mediated diseases. The antibodies are useful for the treatment of
 CC allergic disorders such as allergic rhinitis, conjunctivitis, atopic
 CC dermatitis, atopic asthma and anaphylactic shock. The antibodies are also
 CC useful for regulating B and T cell proliferation and as such are useful
 CC in the treatment of autoimmune diseases and graft versus host disease
 XX
 XX Sequence 141 AA;
 SQ
 Query Match 100.0%; Score 66; DB 2; Length 141;
 Best Local Similarity 100.0%; Pred. NO. 0.0036;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RETVFYWFYFDV 11
 Db 120 RETVFYWFYFDV 130
 RESULT 15
 ADP47150
 ID ADP47150 standard; peptide; 13 AA.
 XX
 AC ADP47150;
 XX
 XX 09-SEP-2004 (first entry)
 DT
 XX Human phospholipase A2-specific mAb heavy chain peptide #15.
 DE
 XX human; monoclonal antibody; phospholipase A2; PLA2;
 KW inflammatory disorder; degenerative disorder;
 KW joint inflammatory reaction; skin inflammatory reaction;
 KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
 KW Alzheimer's disease; atherosclerosis; restenosis; heavy chain.
 XX
 OS Homo sapiens.
 XX
 XX WO2004050850-A2.
 PN
 XX 17-JUN-2004.
 PD
 XX
 XX 02-DEC-2003; 2003WO-US038234.
 PF
 XX 02-DEC-2002; 2002US-0430724P.
 PR
 XX (ABGE-) ARGENIX INC.
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 XX Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;
 PI Jia X, Nocerini MR;
 XX
 XX WPI; 2004-461119/43.
 DR
 XX New human monoclonal antibody that binds to phospholipase A2 (PLA2),
 PT useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
 PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.
 XX
 XX Example 5; SEQ ID NO 65; 128pp; English.
 PS
 XX The invention comprises a human monoclonal antibody that binds to
 CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is
 CC useful in the preparation of a medicament for the treatment of
 CC inflammatory and degenerative disorders stemming from inflammatory
 CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
 CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
 CC amino acid sequence represents a human PLA2-specific monoclonal antibody
 CC heavy chain peptide.
 XX
 XX Sequence 13 AA;
 SQ
 Query Match 78.8%; Score 52; DB 8; Length 13;
 Best Local Similarity 77.8%; Pred. NO. 0.066;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TVFYWFYFDV 11
 Db 5 TIFYWYFDL 13
 RESULT 16
 ADP47171
 ID ADP47171 standard; peptide; 13 AA.
 XX
 AC ADP47171;
 XX
 XX 09-SEP-2004 (first entry)
 DT
 XX Human phospholipase A2-specific mAb heavy chain peptide #36.
 DE
 XX human; monoclonal antibody; phospholipase A2; PLA2;
 KW inflammatory disorder; degenerative disorder;
 KW joint inflammatory reaction; skin inflammatory reaction;
 KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
 KW Alzheimer's disease; atherosclerosis; restenosis; heavy chain.
 XX
 OS Homo sapiens.
 XX
 XX WO2004050850-A2.
 PN
 XX 17-JUN-2004.
 PD
 XX
 XX 02-DEC-2003; 2003WO-US038234.
 PF
 XX 02-DEC-2002; 2002US-0430724P.
 PR
 XX (ABGE-) ARGENIX INC.
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 XX Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;
 PI Jia X, Nocerini MR;
 XX

XX WPI; 2004-461119/43.
 XX New human monoclonal antibody that binds to phospholipase A2 (PLA2),
 XX useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
 XX asthma, Alzheimer's disease, atherosclerosis, or restenosis.
 XX Example 5; SEQ ID NO 86; 128pp; English.
 XX The invention comprises a human monoclonal antibody that binds to
 XX phospholipase A2 (PLA2). The monoclonal antibody of the invention is
 XX useful in the preparation of a medicament for the treatment of
 XX inflammatory and degenerative disorders stemming from inflammatory
 XX reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
 XX asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
 XX amino acid sequence represents a human PLA2-specific monoclonal antibody
 XX heavy chain peptide.
 XX Sequence 13 AA;
 SQ Query Match 78.8%; Score 52; DB 8; Length 13;
 Best Local Similarity 77.8%; Pred. No. 0.066; Length 13;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 TVFYWYFDV 11
 Db 5 TIFYWYFDL 13
 RESULT 17
 ID AAR99470 standard; protein; 137 AA.
 XX AC AAR99470;
 XX DT 14-FEB-1997 (first entry)
 XX DE Monoclonal antibody PA1-3F10 variable heavy chain.
 XX PA1-3F10; antibody; hybridoma; LMBP1322CB; cancer; target; epitope;
 XX killing; colorectal; lung; ovary; cytotoxin; neoplasia.
 XX Mus musculus.
 XX Key Location/Qualifiers
 XX Region 11..40
 XX /label= framework_region
 XX /note= "FR1"
 XX Region 41..45
 XX /label= complementarity_determining_region
 XX /note= "CDR1"
 XX Region 46..59
 XX /label= framework_region
 XX /note= "FR2"
 XX Region 60..76
 XX /label= complementarity_determining_region
 XX /note= "CDR2"
 XX Region 77..108
 XX /label= framework_region
 XX /note= "FR3"
 XX Region 109..120
 XX /label= complementarity_determining_region
 XX /note= "CDR3"
 XX Region 121..131
 XX /label= framework_region
 XX /note= "FR4"
 XX WO9622310-A1.
 XX 25-JUL-1996.
 XX 15-JAN-1996; 96WO-SE000029.

PR 18-JAN-1995; 95SE-00000148.
 XX (BIOI-) BIOINVENT INT AB.
 XX Carlsson R, Jansson B;
 XX WPI; 1996-354478/35.
 XX Monoclonal antibody PA1-3F10 produced by hybridoma BCM LMBP1322CB -
 XX useful to target cancer cells for killing or detection.
 XX Claim 4; Fig 11; 62pp; English.
 XX AAR99469 represents the variable light (VL) chain of monoclonal antibody
 XX PA1-3F10 produced by hybridoma BCM LMBP1322CB. The antibody is directed
 XX against an epitope present on cancer cells, in particular breast, ovary,
 XX lung and colorectal cancer cells. The antibody is useful for detecting
 XX cancer cell epitopes and hence in the diagnosis of cancer. The antibody
 XX can be conjugated to a cytotoxic compound and targetted to cancer cells
 XX to kill them
 XX Sequence 137 AA;
 SQ Query Match 74.2%; Score 49; DB 2; Length 137;
 Best Local Similarity 72.7%; Pred. No. 2.3;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 RETVFWYFDV 11
 Db 110 RSDSFYWFVDV 120
 RESULT 18
 ID ABP66387 standard; protein; 120 AA.
 XX AC ABP66387;
 XX DT 04-DEC-2002 (first entry)
 XX DE Human RSV antibody variable heavy domain.
 XX Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;
 XX complementarity determining region; respiratory syncytial virus;
 XX virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;
 XX immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;
 XX bronchopulmonary dysplasia; congenital heart disease;
 XX congenital immunodeficiency; acquired immunodeficiency.
 XX Homo sapiens.
 XX WO200243660-A2.
 XX 06-JUN-2002.
 XX 28-NOV-2001; 2001WO-US044807.
 XX 28-NOV-2000; 2000US-00724396.
 XX 28-NOV-2000; 2000US-00724531.
 XX (MEDI-) MEDIUMMUNE INC.
 XX Young JF, Koenig S, Johnson LS;
 XX WPI; 2002-706803/76.
 XX Antibody for treating respiratory syncytial virus (RSV) infection,
 XX comprises a variable heavy/light domain or complementarity determining
 XX regions 1 - 3 of variable light/heavy chains, that immunospecifically
 XX binds to RSV antigen.
 XX Claim 1; Page 207; 298pp; English.

CC The invention relates to a novel antibody comprising a variable heavy
 CC (VH) domain, variable light (VL) domain, VH complementarity determining
 CC region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the
 CC antibody immunospecifically binds to a respiratory syncytial virus (RSV)
 CC antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the
 CC invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,
 CC and immunostimulant activity. The polynucleotides of the invention may
 CC be used for preventing, treating or ameliorating one or more symptoms
 CC associated with RSV infection in a mammal, e.g. cystic fibrosis,
 CC bronchopulmonary dysplasia, congenital heart disease, congenital
 CC immunodeficiency or acquired immunodeficiency, or after a bone marrow
 CC transplant. The sequence represents a variable domain of a human RSV
 CC antibody of the invention
 XX
 CC Sequence 120 AA;
 SQ

Query Match 71.2%; Score 47; DB 5; Length 120;
 Best Local Similarity 63.6%; Pred. No. 4.4;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RETVFWYFDV 11
 |: : |||||
 Db 99 RDMIFNWYFDV 109

RESULT 19
 ABP66421
 ID ABP66421 standard; protein; 120 AA.
 XX
 AC ABP66421;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 DE Human RSV antibody variable heavy domain.
 XX
 KW Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;
 KW complementarity determining region; respiratory syncytial virus;
 KW virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;
 KW immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;
 KW bronchopulmonary dysplasia; congenital heart disease;
 KW congenital immunodeficiency; acquired immunodeficiency.
 XX
 OS Homo sapiens.
 XX
 PN WO200243660-A2.
 XX
 PD 06-JUN-2002.
 XX
 PF 28-NOV-2001; 2001WO-US044807.
 XX
 PR 28-NOV-2000; 2000US-00724396.
 XX
 PR 28-NOV-2000; 2000US-00724531.
 XX
 PA (MEDI-) MEDIUMMUNE INC.
 XX
 PI Young JF, Koenig S, Johnson LS;
 XX
 DR WPI; 2002-706803/76.
 XX
 PT Antibody for treating respiratory syncytial virus (RSV) infection,
 PT comprises a variable heavy/light domain or complementarity determining
 PT regions 1 - 3 of variable light/heavy chains, that immunospecifically
 PT binds to RSV antigen.
 XX
 PS Claim 1; Page 219; 298pp; English.
 XX
 CC The invention relates to a novel antibody comprising a variable heavy
 CC (VH) domain, variable light (VL) domain, VH complementarity determining
 CC region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the
 CC antibody immunospecifically binds to a respiratory syncytial virus (RSV)
 CC antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the
 CC invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,
 CC and immunostimulant activity. The polynucleotides of the invention may
 CC be used for preventing, treating or ameliorating one or more symptoms
 CC associated with RSV infection in a mammal, e.g. cystic fibrosis,
 CC bronchopulmonary dysplasia, congenital heart disease, congenital
 CC immunodeficiency or acquired immunodeficiency, or after a bone marrow
 CC transplant. The sequence represents a variable domain of a human RSV
 CC antibody of the invention

CC invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,
 CC and immunostimulant activity. The polynucleotides of the invention may
 CC have a use in a vaccine, and in gene therapy. The antibody is useful for
 CC treating or ameliorating a RSV infection in a human. The antibody is also
 CC useful for preventing, treating or ameliorating one or more symptoms
 CC associated with RSV infection in a mammal, e.g. cystic fibrosis,
 CC bronchopulmonary dysplasia, congenital heart disease, congenital
 CC immunodeficiency or acquired immunodeficiency, or after a bone marrow
 CC transplant. The sequence represents a variable domain of a human RSV
 CC antibody of the invention
 XX
 CC Sequence 120 AA;
 SQ

Query Match 71.2%; Score 47; DB 5; Length 120;
 Best Local Similarity 63.6%; Pred. No. 4.4;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RETVFWYFDV 11
 |: : |||||
 Db 99 RDMIFNWYFDV 109

RESULT 20
 ABP66405
 ID ABP66405 standard; protein; 120 AA.
 XX
 AC ABP66405;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 DE Human RSV antibody variable heavy domain.
 XX
 KW Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;
 KW complementarity determining region; respiratory syncytial virus;
 KW virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;
 KW immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;
 KW bronchopulmonary dysplasia; congenital heart disease;
 KW congenital immunodeficiency; acquired immunodeficiency.
 XX
 OS Homo sapiens.
 XX
 PN WO200243660-A2.
 XX
 PD 06-JUN-2002.
 XX
 PF 28-NOV-2001; 2001WO-US044807.
 XX
 PR 28-NOV-2000; 2000US-00724396.
 XX
 PR 28-NOV-2000; 2000US-00724531.
 XX
 PA (MEDI-) MEDIUMMUNE INC.
 XX
 PI Young JF, Koenig S, Johnson LS;
 XX
 DR WPI; 2002-706803/76.
 XX
 PT Antibody for treating respiratory syncytial virus (RSV) infection,
 PT comprises a variable heavy/light domain or complementarity determining
 PT regions 1 - 3 of variable light/heavy chains, that immunospecifically
 PT binds to RSV antigen.
 XX
 PS Claim 1; Page 213; 298pp; English.
 XX
 CC The invention relates to a novel antibody comprising a variable heavy
 CC (VH) domain, variable light (VL) domain, VH complementarity determining
 CC region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the
 CC antibody immunospecifically binds to a respiratory syncytial virus (RSV)
 CC antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the
 CC invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,
 CC and immunostimulant activity. The polynucleotides of the invention may
 CC have a use in a vaccine, and in gene therapy. The antibody is useful for
 CC treating or ameliorating a RSV infection in a human. The antibody is also
 CC useful for preventing, treating or ameliorating one or more symptoms

CC associated with RSV infection in a mammal, e.g. cystic fibrosis,
 CC bronchopulmonary dysplasia, congenital heart disease, congenital
 CC immunodeficiency or acquired immunodeficiency, or after a bone marrow
 CC transplant. The sequence represents a variable domain of a human RSV
 CC antibody of the invention
 XX Sequence 120 AA;
 SQ

Query Match 71.2%; Score 47; DB 5; Length 120;
 Best Local Similarity 63.6%; Pred. No. 4.4;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RETVFWYFDV 11
 | : | | | | |
 Db 99 RDMIFWYFDV 109

RESULT 21
 ABP66382
 ID ABP66382 standard; protein; 120 AA.
 XX AC ABP66382;
 XX 04-DEC-2002 (first entry)
 DT Human RSV antibody variable heavy domain.
 XX Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;
 KW complementarity determining region; respiratory syncytial virus;
 KW virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;
 KW immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;
 KW bronchopulmonary dysplasia; congenital heart disease;
 KW congenital immunodeficiency; acquired immunodeficiency.
 XX Homo sapiens.
 OS WO200243660-A2.
 FN 06-JUN-2002.
 PD 28-NOV-2001; 2001WO-US044807.
 PF 28-NOV-2000; 2000US-00724396.
 PR 28-NOV-2000; 2000US-00724531.
 XX (MEDI-) MEDIUMMUNE INC.
 PA Young JF, Koenig S, Johnson LS;
 PI WPI; 2002-706803/76.
 XX Antibody for treating respiratory syncytial virus (RSV) infection,
 PT comprises a variable heavy/light domain or complementarity determining
 PT regions 1 - 3 of variable light/heavy chains, that immunospecifically
 PT binds to RSV antigen.
 XX Claim 1; Page 206; 298pp; English.
 PS The invention relates to a novel antibody comprising a variable heavy
 XX (VH) domain, variable light (VL) domain, VH complementarity determining
 CC region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the
 CC antibody immunospecifically binds to a respiratory syncytial virus (RSV)
 CC antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the
 CC invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,
 CC and immunostimulant activity. The polynucleotides of the invention may
 CC have a use in a vaccine, and in gene therapy. The antibody is useful for
 CC treating or ameliorating a RSV infection in a human. The antibody is also
 CC useful for preventing, treating or ameliorating one or more symptoms
 CC associated with RSV infection in a mammal, e.g. cystic fibrosis,
 CC bronchopulmonary dysplasia, congenital heart disease, congenital
 CC immunodeficiency or acquired immunodeficiency, or after a bone marrow
 CC transplant. The sequence represents a variable domain of a human RSV
 CC antibody of the invention

XX SQ Sequence 120 AA;
 SQ

Query Match 71.2%; Score 47; DB 5; Length 120;
 Best Local Similarity 63.6%; Pred. No. 4.4;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RETVFWYFDV 11
 | : | | | | |
 Db 99 RDMIFWYFDV 109

RESULT 22
 ABP66409
 ID ABP66409 standard; protein; 120 AA.
 XX AC ABP66409;
 XX 04-DEC-2002 (first entry)
 DT Human RSV antibody variable heavy domain.
 XX Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;
 KW complementarity determining region; respiratory syncytial virus;
 KW virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;
 KW immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;
 KW bronchopulmonary dysplasia; congenital heart disease;
 KW congenital immunodeficiency; acquired immunodeficiency.
 XX Homo sapiens.
 OS WO200243660-A2.
 FN 06-JUN-2002.
 PD 28-NOV-2001; 2001WO-US044807.
 PF 28-NOV-2000; 2000US-00724396.
 PR 28-NOV-2000; 2000US-00724531.
 XX (MEDI-) MEDIUMMUNE INC.
 PA Young JF, Koenig S, Johnson LS;
 PI WPI; 2002-706803/76.
 XX Antibody for treating respiratory syncytial virus (RSV) infection,
 PT comprises a variable heavy/light domain or complementarity determining
 PT regions 1 - 3 of variable light/heavy chains, that immunospecifically
 PT binds to RSV antigen.
 XX Claim 1; Page 214-215; 298pp; English.
 PS The invention relates to a novel antibody comprising a variable heavy
 XX (VH) domain, variable light (VL) domain, VH complementarity determining
 CC region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the
 CC antibody immunospecifically binds to a respiratory syncytial virus (RSV)
 CC antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the
 CC invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,
 CC and immunostimulant activity. The polynucleotides of the invention may
 CC have a use in a vaccine, and in gene therapy. The antibody is useful for
 CC treating or ameliorating a RSV infection in a human. The antibody is also
 CC useful for preventing, treating or ameliorating one or more symptoms
 CC associated with RSV infection in a mammal, e.g. cystic fibrosis,
 CC bronchopulmonary dysplasia, congenital heart disease, congenital
 CC immunodeficiency or acquired immunodeficiency, or after a bone marrow
 CC transplant. The sequence represents a variable domain of a human RSV
 CC antibody of the invention
 XX SQ Sequence 120 AA;
 SQ

Query Match 71.2%; Score 47; DB 5; Length 120;
 Best Local Similarity 63.6%; Pred. No. 4.4;

```
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 RETVFWYFDV 11
   | : : | | | |
Db 99 RDMIFWYFDV 109

RESULT 23
AAE28076
ID AAE28076 standard; protein; 120 AA.
XX AC AAE28076;
XX DT 13-DEC-2002 (first entry)
XX DE Human modified anti-RSV A13A11 antibody VH domain.
XX KW Human; immunoglobulin; IgG1; passive immunotherapy; gamma globulinaemia;
XX KW vaccination; hypogammaglobulinaemia; autoimmune disease; antibacterial;
XX KW immunosuppressive; lymphoid malignancy; respiratory syncytial virus;
XX KW anti-RSV; systemic infection; graft-versus-host disease; cytostatic;
XX KW virucide; mutant; mutein.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200260919-A2.
XX PD 08-AUG-2002.
XX PF 12-DEC-2001; 2001WO-US048432.
XX PR 12-DEC-2000; 2000US-0254884P.
XX PR 09-MAY-2001; 2001US-0289760P.
XX PA (MEDI-) MEDIMUNE INC.
XX PI Dall'acqua W, Johnson LS, Ward ES;
XX DR WPI; 2002-666925/71.
XX CC Modified immunoglobulins useful in the treatment of autoimmune diseases,
XX CC comprises at least one amino acid modification relative to a wild-type
XX CC immunoglobulin constant domain.
XX PS Disclosure; Page 134; 147pp; English.
XX CC The invention relates to a modified immunoglobulin (IgG1) which comprises
XX CC an IgG constant domain having at least one amino acid modification. The
XX CC immunoglobulins are used in the treatment or prevention of a disease or
XX CC disorder by passive immunotherapy for vaccinating a subject and for in
XX CC vivo diagnosis of a subject. The disease and disorders include a gamma
XX CC globulinaemia, hypogammaglobulinaemia, autoimmune diseases, graft-versus-
XX CC host, lymphoid malignancies and passive immunotherapies and also for the
XX CC treatment of various systemic infections. The present sequence is human
XX CC modified anti-RSV (respiratory syncytial virus) antibody VH domain
XX CC chain variable region)
XX CC Sequence 120 AA;
XX CC Query Match 71.2%; Score 47; DB 5; Length 120;
XX CC Best Local Similarity 63.6%; Pred. No. 4.4;
XX CC Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 RETVFWYFDV 11
   | : : | | | |
Db 99 RDMIFWYFDV 109

RESULT 24
AAE28042
ID AAE28042 standard; protein; 120 AA.
XX AC AAE28042;
XX DT 13-DEC-2002 (first entry)
XX DE Human modified anti-RSV p11d4 antibody VH domain.
XX KW Human; immunoglobulin; IgG1; passive immunotherapy; gamma globulinaemia;
XX KW vaccination; hypogammaglobulinaemia; autoimmune disease; antibacterial;
XX KW immunosuppressive; lymphoid malignancy; respiratory syncytial virus;
XX KW anti-RSV; systemic infection; graft-versus-host disease; cytostatic;
XX KW complementarity determining region; CDR; virucide; mutant; mutein.
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AC AAE28042;
XX DT 13-DEC-2002 (first entry)
XX DE Human modified anti-RSV Ale109 antibody VH domain.
XX KW Human; immunoglobulin; IgG1; passive immunotherapy; gamma globulinaemia;
XX KW vaccination; hypogammaglobulinaemia; autoimmune disease; antibacterial;
XX KW immunosuppressive; lymphoid malignancy; respiratory syncytial virus;
XX KW anti-RSV; systemic infection; graft-versus-host disease; cytostatic;
XX KW complementarity determining region; CDR; virucide; mutant; mutein.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200260919-A2.
XX PD 08-AUG-2002.
XX PF 12-DEC-2001; 2001WO-US048432.
XX PR 12-DEC-2000; 2000US-0254884P.
XX PR 09-MAY-2001; 2001US-0289760P.
XX PA (MEDI-) MEDIMUNE INC.
XX PI Dall'acqua W, Johnson LS, Ward ES;
XX DR WPI; 2002-666925/71.
XX CC Modified immunoglobulins useful in the treatment of autoimmune diseases,
XX CC comprises at least one amino acid modification relative to a wild-type
XX CC immunoglobulin constant domain.
XX PS Disclosure; Page 122-123; 147pp; English.
XX CC The invention relates to a modified immunoglobulin (IgG1) which comprises
XX CC an IgG constant domain having at least one amino acid modification. The
XX CC immunoglobulins are used in the treatment or prevention of a disease or
XX CC disorder by passive immunotherapy for vaccinating a subject and for in
XX CC vivo diagnosis of a subject. The disease and disorders include a gamma
XX CC globulinaemia, hypogammaglobulinaemia, autoimmune diseases, graft-versus-
XX CC host, lymphoid malignancies and passive immunotherapies and also for the
XX CC treatment of various systemic infections. The present sequence is human
XX CC modified anti-RSV (respiratory syncytial virus) antibody VH domain
XX CC Sequence 120 AA;
XX CC Query Match 71.2%; Score 47; DB 5; Length 120;
XX CC Best Local Similarity 63.6%; Pred. No. 4.4;
XX CC Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 RETVFWYFDV 11
   | : : | | | |
Db 99 RDMIFWYFDV 109

RESULT 25
AAE28037
ID AAE28037 standard; protein; 120 AA.
XX AC AAE28037;
XX DT 13-DEC-2002 (first entry)
XX DE Human modified anti-RSV p11d4 antibody VH domain.
XX KW Human; immunoglobulin; IgG1; passive immunotherapy; gamma globulinaemia;
XX KW vaccination; hypogammaglobulinaemia; autoimmune disease; antibacterial;
XX KW immunosuppressive; lymphoid malignancy; respiratory syncytial virus;
XX KW anti-RSV; systemic infection; graft-versus-host disease; cytostatic;
XX KW complementarity determining region; CDR; virucide; mutant; mutein.
```

OS Homo sapiens.
 OS Synthetic.
 PN WO200260919-A2.
 XX
 XX 08-AUG-2002.
 XX
 XX 12-DEC-2001; 2001WO-US048432.
 XX
 XX 12-DEC-2000; 2000US-0254884P.
 XX
 XX 09-MAY-2001; 2001US-0289760P.
 XX
 XX (MEDI-) MEDIMMUNE INC.
 XX
 XX Dall'acqua W, Johnson LS, Ward ES;
 XX
 XX WPI; 2002-666925/71.
 XX
 XX Modified immunoglobulins useful in the treatment of autoimmune diseases,
 PT comprises at least one amino acid modification relative to a wild-type
 PT immunoglobulin constant domain.
 XX
 XX Disclosure; Page 121; 147pp; English.
 PS
 XX The invention relates to a modified immunoglobulin (IgG1) which comprises
 CC an Igg constant domain having at least one amino acid modification. The
 CC immunoglobulins are used in the treatment or prevention of a disease or
 CC disorder by passive immunotherapy for vaccinating a subject and for in
 CC vivo diagnosis of a subject. The disease and disorders include a gamma
 CC globulinaemia, hypogammaglobulinaemia, autoimmune diseases, graft-versus-
 CC host, lymphoid malignancies and passive immunotherapies and also for the
 CC treatment of various systemic infections. The present sequence is human
 CC modified anti-RSV (respiratory syncytial virus) antibody VH domain
 XX
 XX Sequence 120 AA;
 SQ
 Query Match 71.2%; Score 47; DB 5; Length 120;
 Best Local Similarity 63.6%; Pred. No. 4.4;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 RETVFWYFDV 11
 Db : : | | | | |
 99 RDMIFNWFYFDV 109
 RESULT 26
 AAE28060
 ID AAE28060 standard; protein; 120 AA.
 XX
 XX AAE28060;
 XX
 XX 13-DEC-2002 (first entry)
 DT Human modified anti-RSV A8C7 antibody VH domain.
 DE
 DE Human; immunoglobulin; IgG1; passive immunotherapy; gamma globulinaemia;
 XX vaccination; hypogammaglobulinaemia; autoimmune disease; antibacterial;
 XX immunosuppressive; lymphoid malignancy; respiratory syncytial virus;
 XX anti-RSV; systemic infection; graft-versus-host disease; cytostatic;
 XX virucide; mutant; mutein.
 XX
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX WO200260919-A2.
 XX
 XX 08-AUG-2002.
 XX
 XX 12-DEC-2001; 2001WO-US048432.
 XX
 XX 12-DEC-2000; 2000US-0254884P.
 XX
 XX 09-MAY-2001; 2001US-0289760P.
 XX
 XX (MEDI-) MEDIMMUNE INC.
 XX
 XX Dall'acqua W, Johnson LS, Ward ES;
 XX
 XX WPI; 2002-666925/71.
 XX
 XX Modified immunoglobulins useful in the treatment of autoimmune diseases,
 PT comprises at least one amino acid modification relative to a wild-type
 PT immunoglobulin constant domain.
 XX
 XX Disclosure; Page 121; 147pp; English.
 PS
 XX The invention relates to a modified immunoglobulin (IgG1) which comprises
 CC an Igg constant domain having at least one amino acid modification. The
 CC immunoglobulins are used in the treatment or prevention of a disease or
 CC disorder by passive immunotherapy for vaccinating a subject and for in
 CC vivo diagnosis of a subject. The disease and disorders include a gamma
 CC globulinaemia, hypogammaglobulinaemia, autoimmune diseases, graft-versus-
 CC host, lymphoid malignancies and passive immunotherapies and also for the
 CC treatment of various systemic infections. The present sequence is human
 CC modified anti-RSV (respiratory syncytial virus) antibody VH domain
 XX
 XX Sequence 120 AA;
 SQ
 Query Match 71.2%; Score 47; DB 5; Length 120;
 Best Local Similarity 63.6%; Pred. No. 4.4;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 RETVFWYFDV 11
 Db : : | | | | |
 99 RDMIFNWFYFDV 109

PA (MEDI-) MEDIMMUNE INC.
 XX
 XX Dall'acqua W, Johnson LS, Ward ES;
 XX
 XX WPI; 2002-666925/71.
 XX
 XX Modified immunoglobulins useful in the treatment of autoimmune diseases,
 PT comprises at least one amino acid modification relative to a wild-type
 PT immunoglobulin constant domain.
 XX
 XX Disclosure; Page 128; 147pp; English.
 PS
 XX The invention relates to a modified immunoglobulin (IgG1) which comprises
 CC an Igg constant domain having at least one amino acid modification. The
 CC immunoglobulins are used in the treatment or prevention of a disease or
 CC disorder by passive immunotherapy for vaccinating a subject and for in
 CC vivo diagnosis of a subject. The disease and disorders include a gamma
 CC globulinaemia, hypogammaglobulinaemia, autoimmune diseases, graft-versus-
 CC host, lymphoid malignancies and passive immunotherapies and also for the
 CC treatment of various systemic infections. The present sequence is human
 CC modified anti-RSV (respiratory syncytial virus) antibody VH domain (heavy
 CC chain variable region)
 XX
 XX Sequence 120 AA;
 SQ
 Query Match 71.2%; Score 47; DB 5; Length 120;
 Best Local Similarity 63.6%; Pred. No. 4.4;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 RETVFWYFDV 11
 Db : : | | | | |
 99 RDMIFNWFYFDV 109
 RESULT 27
 AAE28064
 ID AAE28064 standard; protein; 120 AA.
 XX
 XX AAE28064;
 XX
 XX 13-DEC-2002 (first entry)
 DT Human modified anti-RSV H3-3F4 antibody VH domain.
 DE
 DE Human; immunoglobulin; IgG1; passive immunotherapy; gamma globulinaemia;
 XX vaccination; hypogammaglobulinaemia; autoimmune disease; antibacterial;
 XX immunosuppressive; lymphoid malignancy; respiratory syncytial virus;
 XX anti-RSV; systemic infection; graft-versus-host disease; cytostatic;
 XX virucide; mutant; mutein.
 XX
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX WO200260919-A2.
 XX
 XX 08-AUG-2002.
 XX
 XX 12-DEC-2001; 2001WO-US048432.
 XX
 XX 12-DEC-2000; 2000US-0254884P.
 XX
 XX 09-MAY-2001; 2001US-0289760P.
 XX
 XX (MEDI-) MEDIMMUNE INC.
 XX
 XX Dall'acqua W, Johnson LS, Ward ES;
 XX
 XX WPI; 2002-666925/71.
 XX
 XX Modified immunoglobulins useful in the treatment of autoimmune diseases,
 PT comprises at least one amino acid modification relative to a wild-type
 PT immunoglobulin constant domain.
 XX
 XX Disclosure; Page 130; 147pp; English.
 PS

XX The invention relates to a modified immunoglobulin (IgG1) which comprises
CC an IGG constant domain having at least one amino acid modification. The
CC immunoglobulins are used in the treatment or prevention of a disease or
CC disorder by passive immunotherapy for vaccinating a subject and for in
CC vivo diagnosis of a subject. The disease and disorders include a gamma
CC globulinaemia, hypogammaglobulinaemia, autoimmune diseases, graft-versus-
CC host, lymphoid malignancies and passive immunotherapies and also for the
CC treatment of various systemic infections. The present sequence is human
CC modified anti-RSV (respiratory syncytial virus) antibody VH domain (heavy
CC chain variable region)

XX SQ Sequence 120 AA;

Query Match 71.2%; Score 47; DB 5; Length 120;
Best Local Similarity 63.6%; Pred. No. 4.4;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RETVFWYFDV 11
| : : : :
Db 99 RDMIFWYFDV 109

RESULT 28

ABU69284
ID ABU69284 standard; protein; 120 AA.

XX AC ABU69284;

DT 03-JUN-2003 (first entry)

DE Respiratory syncytial virus (RSV) antibody #32.

XX Respiratory syncytial virus; RSV; vaccine; antibody;
KW variable heavy domain; VH; variable light domain; VL;
KW complementarity determining region; CDR; CDRI; CDR2; CDR3; RSV infection;
KW cystic fibrosis; bronchopulmonary dysplasia; congenital heart disease;
KW congenital immunodeficiency; acquired immune deficiency;
KW bone marrow transplant.

XX OS Homo sapiens.

XX PN US2002177126-A1.

XX PD 28-NOV-2002.

XX PF 28-NOV-2001; 2001US-00996288.

XX PR 28-NOV-2000; 2000US-00724531.

XX PA (MEDI-) MEDIMUNE INC.

XX PI Young JF, Koenig S, Johnson LS;

XX DR WPI; 2003-340947/32.

XX New antibody comprising a variable heavy (VH) or variable light (VL)
PT domain or complementarity determining region (CDR), such as CDRI, CDR2,
PT or CDR3, useful for preventing or treating a respiratory syncytial virus
PT (RSV) infection.

XX Claim 1; Page 82; 165pp; English.

XX The invention describes an antibody comprising a variable heavy (VH) or
CC variable light (VL) domain or complementarity determining region (CDR),
CC such as CDRI, CDR2, or CDR3, which immunospecifically binds to a
CC respiratory syncytial virus (RSV) antigen and is not SYNAGIS (RTM). The
CC antibody, pharmaceutical compositions and methods are useful for
CC preventing, treating or ameliorating a RSV infection in patients with
CC cystic fibrosis, bronchopulmonary dysplasia, congenital heart disease,
CC congenital immunodeficiency, or acquired immune deficiency, or patients
CC having had a bone marrow transplant or the elderly. This is the amino
CC acid sequence of a respiratory syncytial virus (RSV) antibody

XX SQ Sequence 120 AA;

Query Match 71.2%; Score 47; DB 6; Length 120;
Best Local Similarity 63.6%; Pred. No. 4.4;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RETVFWYFDV 11
| : : : :
Db 99 RDMIFWYFDV 109

RESULT 29

ABU69268

ID ABU69268 standard; protein; 120 AA.

XX AC ABU69268;

DT 03-JUN-2003 (first entry)

DE Respiratory syncytial virus (RSV) antibody #21.

XX Respiratory syncytial virus; RSV; vaccine; antibody;
KW variable heavy domain; VH; variable light domain; VL;
KW complementarity determining region; CDR; CDRI; CDR2; CDR3; RSV infection;
KW cystic fibrosis; bronchopulmonary dysplasia; congenital heart disease;
KW congenital immunodeficiency; acquired immune deficiency;
KW bone marrow transplant.

XX OS Homo sapiens.

XX PN US2002177126-A1.

XX PD 28-NOV-2002.

XX PF 28-NOV-2001; 2001US-00996288.

XX PR 28-NOV-2000; 2000US-00724531.

XX PA (MEDI-) MEDIMUNE INC.

XX PI Young JF, Koenig S, Johnson LS;

XX DR WPI; 2003-340947/32.

XX New antibody comprising a variable heavy (VH) or variable light (VL)
PT domain or complementarity determining region (CDR), such as CDRI, CDR2,
PT or CDR3, useful for preventing or treating a respiratory syncytial virus
PT (RSV) infection.

XX Claim 1; Page 76-77; 165pp; English.

XX The invention describes an antibody comprising a variable heavy (VH) or
CC variable light (VL) domain or complementarity determining region (CDR),
CC such as CDRI, CDR2, or CDR3, which immunospecifically binds to a
CC respiratory syncytial virus (RSV) antigen and is not SYNAGIS (RTM). The
CC antibody, pharmaceutical compositions and methods are useful for
CC preventing, treating or ameliorating a RSV infection in patients with
CC cystic fibrosis, bronchopulmonary dysplasia, congenital heart disease,
CC congenital immunodeficiency, or acquired immune deficiency, or patients
CC having had a bone marrow transplant or the elderly. This is the amino
CC acid sequence of a respiratory syncytial virus (RSV) antibody

XX SQ Sequence 120 AA;

Query Match 71.2%; Score 47; DB 6; Length 120;
Best Local Similarity 63.6%; Pred. No. 4.4;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RETVFWYFDV 11
| : : : :
Db 99 RDMIFWYFDV 109

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RESULT 30
ABU69250
ID ABU69250 standard; protein; 120 AA.
XX
XX AC ABU69250;
XX
XX DT 03-JUN-2003 (first entry)
XX
XX DE Respiratory syncytial virus (RSV) antibody #11.
XX
XX KW Respiratory syncytial virus; RSV; vaccine; antibody;
XX variable heavy domain; VH; variable light domain; VL;
XX complementarity determining region; CDR; CDR1; CDR2; CDR3; RSV infection;
XX cystic fibrosis; bronchopulmonary dysplasia; congenital heart disease;
XX congenital immunodeficiency; acquired immune deficiency;
XX bone marrow transplant.
XX
XX OS Homo sapiens.
XX
XX FN US2002177126-A1.
XX
XX PD 28-NOV-2002.
XX
XX PF 28-NOV-2001; 2001US-00996288.
XX
XX PR 28-NOV-2000; 2000US-00724531.
XX
XX PA (MEDI-) MEDIMUNE INC.
XX
XX PI Young JF, Koenig S, Johnson LS;
XX WPI; 2003-340947/32.
XX
XX PT New antibody comprising a variable heavy (VH) or variable light (VL)
XX domain or complementarity determining region (CDR), such as CDR1, CDR2,
XX or CDR3, useful for preventing or treating a respiratory syncytial virus
XX (RSV) infection.
XX
XX PS Claim 1; Page 71-72; 165pp; English.
XX
XX CC The invention describes an antibody comprising a variable heavy (VH) or
XX variable light (VL) domain or complementarity determining region (CDR),
XX such as CDR1, CDR2, or CDR3, which immunospecifically binds to a
XX respiratory syncytial virus (RSV) antigen and is not SYNAGIS (RTM). The
XX antibody, pharmaceutical compositions and methods are useful for
XX preventing, treating or ameliorating a RSV infection in patients with
XX cystic fibrosis, bronchopulmonary dysplasia, congenital heart disease,
XX congenital immunodeficiency, or acquired immune deficiency, or patients
XX having had a bone marrow transplant or the elderly. This is the amino
XX acid sequence of a respiratory syncytial virus (RSV) antibody
XX
XX SQ Sequence 120 AA;
XX
XX Query Match 71.2%; Score 47; DB 6; Length 120;
XX Best Local Similarity 63.6%; Pred. No. 4.4;
XX Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 1 RETVFWYFDV 11
XX |:| |||||
XX Db 99 RDMIFNWYFDV 109
XX
XX RESULT 32
XX ABU69245
XX ID ABU69245 standard; protein; 120 AA.
XX
XX AC ABU69245;
XX
XX DT 03-JUN-2003 (first entry)
XX
XX DE Respiratory syncytial virus (RSV) antibody #9.
XX
XX KW Respiratory syncytial virus; RSV; vaccine; antibody;
XX variable heavy domain; VH; variable light domain; VL;
XX complementarity determining region; CDR; CDR1; CDR2; CDR3; RSV infection;
XX cystic fibrosis; bronchopulmonary dysplasia; congenital heart disease;
XX congenital immunodeficiency; acquired immune deficiency;
XX bone marrow transplant.
XX
XX OS Homo sapiens.
XX
XX FN US2002177126-A1.
XX
XX

```

PD 28-NOV-2002.
 XX
 PF 28-NOV-2001; 2001US-00996288.
 XX
 PR 28-NOV-2000; 2000US-00724531.
 XX
 PA (MEDI-) IMMUNE INC.
 XX
 PI Young JF, Koenig S, Johnson LS;
 XX WPI; 2003-340947/32.
 DR
 XX New antibody comprising a variable heavy (VH) or variable light (VL)
 PT domain or complementarity determining region (CDR), such as CDR1, CDR2,
 PT or CDR3, useful for preventing or treating a respiratory syncytial virus
 PT (RSV) infection.
 XX
 PS Claim 1; Page 70; 165pp; English.
 CC
 CC The invention describes an antibody comprising a variable heavy (VH) or
 CC variable light (VL) domain or complementarity determining region (CDR),
 CC such as CDR1, CDR2, or CDR3, which immunospecifically binds to a
 CC respiratory syncytial virus (RSV) antigen and is not SYNAGIS (RTM). The
 CC antibody, pharmaceutical compositions and methods are useful for
 CC preventing, treating or ameliorating a RSV infection in patients with
 CC cystic fibrosis, bronchopulmonary dysplasia, congenital heart disease,
 CC congenital immunodeficiency, or acquired immune deficiency, or patients
 CC having had a bone marrow transplant or the elderly. This is the amino
 CC acid sequence of a respiratory syncytial virus (RSV) antibody
 XX
 SQ Sequence 120 AA;
 Query Match 71.2%; Score 47; DB 6; Length 120;
 Best Local Similarity 63.6%; Pred. No. 4.4;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RETVFWYFDV 11
 Db : : |||||
 99 RDMIFWYFDV 109
 RESULT 33
 ADE35779
 ID ADE35779 standard; protein; 120 AA.
 AC ADE35779;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE SYNAGIS antibody based heavy chain domain #13.
 KW respiratory syncytial virus; RSV infection; high affinity antibody;
 KW high avidity antibody; low antibody dose; more effective prophylaxis;
 KW complementarity determining region; CDR; human.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN US2003091584-A1.
 XX
 PD 15-MAY-2003.
 XX
 PF 28-NOV-2001; 2001US-00996265.
 XX
 PR 28-NOV-2000; 2000US-00724396.
 XX
 XX (YOUNG) YOUNG J F.
 PA (KOENIG) KOENIG S.
 PA (JOHN) JOHNSON L S.
 XX
 PI Young JF, Koenig S, Johnson LS;
 XX WPI; 2003-874589/81.
 DR

XX Preventing, treating or ameliorating symptoms associated with respiratory
 PT syncytial virus infection in mammal by administering antibodies or their
 PT fragments that immunospecifically bind to RSV antigens.
 XX
 PS Disclosure; SEQ ID NO 67; 161pp; English.
 XX
 CC The invention relates to a method of preventing, treating or ameliorating
 CC one or more symptoms associated with a respiratory syncytial virus (RSV)
 CC infection in a mammal. A sustained release formulation comprising one or
 CC more antibodies or their fragments that immunospecifically bind to one or
 CC more RSV antigens and a pharmaceutical composition comprising one or more
 CC antibodies or their fragments that immunospecifically bind to one or more
 CC RSV antigens formulated for pulmonary delivery is useful for preventing,
 CC treating or ameliorating one or more symptoms associated with a RSV
 CC infection in a mammal by administering the formulation to the mammal, or
 CC the composition to the lungs of the mammal. The antibodies bind to RSV
 CC antigen with a high affinity and/or high avidity. The methods use lower
 CC doses of antibodies which immunospecifically bind to RSV antigen, and
 CC which provide a more effective prophylaxis. The present sequence
 CC represents the amino acid sequence of an antibody chain domain based on
 CC the SYNAGIS antibody.
 XX
 SQ Sequence 120 AA;
 Query Match 71.2%; Score 47; DB 7; Length 120;
 Best Local Similarity 63.6%; Pred. No. 4.4;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RETVFWYFDV 11
 Db : : |||||
 99 RDMIFWYFDV 109
 RESULT 34
 ADE35767
 ID ADE35767 standard; protein; 120 AA.
 AC ADE35767;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE SYNAGIS antibody based heavy chain domain #12.
 KW respiratory syncytial virus; RSV infection; high affinity antibody;
 KW high avidity antibody; low antibody dose; more effective prophylaxis;
 KW complementarity determining region; CDR; human.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN US2003091584-A1.
 XX
 PD 15-MAY-2003.
 XX
 PF 28-NOV-2001; 2001US-00996265.
 XX
 PR 28-NOV-2000; 2000US-00724396.
 XX
 XX (YOUNG) YOUNG J F.
 PA (KOENIG) KOENIG S.
 PA (JOHN) JOHNSON L S.
 XX
 PI Young JF, Koenig S, Johnson LS;
 XX WPI; 2003-874589/81.
 DR
 XX Preventing, treating or ameliorating symptoms associated with respiratory
 PT syncytial virus infection in mammal by administering antibodies or their
 PT fragments that immunospecifically bind to RSV antigens.
 XX
 PS Disclosure; SEQ ID NO 55; 161pp; English.
 XX

CC The invention relates to a method of preventing, treating or ameliorating
 CC one or more symptoms associated with a respiratory syncytial virus (RSV)
 CC infection in a mammal. A sustained release formulation comprising one or
 CC more antibodies or their fragments that immunospecifically bind to one or
 CC more RSV antigens and a pharmaceutical composition comprising one or more
 CC antibodies or their fragments that immunospecifically bind to one or more
 CC RSV antigens formulated for pulmonary delivery is useful for preventing,
 CC treating or ameliorating one or more symptoms associated with a RSV
 CC infection in a mammal by administering the formulation to the mammal, or
 CC the composition to the lungs of the mammal. The antibodies bind to RSV
 CC antigen with a high affinity and/or high avidity. The methods use lower
 CC doses of antibodies which immunospecifically bind to RSV antigen, and
 CC which provide a more effective prophylaxis. The present sequence
 CC represents the amino acid sequence of a antibody chain domain based on
 CC the SYNAGIS antibody.

XX Sequence 120 AA;

Query Match 71.2%; Score 47; DB 7; Length 120;
 Best Local Similarity 63.6%; Pred. No. 4.4;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RETVFWYFDV 11
 | : : | | | | |
 Db 99 RDMIFNWFYDV 109

RESULT 35

ADE35740
 ID ADE35740 standard; protein; 120 AA.

XX AC ADE35740;

XX 29-JAN-2004 (first entry)

XX SYNAGIS antibody based heavy chain domain #5.

XX respiratory syncytial virus; RSV infection; high affinity antibody;
 XX high avidity antibody; low antibody dose; more effective prophylaxis;
 XX complementarity determining region; CDR; human.

XX Synthetic.
 XX OS Homo sapiens.

XX US2003091584-A1.

XX 15-MAY-2003.

XX 28-NOV-2001; 2001US-00996265.

XX 28-NOV-2000; 2000US-00724396.

XX (YOUNG) YOUNG J F.
 XX (KOENIG) KOENIG S.
 XX (JOHN) JOHNSON L S.

XX Young JF, Koenig S, Johnson LS;

XX WPI; 2003-874589/81.

XX Preventing, treating or ameliorating symptoms associated with respiratory
 XX syncytial virus infection in mammal by administering antibodies or their
 XX fragments that immunospecifically bind to RSV antigens.

XX Disclosure; SEQ ID NO 28; 161pp; English.

XX The invention relates to a method of preventing, treating or ameliorating
 CC one or more symptoms associated with a respiratory syncytial virus (RSV)
 CC infection in a mammal. A sustained release formulation comprising one or
 CC more antibodies or their fragments that immunospecifically bind to one or
 CC more RSV antigens and a pharmaceutical composition comprising one or more
 CC antibodies or their fragments that immunospecifically bind to one or more
 CC RSV antigens formulated for pulmonary delivery is useful for preventing,
 CC treating or ameliorating one or more symptoms associated with a RSV
 CC infection in a mammal by administering the formulation to the mammal, or
 CC the composition to the lungs of the mammal. The antibodies bind to RSV
 CC antigen with a high affinity and/or high avidity. The methods use lower
 CC doses of antibodies which immunospecifically bind to RSV antigen, and
 CC which provide a more effective prophylaxis. The present sequence
 CC represents the amino acid sequence of a antibody chain domain based on
 CC the SYNAGIS antibody.

CC treating or ameliorating one or more symptoms associated with a RSV
 CC infection in a mammal by administering the formulation to the mammal, or
 CC the composition to the lungs of the mammal. The antibodies bind to RSV
 CC antigen with a high affinity and/or high avidity. The methods use lower
 CC doses of antibodies which immunospecifically bind to RSV antigen, and
 CC which provide a more effective prophylaxis. The present sequence
 CC represents the amino acid sequence of a antibody chain domain based on
 CC the SYNAGIS antibody.

XX Sequence 120 AA;

Query Match 71.2%; Score 47; DB 7; Length 120;
 Best Local Similarity 63.6%; Pred. No. 4.4;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RETVFWYFDV 11
 | : : | | | | |
 Db 99 RDMIFNWFYDV 109

RESULT 36

ADE35745
 ID ADE35745 standard; protein; 120 AA.

XX AC ADE35745;

XX 29-JAN-2004 (first entry)

XX SYNAGIS antibody based heavy chain domain #6.

XX respiratory syncytial virus; RSV infection; high affinity antibody;
 XX high avidity antibody; low antibody dose; more effective prophylaxis;
 XX complementarity determining region; CDR; human.

XX Synthetic.
 XX OS Homo sapiens.

XX US2003091584-A1.

XX 15-MAY-2003.

XX 28-NOV-2001; 2001US-00996265.

XX 28-NOV-2000; 2000US-00724396.

XX (YOUNG) YOUNG J F.
 XX (KOENIG) KOENIG S.
 XX (JOHN) JOHNSON L S.

XX Young JF, Koenig S, Johnson LS;

XX WPI; 2003-874589/81.

XX Preventing, treating or ameliorating symptoms associated with respiratory
 XX syncytial virus infection in mammal by administering antibodies or their
 XX fragments that immunospecifically bind to RSV antigens.

XX Disclosure; SEQ ID NO 33; 161pp; English.

XX The invention relates to a method of preventing, treating or ameliorating
 CC one or more symptoms associated with a respiratory syncytial virus (RSV)
 CC infection in a mammal. A sustained release formulation comprising one or
 CC more antibodies or their fragments that immunospecifically bind to one or
 CC more RSV antigens and a pharmaceutical composition comprising one or more
 CC antibodies or their fragments that immunospecifically bind to one or more
 CC RSV antigens formulated for pulmonary delivery is useful for preventing,
 CC treating or ameliorating one or more symptoms associated with a RSV
 CC infection in a mammal by administering the formulation to the mammal, or
 CC the composition to the lungs of the mammal. The antibodies bind to RSV
 CC antigen with a high affinity and/or high avidity. The methods use lower
 CC doses of antibodies which immunospecifically bind to RSV antigen, and
 CC which provide a more effective prophylaxis. The present sequence
 CC represents the amino acid sequence of a antibody chain domain based on
 CC the SYNAGIS antibody.

```
CC the SYNAGIS antibody.
XX
SQ Sequence 120 AA;

Query Match 71.2%; Score 47; DB 7; Length 120;
Best Local Similarity 63.6%; Pred. No. 4.4;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RETVFWYFDV 11
Db 99 RDMIFNWYFDV 109
|: :| |||||

RESULT 37
ADE35763
ID ADE35763 standard; protein; 120 AA.
XX
AC ADE35763;
XX
DT 29-JAN-2004 (first entry)
XX
DE SYNAGIS antibody based heavy chain domain #11.
XX
KW respiratory syncytial virus; RSV infection; high affinity antibody;
KW high avidity antibody; low antibody dose; more effective prophylaxis;
KW complementarity determining region; CDR; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US2003091584-A1.
XX
PD 15-MAY-2003.
XX
PF 28-NOV-2001; 2001US-00996265.
XX
PR 28-NOV-2000; 2000US-00724396.
XX
PA (YOUNG/) YOUNG J F.
PA (KOENIG/) KOENIG S.
PA (JOHN/) JOHNSON L S.
XX
PI Young JF, Koenig S, Johnson LS;
XX
XX WPI; 2003-874589/81.
XX
DR Preventing, treating or ameliorating symptoms associated with respiratory
PT syncytial virus infection in mammal by administering antibodies or their
PT fragments that immunospecifically bind to RSV antigens.
XX
PS Disclosure; SEQ ID NO 51; 161pp; English.
XX
CC The invention relates to a method of preventing, treating or ameliorating
CC one or more symptoms associated with a respiratory syncytial virus (RSV)
CC infection in a mammal. A sustained release formulation comprising one or
CC more antibodies or their fragments that immunospecifically bind to one or
CC more RSV antigens and a pharmaceutical composition comprising one or more
CC antibodies or their fragments that immunospecifically bind to one or more
CC RSV antigens formulated for pulmonary delivery is useful for preventing,
CC treating or ameliorating one or more symptoms associated with a RSV
CC infection in a mammal by administering the formulation to the mammal, or
CC the composition to the lungs of the mammal. The antibodies bind to RSV
CC antigen with a high affinity and/or high avidity. The methods use lower
CC doses of antibodies which immunospecifically bind to RSV antigen, and
CC which provide a more effective prophylaxis. The present sequence
CC represents the amino acid sequence of a antibody chain domain based on
CC the SYNAGIS antibody.
XX
SQ Sequence 120 AA;

Query Match 71.2%; Score 47; DB 7; Length 120;
Best Local Similarity 63.6%; Pred. No. 4.4;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RETVFWYFDV 11
Db 99 RDMIFNWYFDV 109
|: :| |||||

RESULT 37
ADE35763
ID ADE35763 standard; protein; 120 AA.
XX
AC ADE35763;
XX
DT 29-JAN-2004 (first entry)
XX
DE SYNAGIS antibody based heavy chain domain #11.
XX
KW respiratory syncytial virus; RSV infection; high affinity antibody;
KW high avidity antibody; low antibody dose; more effective prophylaxis;
KW complementarity determining region; CDR; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US2003091584-A1.
XX
PD 15-MAY-2003.
XX
PF 28-NOV-2001; 2001US-00996265.
XX
PR 28-NOV-2000; 2000US-00724396.
XX
PA (YOUNG/) YOUNG J F.
PA (KOENIG/) KOENIG S.
PA (JOHN/) JOHNSON L S.
XX
PI Young JF, Koenig S, Johnson LS;
XX
XX WPI; 2003-874589/81.
XX
DR Preventing, treating or ameliorating symptoms associated with respiratory
PT syncytial virus infection in mammal by administering antibodies or their
PT fragments that immunospecifically bind to RSV antigens.
XX
PS Disclosure; SEQ ID NO 51; 161pp; English.
XX
CC The invention relates to a method of preventing, treating or ameliorating
CC one or more symptoms associated with a respiratory syncytial virus (RSV)
CC infection in a mammal. A sustained release formulation comprising one or
CC more antibodies or their fragments that immunospecifically bind to one or
CC more RSV antigens and a pharmaceutical composition comprising one or more
CC antibodies or their fragments that immunospecifically bind to one or more
CC RSV antigens formulated for pulmonary delivery is useful for preventing,
CC treating or ameliorating one or more symptoms associated with a RSV
CC infection in a mammal by administering the formulation to the mammal, or
CC the composition to the lungs of the mammal. The antibodies bind to RSV
CC antigen with a high affinity and/or high avidity. The methods use lower
CC doses of antibodies which immunospecifically bind to RSV antigen, and
CC which provide a more effective prophylaxis. The present sequence
CC represents the amino acid sequence of a antibody chain domain based on
CC the SYNAGIS antibody.
XX
SQ Sequence 120 AA;

Query Match 71.2%; Score 47; DB 8; Length 120;
Best Local Similarity 63.6%; Pred. No. 4.4;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RETVFWYFDV 11
Db 99 RDMIFNWYFDV 109
|: :| |||||

RESULT 39
ADI56902
ID ADI56902 standard; protein; 120 AA.
XX
AC ADI56902;
XX
DT 06-MAY-2004 (first entry)
XX
DE RSV antibody heavy chain variable region #4.
XX
```


KW human; liquid antibody formulation; antibody;
KW respiratory syncytial virus; RSV; RSV infection.

OS Homo sapiens.

PN WO2003106644-A2.

XX 24-DEC-2003.

XX 16-JUN-2003; 2003WO-US018914.

XX 14-JUN-2002; 2002US-0388920P.

XX (MEDI-) MEDIMMUNE INC.

XX Oliver CN, Allan CB, Chang S;

XX WPI; 2004-082183/08.

XX Liquid antibody formulation, useful for treating symptoms associated with
PT respiratory syncytial virus (RSV) infection, comprising antibody or its
PT fragment binding immunospecifically to RSV antigen and histidine.

XX Claim 30; SEQ ID NO 28; 169pp; English.

XX The invention relates to a liquid antibody formulation comprising 15 or
CC more mg/ml of antibody, or its fragment that immunospecifically binds to
CC a respiratory syncytial virus (RSV) antigen and histidine in an aqueous
CC carrier. The formulation is useful for preventing, treating or
CC ameliorating one or more symptoms associated with a RSV infection in a
CC subject, which involves administering a prophylactically or
CC therapeutically effective amount of the formulation. The formulation is a
CC stable liquid formulation of an anti-RSV antibody effective in preventing
CC or treating RSV infection. The present sequence represents the amino acid
CC sequence of a RSV antibody heavy chain variable region.

XX Sequence 120 AA;

Query Match 71.2%; Score 47; DB 8; Length 120;

Best Local Similarity 63.6%; Pred. No. 4.4;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RETVFYWFYFDV 11

Db : : |||||

99 RDMIFNWFYFDV 109

RESULT 40

ADI56929

ID ADI56929 standard; protein; 120 AA.

XX AC ADI56929;

XX 06-MAY-2004 (first entry)

XX RSV antibody heavy chain variable region #11.

XX human; liquid antibody formulation; antibody;

KW respiratory syncytial virus; RSV; RSV infection.

OS Homo sapiens.

PN WO2003106644-A2.

XX 24-DEC-2003.

XX 16-JUN-2003; 2003WO-US018914.

XX 14-JUN-2002; 2002US-0388920P.

XX (MEDI-) MEDIMMUNE INC.

XX Oliver CN, Allan CB, Chang S;

XX WPI; 2004-082183/08.

XX Liquid antibody formulation, useful for treating symptoms associated with
PT respiratory syncytial virus (RSV) infection, comprising antibody or its
PT fragment binding immunospecifically to RSV antigen and histidine.

XX Claim 30; SEQ ID NO 55; 169pp; English.

XX The invention relates to a liquid antibody formulation comprising 15 or
CC more mg/ml of antibody, or its fragment that immunospecifically binds to
CC a respiratory syncytial virus (RSV) antigen and histidine in an aqueous
CC carrier. The formulation is useful for preventing, treating or
CC ameliorating one or more symptoms associated with a RSV infection in a
CC subject, which involves administering a prophylactically or
CC therapeutically effective amount of the formulation. The formulation is a
CC stable liquid formulation of an anti-RSV antibody effective in preventing
CC or treating RSV infection. The present sequence represents the amino acid
CC sequence of a RSV antibody heavy chain variable region.

XX Sequence 120 AA;

Query Match 71.2%; Score 47; DB 8; Length 120;

Best Local Similarity 63.6%; Pred. No. 4.4;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RETVFYWFYFDV 11

Db : : |||||

99 RDMIFNWFYFDV 109

RESULT 41

ADI56925

ID ADI56925 standard; protein; 120 AA.

XX AC ADI56925;

XX 06-MAY-2004 (first entry)

XX RSV antibody heavy chain variable region #10.

XX human; liquid antibody formulation; antibody;

KW respiratory syncytial virus; RSV; RSV infection.

OS Homo sapiens.

PN WO2003106644-A2.

XX 24-DEC-2003.

XX 16-JUN-2003; 2003WO-US018914.

XX 14-JUN-2002; 2002US-0388920P.

XX (MEDI-) MEDIMMUNE INC.

XX Oliver CN, Allan CB, Chang S;

XX WPI; 2004-082183/08.

XX Liquid antibody formulation, useful for treating symptoms associated with
PT respiratory syncytial virus (RSV) infection, comprising antibody or its
PT fragment binding immunospecifically to RSV antigen and histidine.

XX Claim 30; SEQ ID NO 51; 169pp; English.

XX The invention relates to a liquid antibody formulation comprising 15 or
CC more mg/ml of antibody, or its fragment that immunospecifically binds to
CC a respiratory syncytial virus (RSV) antigen and histidine in an aqueous
CC carrier. The formulation is useful for preventing, treating or
CC ameliorating one or more symptoms associated with a RSV infection in a
CC subject, which involves administering a prophylactically or
CC therapeutically effective amount of the formulation. The formulation is a

CC stable liquid formulation of an anti-RSV antibody effective in preventing
CC or treating RSV infection. The present sequence represents the amino acid
CC sequence of a RSV antibody heavy chain variable region.

XX Sequence 120 AA;

Query Match 71.2%; Score 47; DB 8; Length 120;
Best Local Similarity 63.6%; Pred. No. 4.4;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RETVFWYFDV 11
| : : |||||
Db 99 RDMIFWYFDV 109

RESULT 42

ADI56907
ID ADI56907 standard; protein; 120 AA.

XX AC ADI56907;

XX DT 06-MAY-2004 (first entry)

XX DE RSV antibody heavy chain variable region #5.

XX KW human; liquid antibody formulation; antibody;
XX KM respiratory syncytial virus; RSV; RSV infection.

XX OS Homo sapiens.

XX PN WO2003106644-A2.

XX PD 24-DEC-2003.

XX PF 16-JUN-2003; 2003WO-US018914.

XX PR 14-JUN-2002; 2002US-0388920P.

XX PA (MEDI-) MEDIMUNE INC.

XX PI Oliver CN, Allan CB, Chang S;

XX DR WPI; 2004-082183/08.

XX PT Liquid antibody formulation, useful for treating symptoms associated with
XX respiratory syncytial virus (RSV) infection, comprising antibody or its
XX fragment binding immunospecifically to RSV antigen and histidine.

XX PS Claim 30; SEQ ID NO 33; 169pp; English.

XX CC The invention relates to a liquid antibody formulation comprising 15 or
XX more mg/ml of antibody, or its fragment that immunospecifically binds to
XX a respiratory syncytial virus (RSV) antigen and histidine in an aqueous
XX carrier. The formulation is useful for preventing, treating or
XX ameliorating one or more symptoms associated with a RSV infection in a
XX subject, which involves administering a prophylactically or
XX therapeutically effective amount of the formulation. The formulation is a
XX stable liquid formulation of an anti-RSV antibody effective in preventing
XX or treating RSV infection. The present sequence represents the amino acid
XX sequence of a RSV antibody heavy chain variable region.

XX SQ Sequence 120 AA;

Query Match 71.2%; Score 47; DB 8; Length 120;
Best Local Similarity 63.6%; Pred. No. 4.4;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RETVFWYFDV 11
| : : |||||
Db 99 RDMIFWYFDV 109

RESULT 43

ADT89230

ID ADT89230 standard; protein; 120 AA.

XX AC ADT89230;

XX DT 16-DEC-2004 (first entry)

XX DE Humanised RSV antibody (Ale109) VH domain protein.

XX KW Stabilised glycoprotein; leukaemia; neoplasms; fibrosarcoma;
XX renal cell carcinoma; osteogenic sarcoma; rhabdomyosarcoma;
XX Ewing's tumour; squamous cell carcinoma; hepatoma; Wilms' tumour; glioma;
XX astrocytoma; acoustic neuroma; neuroblastoma; retinoblastoma;
XX inflammatory disorder; rheumatoid arthritis; spondyloarthropathy;
XX inflammatory bowel disease; asthma; humanised; antibody; virucide;
XX antibacterial; cytostatic; antiinflammatory; antirheumatic;
XX antiarthritic; variable heavy chain; VH.

XX OS Respiratory syncytial virus.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN US2004191265-A1.

XX PD 30-SEP-2004.

XX PF 05-JAN-2004; 2004US-00751744.

XX PR 06-JAN-2003; 2003US-0438162P.

XX PA (SCHE/) SCHERNMAN M A.

XX PA (CASA/) CASAS-FINET J.

XX PA (FENG/) FENG J.

XX PA (TOUS/) TOUS G.

XX PI Schernman MA, Casas-Finet J, Feng J, Tous G;

XX DR WPI; 2004-698665/68.

XX PT New modified immunoglobulin G (IgG) having modified hinge region
XX comprising amino acid modifications corresponding to specific positions
XX of IgG1 of wild-type, useful for treating viral infection caused by
XX respiratory syncytial virus.

XX PS Disclosure; SEQ ID NO 33; 66pp; English.

XX CC The present invention is based upon the development of a novel method of
XX analysing and identifying glycoprotein (limited to immunoglobulins)
XX degradation products. The inventors have identified a portion of the
XX hinge region of the heavy chain immunoglobulin G1 (IgG1) constant domain
XX as a site of immunoglobulin degradation. This method leads to the
XX identification and production of stabilised immunoglobulin molecules with
XX increased stability and/or serum half life. The invention is useful for
XX treating, preventing or ameliorating one or more symptoms associated with
XX viral infection caused by respiratory syncytial virus (RSV) in human and
XX preventing viral or bacterial antigen from binding to its host cell
XX receptor. The invention is also useful for preventing, inhibiting or
XX reducing the growth or metastasis of cancerous cells such as leukaemia,
XX neoplasms, fibrosarcoma, renal cell carcinoma, osteogenic sarcoma,
XX rhabdomyosarcoma, Ewing's tumour, squamous cell carcinoma, hepatoma,
XX Wilms' tumour, glioma, astrocytoma, acoustic neuroma, neuroblastoma and
XX retinoblastoma and inflammatory disorders such as rheumatoid arthritis,
XX spondyloarthropathies, inflammatory bowel disease and asthma. The present
XX sequence is the humanised RSV antibody variable heavy chain (VH) domain
XX protein.

XX SQ Sequence 120 AA;

Query Match 71.2%; Score 47; DB 8; Length 120;
Best Local Similarity 63.6%; Pred. No. 4.4;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RETVFWYFDV 11

1 : : |||||
99 RDMIFNWFYFDV 109

RESULT 44

ADT89225
ID ADT89225 standard; protein; 120 AA.

XX AC ADT89225;

XX DT 16-DEC-2004 (first entry)

XX DE Humanised RSV antibody (plld4) VH domain protein.

XX KW Stabilised glycoprotein; leukaemia; neoplasms; fibrosarcoma;
XX KW renal cell carcinoma; osteogenic sarcoma; rhabdomyosarcoma;
XX KW Ewing's tumour; squamous cell carcinoma; hepatoma; Wilms' glioma;
XX KW astrocytoma; acoustic neuroma; neuroblastoma; retinoblastoma;
XX KW inflammatory disorder; rheumatoid arthritis; spondyloarthritis;
XX KW inflammatory bowel disease; asthma; humanised; antibody; virucide;
XX KW antibacterial; cytostatic; antiinflammatory; antirheumatic;
XX KW antiarthritic; variable heavy chain; VH.

XX OS Respiratory syncytial virus.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN US2004191265-A1.

XX PD 30-SEP-2004.

XX PF 05-JAN-2004; 2004US-00751744.

XX PR 06-JAN-2003; 2003US-0438162P.

XX PA (SCHE/) SCHERNMAN M A.

XX PA (CASA/) CASAS-FINET J.

XX PA (FENG/) FENG J.

XX PA (TOUS/) TOUS G.

XX PI Schernman MA, Casas-Finet J, Feng J, Tous G;

XX DR WPI; 2004-698665/68.

XX PS New modified immunoglobulin G (IgG) having modified hinge region
XX PT comprising amino acid modifications corresponding to specific positions
XX PT of IgG1 of wild-type, useful for treating viral infection caused by
XX PT respiratory syncytial virus.

XX PS Disclosure; SEQ ID NO 28; 66pp; English.

XX CC The present invention is based upon the development of a novel method of
XX CC analysing and identifying glycoprotein (limited to immunoglobulins)
XX CC degradation products. The inventors have identified a portion of the
XX CC hinge region of the heavy chain immunoglobulin G1 (IgG1) constant domain
XX CC as a site of immunoglobulin degradation. This method leads to the
XX CC identification and production of stabilised immunoglobulin molecules with
XX CC increased stability and/or serum half life. The invention is useful for
XX CC treating, preventing or ameliorating one or more symptoms associated with
XX CC viral infection caused by respiratory syncytial virus (RSV) in human and
XX CC preventing viral or bacterial antigen from binding to its host cell
XX CC receptor. The invention is also useful for preventing, inhibiting or
XX CC reducing the growth or metastasis of cancerous cells such as leukaemia,
XX CC neoplasms, fibrosarcoma, renal cell carcinoma, osteogenic sarcoma,
XX CC rhabdomyosarcoma, Ewing's tumour, squamous cell carcinoma, hepatoma,
XX CC Wilms' tumour, glioma, astrocytoma, acoustic neuroma, neuroblastoma and
XX CC retinoblastoma and inflammatory disorders such as rheumatoid arthritis,
XX CC spondyloarthropathies, inflammatory bowel disease and asthma. The present
XX CC sequence is the humanised RSV antibody variable heavy chain (VH) domain
XX CC protein.

XX SQ Sequence 120 AA;

Query Match 71.2%; Score 47; DB 8; Length 120;
Best Local Similarity 63.6%; Pred. No. 4.4;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RETVPYWFYFDV 11

DB 99 RDMIFNWFYFDV 109

RESULT 45

ADT89264
ID ADT89264 standard; protein; 120 AA.

XX AC ADT89264;

XX DT 16-DEC-2004 (first entry)

XX DE Humanised RSV antibody (A13A11) VH domain protein.

XX KW Stabilised glycoprotein; leukaemia; neoplasms; fibrosarcoma;
XX KW renal cell carcinoma; osteogenic sarcoma; rhabdomyosarcoma;
XX KW Ewing's tumour; squamous cell carcinoma; hepatoma; Wilms' glioma;
XX KW astrocytoma; acoustic neuroma; neuroblastoma; retinoblastoma;
XX KW inflammatory disorder; rheumatoid arthritis; spondyloarthritis;
XX KW inflammatory bowel disease; asthma; humanised; antibody; virucide;
XX KW antibacterial; cytostatic; antiinflammatory; antirheumatic;
XX KW antiarthritic; variable heavy chain; VH.

XX OS Respiratory syncytial virus.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN US2004191265-A1.

XX PD 30-SEP-2004.

XX PF 05-JAN-2004; 2004US-00751744.

XX PR 06-JAN-2003; 2003US-0438162P.

XX PA (SCHE/) SCHERNMAN M A.

XX PA (CASA/) CASAS-FINET J.

XX PA (FENG/) FENG J.

XX PA (TOUS/) TOUS G.

XX PI Schernman MA, Casas-Finet J, Feng J, Tous G;

XX DR WPI; 2004-698665/68.

XX PT New modified immunoglobulin G (IgG) having modified hinge region
XX PT comprising amino acid modifications corresponding to specific positions
XX PT of IgG1 of wild-type, useful for treating viral infection caused by
XX PT respiratory syncytial virus.

XX PS Disclosure; SEQ ID NO 67; 66pp; English.

XX CC The present invention is based upon the development of a novel method of
XX CC analysing and identifying glycoprotein (limited to immunoglobulins)
XX CC degradation products. The inventors have identified a portion of the
XX CC hinge region of the heavy chain immunoglobulin G1 (IgG1) constant domain
XX CC as a site of immunoglobulin degradation. This method leads to the
XX CC identification and production of stabilised immunoglobulin molecules with
XX CC increased stability and/or serum half life. The invention is useful for
XX CC treating, preventing or ameliorating one or more symptoms associated with
XX CC viral infection caused by respiratory syncytial virus (RSV) in human and
XX CC preventing viral or bacterial antigen from binding to its host cell
XX CC receptor. The invention is also useful for preventing, inhibiting or
XX CC reducing the growth or metastasis of cancerous cells such as leukaemia,
XX CC neoplasms, fibrosarcoma, renal cell carcinoma, osteogenic sarcoma,
XX CC rhabdomyosarcoma, Ewing's tumour, squamous cell carcinoma, hepatoma,
XX CC Wilms' tumour, glioma, astrocytoma, acoustic neuroma, neuroblastoma and
XX CC retinoblastoma and inflammatory disorders such as rheumatoid arthritis,
XX CC spondyloarthropathies, inflammatory bowel disease and asthma. The present
XX CC sequence is the humanised RSV antibody variable heavy chain (VH) domain
XX CC protein.

CC sequence is the humanised RSV antibody variable heavy chain (VH) domain
 CC protein.
 XX
 SQ Sequence 120 AA;
 Query Match 71.2%; Score 47; DB 8; Length 120;
 Best Local Similarity 63.6%; Pred. No. 4.4;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RETVFYWFYDFV 11
 |: :| |||||
 Db 99 RDMIFNWFYDFV 109
 RESULT 46
 ADT89252
 ID ADT89252 standard; protein; 120 AA.
 XX
 AC ADT89252;
 XX
 DT 16-DEC-2004 (first entry)
 DE Humanised RSV antibody (H3-3F4) VH domain protein.
 XX
 KW Stabilised glycoprotein; leukaemia; neoplasms; fibrosarcoma;
 KW renal cell carcinoma; osteogenic sarcoma; rhabdomyosarcoma;
 KW Ewing's tumour; squamous cell carcinoma; hepatoma; glioma;
 KW astrocytoma; acoustic neuroma; neuroblastoma; retinoblastoma;
 KW inflammatory disorder; rheumatoid arthritis; spondyloarthritis;
 KW inflammatory bowel disease; asthma; humanised; antibody; virucide;
 KW antibacterial; cytostatic; antiinflammatory; antirheumatic;
 KW antiarthritic; variable heavy chain; VH.
 XX
 OS Respiratory syncytial virus.
 OS Homo sapiens.
 OS Synthetic.
 OS
 XX US2004191265-A1.
 XX
 PD 30-SEP-2004.
 XX
 PF 05-JAN-2004; 2004US-00751744.
 XX
 PR 06-JAN-2003; 2003US-0438162P.
 XX
 PA (SCHE/) SCHENNERMAN M A.
 PA (CASA/) CASAS-FINET J.
 PA (FENG/) FENG J.
 PA (TOUS/) TOUS G.
 XX
 PI Schenerman MA, Casas-Finet J, Feng J, Tous G;
 DR WPI; 2004-698665/68.
 XX
 PT New modified immunoglobulin G (IgG) having modified hinge region
 PT comprising amino acid modifications corresponding to specific positions
 PT of IgG1 of wild-type, useful for treating viral infection caused by
 PT respiratory syncytial virus.
 XX
 PS Disclosure; SEQ ID NO 55; 66pp; English.
 XX
 CC The present invention is based upon the development of a novel method of
 CC analysing and identifying glycoprotein (limited to immunoglobulins)
 CC degradation products. The inventors have identified a portion of the
 CC hinge region of the heavy chain immunoglobulin G1 (IgG1) constant domain
 CC as a site of immunoglobulin degradation. This method leads to the
 CC identification and production of stabilised immunoglobulin molecules with
 CC increased stability and/or serum half life. The invention is useful for
 CC treating, preventing or ameliorating one or more symptoms associated with
 CC viral infection caused by respiratory syncytial virus (RSV) in human and
 CC preventing viral or bacterial antigen from binding to its host cell
 CC receptor. The invention is also useful for preventing, inhibiting or
 CC reducing the growth or metastasis of cancerous cells such as leukaemia,

CC neoplasms, fibrosarcoma, renal cell carcinoma, osteogenic sarcoma.
 CC rhabdomyosarcoma, Ewing's tumour, squamous cell carcinoma, hepatoma,
 CC Wilms' tumour, glioma, astrocytoma, acoustic neuroma, neuroblastoma and
 CC retinoblastoma and inflammatory disorders such as rheumatoid arthritis,
 CC spondyloarthritis, inflammatory bowel disease and asthma. The present
 CC sequence is the humanised RSV antibody variable heavy chain (VH) domain
 CC protein.
 XX
 SQ Sequence 120 AA;
 Query Match 71.2%; Score 47; DB 8; Length 120;
 Best Local Similarity 63.6%; Pred. No. 4.4;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RETVFYWFYDFV 11
 |: :| |||||
 Db 99 RDMIFNWFYDFV 109
 RESULT 47
 ADT89248
 ID ADT89248 standard; protein; 120 AA.
 XX
 AC ADT89248;
 XX
 DT 16-DEC-2004 (first entry)
 DE Humanised RSV antibody (A8C7) VH domain protein.
 XX
 KW Stabilised glycoprotein; leukaemia; neoplasms; fibrosarcoma;
 KW renal cell carcinoma; osteogenic sarcoma; rhabdomyosarcoma;
 KW Ewing's tumour; squamous cell carcinoma; hepatoma; Wilms' tumour; glioma;
 KW astrocytoma; acoustic neuroma; neuroblastoma; retinoblastoma;
 KW inflammatory disorder; rheumatoid arthritis; spondyloarthritis;
 KW inflammatory bowel disease; asthma; humanised; antibody; virucide;
 KW antibacterial; cytostatic; antiinflammatory; antirheumatic;
 KW antiarthritic; variable heavy chain; VH.
 XX
 OS Respiratory syncytial virus.
 OS Homo sapiens.
 OS Synthetic.
 OS
 XX US2004191265-A1.
 XX
 PD 30-SEP-2004.
 XX
 PF 05-JAN-2004; 2004US-00751744.
 XX
 PR 06-JAN-2003; 2003US-0438162P.
 XX
 PA (SCHE/) SCHENNERMAN M A.
 PA (CASA/) CASAS-FINET J.
 PA (FENG/) FENG J.
 PA (TOUS/) TOUS G.
 XX
 PI Schenerman MA, Casas-Finet J, Feng J, Tous G;
 DR WPI; 2004-698665/68.
 XX
 PT New modified immunoglobulin G (IgG) having modified hinge region
 PT comprising amino acid modifications corresponding to specific positions
 PT of IgG1 of wild-type, useful for treating viral infection caused by
 PT respiratory syncytial virus.
 XX
 PS Disclosure; SEQ ID NO 51; 66pp; English.
 XX
 CC The present invention is based upon the development of a novel method of
 CC analysing and identifying glycoprotein (limited to immunoglobulins)
 CC degradation products. The inventors have identified a portion of the
 CC hinge region of the heavy chain immunoglobulin G1 (IgG1) constant domain
 CC as a site of immunoglobulin degradation. This method leads to the
 CC identification and production of stabilised immunoglobulin molecules with
 CC increased stability and/or serum half life. The invention is useful for

CC treating, preventing or ameliorating one or more symptoms associated with
 CC viral infection caused by respiratory syncytial virus (RSV) in human and
 CC preventing viral or bacterial antigen from binding to its host cell
 CC receptor. The invention is also useful for preventing, inhibiting or
 CC reducing the growth or metastasis of cancerous cells such as leukaemia,
 CC neoplasms, fibrosarcoma, renal cell carcinoma, osteogenic sarcoma,
 CC rhabdomyosarcoma, Ewing's tumour, squamous cell carcinoma, hepatoma,
 CC Wilms' tumour, glioma, astrocytoma, acoustic neuroma, neuroblastoma and
 CC retinoblastoma and inflammatory disorders such as rheumatoid arthritis,
 CC spondyloarthropathies, inflammatory bowel disease and asthma. The present
 CC sequence is the humanised RSV antibody variable heavy chain (VH) domain
 CC protein.

XX SQ Sequence 120 AA;

Query Match 71.2%; Score 47; DB 8; Length 120;
 Best Local Similarity 63.6%; Pred. No. 4.4;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RETVPYWFYFDV 11
 | : | | | | |
 Db 99 RDMIFNWFYFDV 109

RESULT 48
 ADW19905
 ID ADW19905 standard; protein; 120 AA.

XX AC ADW19905;

XX DT 24-MAR-2005 (first entry)

XX RSV antigen binding antibody variable heavy domain, SEQ ID 51.

XX respiratory syncytial virus infection; delivery mechanism;

XX respiratory-gen.; virucide; vaccine; gene therapy;

XX heavy chain variable region.

XX OS Homo sapiens.

XX US2005002926-A1.

XX 06-JAN-2005.

XX 26-JUL-2004; 2004US-00900230.

XX 28-NOV-2000; 2000US-00724396.

XX 28-NOV-2001; 2001US-00996265.

XX (MEDI-) MEDIMMUNE INC.

XX Young JF, Koenig S, Johnson LS, Huse WD, Watkins JD, Wu H;

XX WPI; 2005-065188/07.

XX Preventing, treating or ameliorating symptoms associated with a
 XX respiratory syncytial virus (RSV) infection by administering antibodies
 XX that immunospecifically bind to one or more RSV antigens.

XX Disclosure; SEQ ID NO 51; 160pp; English.

XX The invention relates to a novel method for preventing, treating or
 CC ameliorating one or more symptoms associated with a respiratory syncytial
 CC virus (RSV) infection in a mammal. The method comprises administering to
 CC the mammal a dose of one or more antibodies or their fragments that
 CC immunospecifically binds to one or more RSV antigens, where the effective
 CC amount is less than 15 mg/kg of the antibodies or antibody fragments. The
 CC invention further comprises: a sustained release formulation comprising
 CC one or more antibodies or their fragments that immunospecifically binds
 CC to one or more RSV antigens; and a pharmaceutical composition comprising
 CC one or more antibodies or their fragments that immunospecifically binds
 CC to one or more RSV antigens formulated for pulmonary delivery. The
 CC methods and compositions have respiratory-gen. and virucide activities.

CC The antibodies can be used in the creation of a vaccine. The compositions
 CC may be used in gene therapy. The methods and compositions of the present
 CC invention are useful for the diagnosis, prevention and/or treatment of
 CC RSV infection. This sequence represents an RSV antigen binding variable
 CC heavy domain of the invention.

XX SQ Sequence 120 AA;

Query Match 71.2%; Score 47; DB 9; Length 120;
 Best Local Similarity 63.6%; Pred. No. 4.4;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RETVPYWFYFDV 11
 | : | | | | |
 Db 99 RDMIFNWFYFDV 109

RESULT 49

ADW19887
 ID ADW19887 standard; protein; 120 AA.

XX AC ADW19887;

XX DT 24-MAR-2005 (first entry)

XX RSV antigen binding antibody variable heavy domain, SEQ ID 33.

XX respiratory syncytial virus infection; delivery mechanism;

XX respiratory-gen.; virucide; vaccine; gene therapy;

XX heavy chain variable region.

XX OS Homo sapiens.

XX US2005002926-A1.

XX 06-JAN-2005.

XX 26-JUL-2004; 2004US-00900230.

XX 28-NOV-2000; 2000US-00724396.

XX 28-NOV-2001; 2001US-00996265.

XX (MEDI-) MEDIMMUNE INC.

XX Young JF, Koenig S, Johnson LS, Huse WD, Watkins JD, Wu H;

XX WPI; 2005-065188/07.

XX Preventing, treating or ameliorating symptoms associated with a
 XX respiratory syncytial virus (RSV) infection by administering antibodies
 XX that immunospecifically bind to one or more RSV antigens.

XX Disclosure; SEQ ID NO 33; 160pp; English.

XX The invention relates to a novel method for preventing, treating or
 CC ameliorating one or more symptoms associated with a respiratory syncytial
 CC virus (RSV) infection in a mammal. The method comprises administering to
 CC the mammal a dose of one or more antibodies or their fragments that
 CC immunospecifically binds to one or more RSV antigens, where the effective
 CC amount is less than 15 mg/kg of the antibodies or antibody fragments. The
 CC invention further comprises: a sustained release formulation comprising
 CC one or more antibodies or their fragments that immunospecifically binds
 CC to one or more RSV antigens; and a pharmaceutical composition comprising
 CC one or more antibodies or their fragments that immunospecifically binds
 CC to one or more RSV antigens formulated for pulmonary delivery. The
 CC methods and compositions have respiratory-gen. and virucide activities.
 CC The antibodies can be used in the creation of a vaccine. The compositions
 CC may be used in gene therapy. The methods and compositions of the present
 CC invention are useful for the diagnosis, prevention and/or treatment of
 CC RSV infection. This sequence represents an RSV antigen binding variable
 CC heavy domain of the invention.

XX SQ Sequence 120 AA;

Query Match 71.2%; Score 47; DB 9; Length 120;
Best Local Similarity 63.6%; Pred. No. 4.4;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RETVFWYFDV 11
|: :| |||||
DB 99 RDMIFNWFYFDV 109

Db 99 RDMIFNWFYFDV 109

Search completed: February 23, 2006, 09:40:58
Job time : 103.769 secs

RESULT 50
ADW19882
ID ADW19882 standard; protein; 120 AA.
XX
AC ADW19882;
XX
DT 24-MAR-2005 (first entry)
XX
DE RSV antigen binding antibody variable heavy domain, SEQ ID 28.
XX
KW respiratory syncytial virus infection; delivery mechanism;
KW respiratory-gen.; virucide; vaccine; gene therapy;
KW heavy chain variable region.
XX

OS Homo sapiens.
XX
XX US2005002926-A1.
XX
XX 06-JAN-2005.
XX
XX 26-JUL-2004; 2004US-00900230.
XX
XX 28-NOV-2000; 2000US-00724396.
XX
XX 28-NOV-2001; 2001US-00996265.
XX
XX (MEDI-) MEDIMUNE INC.
XX
XX Young JF, Koenig S, Johnson LS, Huse WD, Watkins JD, Wu H;
XX WPI; 2005-065188/07.
XX
XX Preventing, treating or ameliorating symptoms associated with a
XX respiratory syncytial virus (RSV) infection by administering antibodies
XX that immunospecifically bind to one or more RSV antigens.
XX
XX Disclosure; SEQ ID NO 28; 160pp; English.

XX The invention relates to a novel method for preventing, treating or
XX ameliorating one or more symptoms associated with a respiratory syncytial
XX virus (RSV) infection in a mammal. The method comprises administering to
XX the mammal a dose of one or more antibodies or their fragments that
XX immunospecifically binds to one or more RSV antigens, where the effective
XX amount is less than 15 mg/kg of the antibodies or antibody fragments. The
XX invention further comprises: a sustained release formulation comprising
XX one or more antibodies or their fragments that immunospecifically binds
XX to one or more RSV antigens; and a pharmaceutical composition comprising
XX one or more antibodies or their fragments that immunospecifically binds
XX to one or more RSV antigens formulated for pulmonary delivery. The
XX methods and compositions have respiratory-gen. and virucide activities.
XX The antibodies can be used in the creation of a vaccine. The compositions
XX may be used in gene therapy. The methods and compositions of the present
XX invention are useful for the diagnosis, prevention and/or treatment of
XX RSV infection. This sequence represents an RSV antigen binding variable
XX heavy domain of the invention.

XX Sequence 120 AA;

Query Match 71.2%; Score 47; DB 9; Length 120;
Best Local Similarity 63.6%; Pred. No. 4.4;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RETVFWYFDV 11
|: :| |||||

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OM protein - protein search, using sw model

Run on: February 23, 2006, 09:41:24 ; Search time 15.5692 Seconds
(without alignment)
67.979 Million cell updates/sec

Title: US-10-723-872-26
Perfect score: 66
Sequence: 1 RETVFWYFDV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 51 | 77.3 | 91 | 2 PH1004 | Ig heavy chain V r |
| 2 | 47 | 71.2 | 123 | 2 B30540 | Ig heavy chain V r |
| 3 | 44 | 66.7 | 31 | 2 B49038 | Ig lambda chain V |
| 4 | 44 | 66.7 | 38 | 2 C49038 | Ig lambda chain V |
| 5 | 44 | 66.7 | 56 | 2 E49038 | Ig lambda chain V |
| 6 | 44 | 66.7 | 58 | 2 D49038 | Ig lambda chain V |
| 7 | 44 | 66.7 | 124 | 2 G30539 | Ig heavy chain V r |
| 8 | 44 | 66.7 | 124 | 2 F30539 | Ig heavy chain V r |
| 9 | 44 | 66.7 | 124 | 2 H30539 | Ig heavy chain V r |
| 10 | 44 | 66.7 | 124 | 2 T40165 | translation elonga |
| 11 | 42 | 63.6 | 108 | 2 PH1006 | Ig heavy chain V r |
| 12 | 42 | 63.6 | 111 | 2 S13687 | Ig heavy chain V r |
| 13 | 41 | 62.1 | 17 | 2 S26744 | Ig heavy chain J r |
| 14 | 41 | 62.1 | 91 | 2 S13689 | Ig heavy chain V r |
| 15 | 41 | 62.1 | 101 | 2 S13692 | Ig heavy chain V r |
| 16 | 41 | 62.1 | 106 | 2 PH1002 | Ig heavy chain V r |
| 17 | 41 | 62.1 | 107 | 2 PH0987 | Ig heavy chain V r |
| 18 | 41 | 62.1 | 110 | 2 S13688 | Ig heavy chain V r |
| 19 | 41 | 62.1 | 111 | 2 S13693 | Ig heavy chain V r |
| 20 | 41 | 62.1 | 111 | 2 S26463 | Ig heavy chain V r |
| 21 | 41 | 62.1 | 112 | 2 S13686 | Ig heavy chain V r |
| 22 | 41 | 62.1 | 112 | 2 S26327 | Ig heavy chain V r |
| 23 | 41 | 62.1 | 112 | 2 S13690 | Ig heavy chain V r |
| 24 | 41 | 62.1 | 112 | 2 PH1022 | Ig heavy chain V r |
| 25 | 41 | 62.1 | 112 | 2 S13685 | Ig heavy chain V r |
| 26 | 41 | 62.1 | 113 | 2 PH1018 | Ig heavy chain V r |
| 27 | 41 | 62.1 | 115 | 2 S13694 | Ig heavy chain V r |
| 28 | 41 | 62.1 | 116 | 2 S13691 | Ig heavy chain V r |
| 29 | 41 | 62.1 | 117 | 1 MEMSJ5 | Ig heavy chain V r |

| | | | | | |
|-----|------|------|---|--------|--------------------|
| 30 | 62.1 | 121 | 2 | D30556 | Ig heavy chain V r |
| 31 | 62.1 | 122 | 1 | B30515 | Ig heavy chain V r |
| 32 | 62.1 | 123 | 1 | AVMS13 | Ig heavy chain V r |
| 33 | 62.1 | 123 | 1 | AVMSH8 | Ig heavy chain V r |
| 34 | 62.1 | 123 | 1 | AVMS15 | Ig heavy chain V r |
| 35 | 62.1 | 123 | 2 | PL0017 | Ig heavy chain V-D |
| 36 | 62.1 | 123 | 2 | B30540 | Ig heavy chain V r |
| 37 | 62.1 | 123 | 2 | B30556 | Ig heavy chain V r |
| 38 | 62.1 | 123 | 2 | D30539 | Ig heavy chain V r |
| 39 | 62.1 | 123 | 2 | B30560 | Ig heavy chain V r |
| 40 | 62.1 | 124 | 1 | AVMS51 | Ig heavy chain V r |
| 41 | 62.1 | 137 | 2 | S03326 | Ig heavy chain pre |
| 42 | 62.1 | 181 | 2 | A28782 | cytochrome-c oxida |
| 43 | 62.1 | 284 | 2 | G22848 | cytochrome-c oxida |
| 44 | 62.1 | 287 | 2 | A25877 | cytochrome-c oxida |
| 45 | 62.1 | 435 | 2 | E82848 | alpha-ketoglutarat |
| 46 | 60.6 | 18 | 2 | A25941 | Ig heavy chain J-H |
| 47 | 60.6 | 162 | 2 | T37538 | hypothetical prote |
| 48 | 60.6 | 364 | 2 | AE3196 | conserved hypotet |
| 49 | 60.6 | 381 | 2 | G89009 | protein R08F11.5 l |
| 50 | 60.6 | 432 | 2 | A83616 | dicarboxylic acid |
| 51 | 60.6 | 570 | 2 | S42708 | proline transport |
| 52 | 60.6 | 570 | 2 | S04547 | probable transmem |
| 53 | 60.6 | 629 | 2 | T39285 | Ig heavy chain V r |
| 54 | 59.1 | 124 | 2 | E30539 | hypothetical prote |
| 55 | 59.1 | 325 | 2 | T31989 | general l-amino ac |
| 56 | 59.1 | 397 | 2 | AD3403 | hypothetical prote |
| 57 | 59.1 | 497 | 2 | A96828 | prophage p12 prote |
| 58 | 59.1 | 533 | 2 | D86756 | penicillin-binding |
| 59 | 59.1 | 749 | 2 | S75331 | hypothetical prote |
| 60 | 59.1 | 1153 | 2 | B97718 | hypothetical prote |
| 61 | 59.1 | 1155 | 2 | B71720 | phospho-beta-gluc |
| 62 | 57.6 | 98 | 2 | F97952 | Ig heavy chain V r |
| 63 | 57.6 | 111 | 2 | D30515 | Ig heavy chain V r |
| 64 | 57.6 | 113 | 2 | PH1663 | Ig heavy chain V r |
| 65 | 57.6 | 138 | 2 | S31666 | probable transcrip |
| 66 | 57.6 | 225 | 2 | C70500 | probable dnaJ-like |
| 67 | 57.6 | 256 | 2 | A81370 | conserved hypotet |
| 68 | 57.6 | 304 | 2 | AF2615 | hypothetical prote |
| 69 | 57.6 | 313 | 2 | E97397 | hypothetical prote |
| 70 | 57.6 | 357 | 2 | E98133 | hypothetical prote |
| 71 | 57.6 | 357 | 2 | AG3154 | conserved hypotet |
| 72 | 57.6 | 368 | 2 | G65119 | hypothetical 40.4 |
| 73 | 57.6 | 393 | 2 | B85992 | probable transport |
| 74 | 57.6 | 399 | 2 | F91146 | probable transport |
| 75 | 57.6 | 402 | 2 | T37694 | hypothetical prote |
| 76 | 57.6 | 435 | 2 | T43749 | cytochrome oxidase |
| 77 | 57.6 | 474 | 2 | G97033 | beta-glucosidase h |
| 78 | 57.6 | 477 | 2 | G69760 | serine-type carbox |
| 79 | 57.6 | 480 | 2 | T50511 | probable Serine/Th |
| 80 | 57.6 | 588 | 2 | E96633 | conserved hypotet |
| 81 | 57.6 | 657 | 2 | AG3170 | conserved hypotet |
| 82 | 57.6 | 776 | 2 | S45495 | lp4 protein - fis |
| 83 | 57.6 | 1450 | 2 | A44027 | 165K myofibrillar |
| 84 | 57.6 | 3005 | 2 | T08841 | apolipoprotein D p |
| 85 | 57.6 | 189 | 2 | A60958 | probable amino aci |
| 86 | 56.1 | 238 | 1 | H83371 | alcohol dehydrogen |
| 87 | 56.1 | 278 | 1 | S07246 | alcohol dehydrogen |
| 88 | 56.1 | 279 | 1 | B42180 | alcohol dehydrogen |
| 89 | 56.1 | 279 | 1 | B40731 | alcohol dehydrogen |
| 90 | 56.1 | 279 | 1 | D40731 | alcohol dehydrogen |
| 91 | 56.1 | 281 | 1 | S16454 | alcohol dehydrogen |
| 92 | 56.1 | 288 | 2 | S36953 | cytochrome-c oxida |
| 93 | 56.1 | 288 | 2 | S36954 | cytochrome-c oxida |
| 94 | 56.1 | 288 | 2 | S36955 | complement C5a ana |
| 95 | 56.1 | 351 | 1 | A46525 | hypothetical prote |
| 96 | 56.1 | 362 | 2 | F95275 | conserved hypotet |
| 97 | 56.1 | 401 | 2 | G82210 | amino acid A8C tra |
| 98 | 56.1 | 426 | 2 | C69831 | conserved hypotet |
| 99 | 56.1 | 432 | 2 | D85905 | alpha-ketoglutarat |
| 100 | 56.1 | 432 | 2 | JN0080 | alpha-ketoglutarat |
| 101 | 56.1 | 432 | 2 | F91060 | alpha-ketoglutarat |
| 102 | 56.1 | 845 | 2 | T25657 | hypothetical prote |

| | | | | | | | | | | | | | |
|-----|------|------|------|---|--------|--------------------|-----|------|------|------|---|--------|----------------------|
| 103 | 37 | 56.1 | 1021 | 2 | T23252 | hypothetical prote | 176 | 35 | 53.0 | 519 | 2 | A44783 | ecto-ATPase precu |
| 104 | 37 | 56.1 | 1714 | 1 | J18644 | multifunctional am | 177 | 35 | 53.0 | 523 | 1 | S61713 | carboxypeptidase C |
| 105 | 36.5 | 55.3 | 1288 | 2 | J50363 | mitogen-activated | 178 | 35 | 53.0 | 527 | 2 | C71098 | hypothetical prote |
| 106 | 36 | 54.5 | 76 | 2 | S06878 | Alzheimer's diseas | 179 | 35 | 53.0 | 536 | 2 | T16023 | hypothetical prote |
| 107 | 36 | 54.5 | 76 | 2 | S04655 | Alzheimer's diseas | 180 | 35 | 53.0 | 556 | 2 | S21347 | hypothetical prote |
| 108 | 36 | 54.5 | 100 | 2 | A32282 | Alzheimer's diseas | 181 | 35 | 53.0 | 603 | 2 | S76615 | hypothetical prote |
| 109 | 36 | 54.5 | 106 | 2 | F32513 | Alzheimer's diseas | 182 | 35 | 53.0 | 685 | 2 | S16783 | probable RNA-direc |
| 110 | 36 | 54.5 | 106 | 2 | F32513 | Ig heavy chain V r | 183 | 35 | 53.0 | 686 | 2 | S60749 | probable ligand-ga |
| 111 | 36 | 54.5 | 108 | 2 | PH1656 | Ig heavy chain V r | 184 | 35 | 53.0 | 691 | 2 | G82144 | hemolysin-related |
| 112 | 36 | 54.5 | 110 | 2 | A30519 | T-cell receptor be | 185 | 35 | 53.0 | 1074 | 2 | T45094 | probable arabinosy |
| 113 | 36 | 54.5 | 115 | 2 | A36296 | T-cell receptor be | 186 | 35 | 53.0 | 1281 | 1 | GNMSLL | retrovirus-related |
| 114 | 36 | 54.5 | 116 | 2 | E30563 | T-cell receptor be | 187 | 35 | 53.0 | 2064 | 2 | G82562 | bacteriocin XF2407 |
| 115 | 36 | 54.5 | 119 | 2 | PL0089 | Ig heavy chain V r | 188 | 35 | 53.0 | 3396 | 1 | A42551 | genome polyprotein |
| 116 | 36 | 54.5 | 123 | 1 | AVMSG6 | Ig heavy chain V r | 189 | 34.5 | 52.3 | 101 | 2 | PH0983 | Ig heavy chain V r |
| 117 | 36 | 54.5 | 124 | 2 | A30539 | Ig heavy chain V r | 190 | 34.5 | 52.3 | 161 | 2 | S61624 | probable membrane |
| 118 | 36 | 54.5 | 125 | 2 | C30540 | Ig heavy chain V r | 191 | 34 | 51.5 | 30 | 2 | B97906 | phospho-beta-gluc |
| 119 | 36 | 54.5 | 131 | 2 | A20722 | T-cell receptor be | 192 | 34 | 51.5 | 52 | 2 | T06503 | hypothetical prote |
| 120 | 36 | 54.5 | 174 | 2 | S05574 | streptothricin ace | 193 | 34 | 51.5 | 104 | 2 | I48151 | adrenergic alpha2 |
| 121 | 36 | 54.5 | 206 | 2 | AF2888 | transcription regu | 194 | 34 | 51.5 | 109 | 2 | C30515 | Ig heavy chain V r |
| 122 | 36 | 54.5 | 208 | 2 | C95968 | probable transcrip | 195 | 34 | 51.5 | 111 | 2 | PH1019 | Ig heavy chain V r |
| 123 | 36 | 54.5 | 234 | 2 | T28861 | hypothetical prote | 196 | 34 | 51.5 | 113 | 2 | S26465 | Ig heavy chain V r |
| 124 | 36 | 54.5 | 239 | 2 | C97864 | hypothetical prote | 197 | 34 | 51.5 | 113 | 2 | PH1029 | Ig heavy chain V r |
| 125 | 36 | 54.5 | 332 | 2 | B81452 | NADH2 dehydrogen | 198 | 34 | 51.5 | 114 | 2 | C32967 | Ig heavy chain V r |
| 126 | 36 | 54.5 | 364 | 2 | T25456 | hypothetical prote | 199 | 34 | 51.5 | 114 | 2 | C32967 | Ig heavy chain V r |
| 127 | 36 | 54.5 | 402 | 1 | VGBE50 | glycoprotein D pre | 200 | 34 | 51.5 | 116 | 2 | S26328 | Ig heavy chain V r |
| 128 | 36 | 54.5 | 465 | 2 | G86244 | Serine carboxypept | 201 | 34 | 51.5 | 116 | 2 | S20645 | Ig heavy chain V r |
| 129 | 36 | 54.5 | 470 | 2 | B96637 | hypothetical prote | 202 | 34 | 51.5 | 118 | 2 | A32530 | Ig heavy chain V r |
| 130 | 36 | 54.5 | 473 | 2 | H72744 | probable D-lactate | 203 | 34 | 51.5 | 119 | 2 | PL0086 | Ig heavy chain V r |
| 131 | 36 | 54.5 | 481 | 2 | T48516 | probable oligopept | 204 | 34 | 51.5 | 122 | 1 | AVMS63 | Ig heavy chain V r |
| 132 | 36 | 54.5 | 482 | 2 | AB1421 | beta-glucosidase h | 205 | 34 | 51.5 | 122 | 2 | A30556 | Ig heavy chain V r |
| 133 | 36 | 54.5 | 482 | 2 | A43828 | probable serine ca | 206 | 34 | 51.5 | 122 | 2 | PH0535 | Ig heavy chain V r |
| 134 | 36 | 54.5 | 484 | 4 | A32761 | hypothetical Alzhe | 207 | 34 | 51.5 | 122 | 2 | PH0887 | Ig heavy chain V r |
| 135 | 36 | 54.5 | 541 | 2 | F72051 | apolipoprotein N-a | 208 | 34 | 51.5 | 122 | 2 | I30535 | Ig heavy chain V r |
| 136 | 36 | 54.5 | 541 | 2 | B65572 | apolipoprotein N-a | 209 | 34 | 51.5 | 123 | 2 | I30538 | Ig heavy chain V r |
| 137 | 36 | 54.5 | 552 | 2 | JC7666 | serine-type carbox | 210 | 34 | 51.5 | 123 | 2 | PT0387 | Ig heavy chain V r |
| 138 | 36 | 54.5 | 562 | 2 | JU0033 | hypothetical li pr | 211 | 34 | 51.5 | 123 | 2 | PT0385 | Ig heavy chain V r |
| 139 | 36 | 54.5 | 659 | 2 | AG1806 | AA3-600 quinol oxi | 212 | 34 | 51.5 | 123 | 2 | PT0383 | Ig heavy chain V r |
| 140 | 36 | 54.5 | 659 | 2 | AG1434 | AA3-600 quinol oxi | 213 | 34 | 51.5 | 123 | 2 | PT0386 | Ig heavy chain V r |
| 141 | 36 | 54.5 | 765 | 2 | B88924 | protein R02C2.3 [i | 214 | 34 | 51.5 | 123 | 2 | PT0354 | Ig heavy chain V r |
| 142 | 36 | 54.5 | 770 | 1 | QRHUN4 | Alzheimer's diseas | 215 | 34 | 51.5 | 125 | 2 | PT0353 | Ig heavy chain V r |
| 143 | 36 | 54.5 | 1289 | 2 | C70044 | probable phosphoes | 216 | 34 | 51.5 | 167 | 2 | G82892 | hypothetical prote |
| 144 | 35.5 | 53.8 | 106 | 2 | PH1005 | Ig heavy chain V r | 217 | 34 | 51.5 | 172 | 2 | H81375 | probable integral |
| 145 | 35.5 | 53.8 | 531 | 2 | S30011 | probable membrane | 218 | 34 | 51.5 | 181 | 2 | T27769 | hypothetical prote |
| 146 | 35.5 | 53.8 | 946 | 2 | S48397 | hypothetical prote | 219 | 34 | 51.5 | 196 | 2 | S25784 | hypothetical prote |
| 147 | 35 | 53.0 | 74 | 1 | FLYB4 | photosystem I chai | 220 | 34 | 51.5 | 209 | 2 | B84501 | hypothetical prote |
| 148 | 35 | 53.0 | 96 | 2 | A88086 | protein Tf1F1.3 [i | 221 | 34 | 51.5 | 210 | 2 | B89958 | hypothetical prote |
| 149 | 35 | 53.0 | 107 | 2 | PH1013 | Ig heavy chain V r | 222 | 34 | 51.5 | 210 | 2 | S39645 | hypothetical prote |
| 150 | 35 | 53.0 | 117 | 1 | MHMS4E | Ig heavy chain V r | 223 | 34 | 51.5 | 210 | 2 | C84054 | acetoin utilizatio |
| 151 | 35 | 53.0 | 117 | 2 | S09961 | Ig heavy chain V-D | 224 | 34 | 51.5 | 226 | 2 | C29504 | hypothetical 24K p |
| 152 | 35 | 53.0 | 123 | 2 | C30556 | Ig heavy chain V r | 225 | 34 | 51.5 | 244 | 2 | A82344 | hypothetical prote |
| 153 | 35 | 53.0 | 140 | 2 | T01407 | Ig heavy chain (my | 226 | 34 | 51.5 | 245 | 2 | AB0499 | ABC transporter pe |
| 154 | 35 | 53.0 | 142 | 2 | S71107 | cell-cell adhesio | 227 | 34 | 51.5 | 252 | 2 | T48681 | hypothetical prote |
| 155 | 35 | 53.0 | 227 | 2 | H90553 | hypothetical prote | 228 | 34 | 51.5 | 256 | 1 | S20713 | alcohol dehydrogen |
| 156 | 35 | 53.0 | 231 | 2 | PC4155 | Ig gamma-2b chain | 229 | 34 | 51.5 | 257 | 2 | T06139 | probable receptor- |
| 157 | 35 | 53.0 | 265 | 2 | S69335 | carcinoembryonic a | 230 | 34 | 51.5 | 261 | 2 | H70740 | hypothetical prote |
| 158 | 35 | 53.0 | 282 | 2 | AF0332 | hypothetical prote | 231 | 34 | 51.5 | 266 | 2 | B84351 | pseudouridylylate sy |
| 159 | 35 | 53.0 | 303 | 2 | T41056 | conserved hypoteth | 232 | 34 | 51.5 | 269 | 1 | JN0565 | alcohol dehydrogen |
| 160 | 35 | 53.0 | 308 | 2 | AC3604 | n-acetylglucosamin | 233 | 34 | 51.5 | 272 | 1 | S20716 | alcohol dehydrogen |
| 161 | 35 | 53.0 | 310 | 2 | A86239 | protein Tf10024.17 | 234 | 34 | 51.5 | 273 | 1 | JN0567 | alcohol dehydrogen |
| 162 | 35 | 53.0 | 340 | 2 | PH0217 | reverse transcript | 235 | 34 | 51.5 | 279 | 2 | S28662 | hypothetical prote |
| 163 | 35 | 53.0 | 384 | 2 | B70690 | hypothetical prote | 236 | 34 | 51.5 | 329 | 2 | G84074 | hypothetical prote |
| 164 | 35 | 53.0 | 418 | 2 | T51129 | hypothetical prote | 237 | 34 | 51.5 | 331 | 2 | E90240 | conserved hypoteth |
| 165 | 35 | 53.0 | 435 | 2 | G84479 | hypothetical prote | 238 | 34 | 51.5 | 340 | 2 | AI0195 | DNA-directed DNA p |
| 166 | 35 | 53.0 | 436 | 2 | T30311 | xyianase (EC 3.2.1 | 239 | 34 | 51.5 | 346 | 2 | T31760 | hypothetical prote |
| 167 | 35 | 53.0 | 458 | 2 | S68177 | C-CAM2a protein is | 240 | 34 | 51.5 | 355 | 2 | F72279 | conserved hypoteth |
| 168 | 35 | 53.0 | 458 | 2 | S23969 | cell-adhesion mole | 241 | 34 | 51.5 | 370 | 2 | A05034 | hypothetical prote |
| 169 | 35 | 53.0 | 463 | 2 | D87624 | sodium-galactoside | 242 | 34 | 51.5 | 378 | 2 | B88504 | protein B0361.6 [i |
| 170 | 35 | 53.0 | 465 | 2 | C42603 | phospho-beta-gluc | 243 | 34 | 51.5 | 400 | 2 | AI0104 | probable galactosi |
| 171 | 35 | 53.0 | 500 | 2 | S41859 | xylan 1,4-beta-xyl | 244 | 34 | 51.5 | 404 | 2 | T27161 | hypothetical prote |
| 172 | 35 | 53.0 | 503 | 2 | T50791 | hypothetical prote | 245 | 34 | 51.5 | 416 | 2 | T02194 | probable pectinase |
| 173 | 35 | 53.0 | 508 | 1 | S46008 | probable carboxype | 246 | 34 | 51.5 | 420 | 2 | T47998 | pectinacetylestera |
| 174 | 35 | 53.0 | 510 | 2 | G71365 | probable carnitine | 247 | 34 | 51.5 | 424 | 2 | F69476 | acetylornithine am |
| 175 | 35 | 53.0 | 513 | 2 | S21976 | probable RNA-direc | 248 | 34 | 51.5 | 426 | 2 | JC7773 | IL-13Ra1pha 1 prot |

| | | | | | | | | | | | | | |
|-----|------|------|------|---|--------|---------------------|-----|----|------|-----|---|--------|--------------------|
| 249 | 34 | 51.5 | 435 | 2 | D82955 | probable MFS dicar | 322 | 33 | 50.0 | 117 | 2 | PL0249 | Ig heavy chain V r |
| 250 | 34 | 51.5 | 450 | 2 | A34169 | alpha-2A-adrenergic | 323 | 33 | 50.0 | 128 | 2 | C82474 | MutT/nudix family |
| 251 | 34 | 51.5 | 450 | 2 | A38316 | alpha-2-adrenergic | 324 | 33 | 50.0 | 130 | 2 | H70454 | conserved hypothet |
| 252 | 34 | 51.5 | 450 | 2 | I49481 | alpha-2-adrenergic | 325 | 33 | 50.0 | 149 | 2 | D97926 | hypothetical prote |
| 253 | 34 | 51.5 | 450 | 2 | JH0190 | alpha-2-adrenergic | 326 | 33 | 50.0 | 153 | 2 | AC1431 | hypothetical prote |
| 254 | 34 | 51.5 | 450 | 2 | B40392 | alpha-2-adrenergic | 327 | 33 | 50.0 | 153 | 2 | AI1804 | hypothetical prote |
| 255 | 34 | 51.5 | 454 | 2 | S72481 | probable transpos | 328 | 33 | 50.0 | 183 | 2 | T38917 | hypothetical prote |
| 256 | 34 | 51.5 | 456 | 2 | AH0842 | probable glycopor | 329 | 33 | 50.0 | 183 | 2 | B84070 | hypothetical prote |
| 257 | 34 | 51.5 | 458 | 2 | I49480 | alpha-2C-adrenerg | 330 | 33 | 50.0 | 189 | 2 | S49581 | apolipoprotein D - |
| 258 | 34 | 51.5 | 458 | 2 | A48392 | alpha-2C4 adrenoce | 331 | 33 | 50.0 | 200 | 2 | B82738 | conserved hypothet |
| 259 | 34 | 51.5 | 458 | 2 | A37869 | alpha-2B-adrenerg | 332 | 33 | 50.0 | 201 | 2 | AC0255 | probable phage pro |
| 260 | 34 | 51.5 | 458 | 2 | A40392 | alpha-2-adrenergic | 333 | 33 | 50.0 | 210 | 2 | A84016 | hypothetical prote |
| 261 | 34 | 51.5 | 459 | 2 | AC0075 | probable membrane | 334 | 33 | 50.0 | 214 | 2 | F59404 | plectin isoform pl |
| 262 | 34 | 51.5 | 461 | 2 | A31237 | alpha-2C-adrenerg | 335 | 33 | 50.0 | 216 | 2 | C70649 | hypothetical prote |
| 263 | 34 | 51.5 | 461 | 2 | T03561 | hypothetical prote | 336 | 33 | 50.0 | 220 | 2 | A72153 | Q2L protein - vari |
| 264 | 34 | 51.5 | 464 | 2 | A88000 | protein Y54E5A.3 [| 337 | 33 | 50.0 | 220 | 2 | H42504 | M2L protein - vacc |
| 265 | 34 | 51.5 | 464 | 2 | S75831 | hypothetical prote | 338 | 33 | 50.0 | 220 | 2 | T28457 | hypothetical prote |
| 266 | 34 | 51.5 | 470 | 2 | B90481 | glycosyltransferas | 339 | 33 | 50.0 | 220 | 2 | I36838 | O2L protein - vari |
| 267 | 34 | 51.5 | 471 | 2 | D96991 | 6-phospho-beta-glu | 340 | 33 | 50.0 | 221 | 2 | T24494 | hypothetical prote |
| 268 | 34 | 51.5 | 481 | 2 | B84860 | hypothetical prote | 341 | 33 | 50.0 | 223 | 2 | D75040 | hypothetical prote |
| 269 | 34 | 51.5 | 495 | 2 | A97022 | probably membrane | 342 | 33 | 50.0 | 225 | 2 | C70192 | conserved hypothet |
| 270 | 34 | 51.5 | 500 | 2 | D87541 | beta-xylosidase [i | 343 | 33 | 50.0 | 227 | 2 | AB1593 | B. subtilis BBSX p |
| 271 | 34 | 51.5 | 524 | 2 | S76140 | hypothetical prote | 344 | 33 | 50.0 | 245 | 2 | T37640 | conserved hypothet |
| 272 | 34 | 51.5 | 535 | 2 | A82710 | MFS permease [limp | 345 | 33 | 50.0 | 247 | 2 | T16061 | hypothetical prote |
| 273 | 34 | 51.5 | 539 | 2 | T22041 | hypothetical prote | 346 | 33 | 50.0 | 256 | 2 | G71121 | hypothetical prote |
| 274 | 34 | 51.5 | 545 | 2 | T12553 | hypothetical prote | 347 | 33 | 50.0 | 259 | 2 | H70575 | hypothetical prote |
| 275 | 34 | 51.5 | 548 | 2 | A54510 | 63K antigen - nema | 348 | 33 | 50.0 | 262 | 2 | S43493 | cytochrome-c oxida |
| 276 | 34 | 51.5 | 548 | 2 | A28209 | 60K filarial antig | 349 | 33 | 50.0 | 271 | 2 | E64694 | hypothetical prote |
| 277 | 34 | 51.5 | 552 | 2 | AB2361 | hypothetical prote | 350 | 33 | 50.0 | 282 | 2 | D82520 | hypothetical prote |
| 278 | 34 | 51.5 | 552 | 2 | T51439 | oligopeptide trans | 351 | 33 | 50.0 | 304 | 2 | G70392 | thiosulfate sulfur |
| 279 | 34 | 51.5 | 583 | 2 | F97492 | probable transport | 352 | 33 | 50.0 | 335 | 2 | AG2569 | hypothetical prote |
| 280 | 34 | 51.5 | 613 | 2 | F69424 | conserved hypothet | 353 | 33 | 50.0 | 337 | 2 | AC0377 | probable mannosylt |
| 281 | 34 | 51.5 | 626 | 1 | SYNCA | acetate-CoA ligase | 354 | 33 | 50.0 | 340 | 2 | T23562 | hypothetical prote |
| 282 | 34 | 51.5 | 670 | 2 | T43784 | NADH2 dehydrogen | 355 | 33 | 50.0 | 342 | 2 | T15541 | hypothetical prote |
| 283 | 34 | 51.5 | 713 | 1 | ABBSXR | cyclomalcodeoxin | 356 | 33 | 50.0 | 363 | 2 | D83566 | hypothetical prote |
| 284 | 34 | 51.5 | 746 | 2 | S18186 | genome polyprotein | 357 | 33 | 50.0 | 368 | 2 | S01651 | probable RNA-direc |
| 285 | 34 | 51.5 | 778 | 2 | T31037 | hypothetical prote | 358 | 33 | 50.0 | 383 | 2 | H75129 | probable transamin |
| 286 | 34 | 51.5 | 816 | 1 | A59003 | phosphoinositide 3 | 359 | 33 | 50.0 | 384 | 2 | H81198 | conserved hypothet |
| 287 | 34 | 51.5 | 823 | 2 | S44873 | ZC21.2 protein - C | 360 | 33 | 50.0 | 386 | 2 | E71001 | probable transamin |
| 288 | 34 | 51.5 | 888 | 2 | B87270 | TonB-dependent rec | 361 | 33 | 50.0 | 387 | 2 | A81452 | exodeoxyribonuclea |
| 289 | 34 | 51.5 | 932 | 2 | T48489 | receptor-like prot | 362 | 33 | 50.0 | 398 | 2 | T30013 | hypothetical prote |
| 290 | 34 | 51.5 | 936 | 2 | T26521 | hypothetical prote | 363 | 33 | 50.0 | 400 | 1 | A39130 | nicotinate phospho |
| 291 | 34 | 51.5 | 976 | 2 | B84659 | probable receptor- | 364 | 33 | 50.0 | 400 | 1 | JQ0756 | nicotinate phospho |
| 292 | 34 | 51.5 | 988 | 2 | T24668 | hypothetical prote | 365 | 33 | 50.0 | 400 | 2 | AB0617 | nicotinate phospho |
| 293 | 34 | 51.5 | 1043 | 2 | T19734 | hypothetical prote | 366 | 33 | 50.0 | 400 | 2 | F90755 | nicotinate phospho |
| 294 | 34 | 51.5 | 1070 | 2 | B86922 | probable arabinosy | 367 | 33 | 50.0 | 400 | 2 | D85619 | nicotinate phospho |
| 295 | 34 | 51.5 | 1094 | 2 | E70697 | probable arabinosy | 368 | 33 | 50.0 | 400 | 2 | B81775 | hypothetical integ |
| 296 | 34 | 51.5 | 1123 | 2 | T48586 | hypothetical prote | 369 | 33 | 50.0 | 401 | 2 | S73511 | hypothetical prote |
| 297 | 34 | 51.5 | 1226 | 2 | T24045 | hypothetical prote | 370 | 33 | 50.0 | 405 | 2 | G89075 | protein K04A8.10 [|
| 298 | 34 | 51.5 | 2227 | 1 | GNNYHB | genome polyprotein | 371 | 33 | 50.0 | 408 | 2 | T29949 | hypothetical prote |
| 299 | 34 | 51.5 | 2227 | 1 | GNNYHM | genome polyprotein | 372 | 33 | 50.0 | 416 | 2 | T45051 | hypothetical prote |
| 300 | 34 | 51.5 | 2227 | 1 | GNNYHR | genome polyprotein | 373 | 33 | 50.0 | 420 | 2 | H96534 | probable Na+/H+ an |
| 301 | 34 | 51.5 | 2227 | 1 | GNNYMK | genome polyprotein | 374 | 33 | 50.0 | 422 | 2 | A83184 | probable protein m |
| 302 | 34 | 51.5 | 2230 | 1 | GNNYSA | genome polyprotein | 375 | 33 | 50.0 | 423 | 2 | S58480 | agrC protein - Sta |
| 303 | 34 | 51.5 | 4859 | 2 | S74173 | ryanodine receptor | 376 | 33 | 50.0 | 431 | 2 | T18753 | hypothetical prote |
| 304 | 34 | 51.5 | 4868 | 2 | B54161 | ryanodine-binding | 377 | 33 | 50.0 | 432 | 2 | I50829 | alpha-2-adrenocept |
| 305 | 34 | 51.5 | 4869 | 2 | S66572 | ryanodine receptor | 378 | 33 | 50.0 | 437 | 2 | D83329 | conserved hypothet |
| 306 | 34 | 51.5 | 4872 | 2 | S27272 | ryanodine receptor | 379 | 33 | 50.0 | 440 | 2 | T22773 | hypothetical prote |
| 307 | 34 | 51.5 | 4967 | 2 | S72269 | ryanodine receptor | 380 | 33 | 50.0 | 448 | 2 | I51883 | alpha-2B-adrenerg |
| 308 | 34 | 51.5 | 4969 | 2 | A37113 | ryanodine receptor | 381 | 33 | 50.0 | 450 | 2 | A37223 | alpha-2B-adrenerg |
| 309 | 34 | 51.5 | 5032 | 1 | A35041 | ryanodine receptor | 382 | 33 | 50.0 | 453 | 2 | A35642 | alpha-2B-adrenerg |
| 310 | 34 | 51.5 | 5035 | 1 | I46646 | ryanodine receptor | 383 | 33 | 50.0 | 454 | 2 | AD2460 | hypothetical prote |
| 311 | 34 | 51.5 | 5037 | 1 | A54161 | ryanodine-binding | 384 | 33 | 50.0 | 455 | 2 | S28221 | alpha-2-C2 adrener |
| 312 | 34 | 51.5 | 5037 | 2 | B35041 | ryanodine receptor | 385 | 33 | 50.0 | 460 | 1 | S51516 | serine-type carbox |
| 313 | 33.5 | 50.8 | 1699 | 2 | T14074 | complement compone | 386 | 33 | 50.0 | 474 | 2 | S41117 | nitric-oxide reduc |
| 314 | 33 | 50.0 | 50 | 2 | C90521 | hypothetical prote | 387 | 33 | 50.0 | 481 | 2 | B85791 | probable transport |
| 315 | 33 | 50.0 | 51 | 2 | H95056 | hypothetical prote | 388 | 33 | 50.0 | 481 | 2 | F90942 | probable transport |
| 316 | 33 | 50.0 | 70 | 2 | PL0250 | Ig heavy chain V r | 389 | 33 | 50.0 | 481 | 2 | A64941 | probable transport |
| 317 | 33 | 50.0 | 89 | 2 | T50245 | hypothetical prote | 390 | 33 | 50.0 | 504 | 2 | C85485 | probable carnitine |
| 318 | 33 | 50.0 | 103 | 2 | F83918 | hypothetical prote | 391 | 33 | 50.0 | 504 | 2 | C90634 | probable carnitine |
| 319 | 33 | 50.0 | 110 | 2 | B41323 | ribulose-bisphosph | 392 | 33 | 50.0 | 504 | 2 | H64724 | probable carnitine |
| 320 | 33 | 50.0 | 110 | 2 | PH1674 | Ig heavy chain V r | 393 | 33 | 50.0 | 505 | 2 | AD0511 | probable carnitine |
| 321 | 33 | 50.0 | 117 | 2 | PL0252 | Ig heavy chain V r | 394 | 33 | 50.0 | 512 | 2 | T33463 | probable serine ca |

| | | | | | | | | | | | | | |
|-----|------|------|------|---|--------|---------------------|-----|----|------|-----|---|--------|---------------------|
| 395 | 33 | 50.0 | 534 | 2 | T19951 | hypotheical prote | 468 | 32 | 48.5 | 179 | 2 | T18101 | hypotheical prote |
| 396 | 33 | 50.0 | 540 | 2 | B82219 | transporter, BCC7 | 469 | 32 | 48.5 | 183 | 2 | H71675 | probable ribosomal |
| 397 | 33 | 50.0 | 548 | 2 | AG0304 | probable BCC7-fami | 470 | 32 | 48.5 | 192 | 2 | AI2271 | transcription regu |
| 398 | 33 | 50.0 | 551 | 2 | AC2311 | hypotheical prote | 471 | 32 | 48.5 | 200 | 2 | T26233 | hypotheical prote |
| 399 | 33 | 50.0 | 560 | 2 | G97264 | PIS system lactose | 472 | 32 | 48.5 | 217 | 2 | H86402 | 24.0K hypotheical |
| 400 | 33 | 50.0 | 569 | 2 | B70113 | hypotheical prote | 473 | 32 | 48.5 | 211 | 2 | S76528 | hypotheical prote |
| 401 | 33 | 50.0 | 574 | 2 | C86400 | hypotheical prote | 474 | 32 | 48.5 | 236 | 2 | D72355 | conserved hypotet |
| 402 | 33 | 50.0 | 578 | 2 | T35264 | probable BCC7 fami | 475 | 32 | 48.5 | 244 | 2 | A84687 | probable homeodoma |
| 403 | 33 | 50.0 | 580 | 2 | T20716 | hypotheical prote | 476 | 32 | 48.5 | 249 | 2 | F96511 | hypotheical prote |
| 404 | 33 | 50.0 | 587 | 2 | G86322 | hypotheical prote | 477 | 32 | 48.5 | 256 | 2 | A90131 | hypotheical prote |
| 405 | 33 | 50.0 | 604 | 2 | T36366 | hypotheical prote | 478 | 32 | 48.5 | 260 | 1 | OTXL3 | cytochrome-c oxida |
| 406 | 33 | 50.0 | 632 | 1 | JC4319 | 2-oxoacid-ferredox | 479 | 32 | 48.5 | 265 | 2 | S25951 | cytochrome-c oxida |
| 407 | 33 | 50.0 | 651 | 2 | T50289 | WD repeat protein | 480 | 32 | 48.5 | 269 | 2 | S10080 | cytochrome-c oxida |
| 408 | 33 | 50.0 | 653 | 2 | A83154 | probable choline t | 481 | 32 | 48.5 | 274 | 2 | S17804 | hypotheical prote |
| 409 | 33 | 50.0 | 660 | 2 | G90330 | amine oxidase (cop | 482 | 32 | 48.5 | 274 | 2 | T20786 | hypotheical prote |
| 410 | 33 | 50.0 | 661 | 2 | F90360 | hypotheical prote | 483 | 32 | 48.5 | 282 | 2 | T14225 | NADH2 dehydrogenas |
| 411 | 33 | 50.0 | 670 | 2 | S78182 | NADH2 dehydrogenas | 484 | 32 | 48.5 | 283 | 2 | T07678 | xyloglucan endo-1, |
| 412 | 33 | 50.0 | 691 | 2 | T29951 | hypotheical prote | 485 | 32 | 48.5 | 289 | 2 | A83608 | polyamine transpor |
| 413 | 33 | 50.0 | 704 | 2 | S46000 | probable membrane | 486 | 32 | 48.5 | 289 | 2 | F71402 | xyloglucan endo-1, |
| 414 | 33 | 50.0 | 723 | 2 | I39066 | N-methyl-D-asparta | 487 | 32 | 48.5 | 292 | 2 | T00829 | wuschel protein - |
| 415 | 33 | 50.0 | 727 | 2 | T47541 | beta-galactosidase | 488 | 32 | 48.5 | 293 | 2 | D84558 | probable homeodoma |
| 416 | 33 | 50.0 | 728 | 2 | 165413 | sodium-dependent n | 489 | 32 | 48.5 | 294 | 2 | S55168 | hypotheical prote |
| 417 | 33 | 50.0 | 730 | 2 | 152632 | sodium-dependent n | 490 | 32 | 48.5 | 295 | 2 | E84425 | probable homeodoma |
| 418 | 33 | 50.0 | 733 | 2 | T03117 | glycoprotein H - a | 491 | 32 | 48.5 | 299 | 2 | T22838 | hypotheical prote |
| 419 | 33 | 50.0 | 737 | 1 | S64767 | probable serine/th | 492 | 32 | 48.5 | 305 | 2 | G84568 | probable xylogluca |
| 420 | 33 | 50.0 | 747 | 2 | JH0773 | Alzheimer's diseas | 493 | 32 | 48.5 | 307 | 2 | A71602 | rifin PR80955w - m |
| 421 | 33 | 50.0 | 793 | 2 | C72219 | DNA mismatch repai | 494 | 32 | 48.5 | 309 | 2 | A43865 | cell wall-associat |
| 422 | 33 | 50.0 | 859 | 2 | S70584 | nitrate reductase | 495 | 32 | 48.5 | 309 | 2 | T27794 | hypotheical prote |
| 423 | 33 | 50.0 | 867 | 1 | JQ1525 | nitrate reductase | 496 | 32 | 48.5 | 311 | 2 | G70676 | hypotheical prote |
| 424 | 33 | 50.0 | 868 | 1 | JC4283 | nitrate reductase | 497 | 32 | 48.5 | 317 | 2 | AD3585 | ferric anguibactin |
| 425 | 33 | 50.0 | 871 | 2 | AE3085 | two component sens | 498 | 32 | 48.5 | 323 | 2 | T45279 | oligopeptide trans |
| 426 | 33 | 50.0 | 880 | 2 | D98201 | hypotheical prote | 499 | 32 | 48.5 | 325 | 2 | E65084 | hypotheical prote |
| 427 | 33 | 50.0 | 894 | 2 | S52857 | nitrate reductase | 500 | 32 | 48.5 | 332 | 2 | JT0585 | minor endoglucanas |
| 428 | 33 | 50.0 | 915 | 2 | A43802 | cellulase (EC 3.2. | 501 | 32 | 48.5 | 332 | 2 | T19457 | hypotheical prote |
| 429 | 33 | 50.0 | 934 | 2 | H90195 | leucyl-tRNA synthe | 502 | 32 | 48.5 | 335 | 1 | A39862 | probable membrane |
| 430 | 33 | 50.0 | 944 | 2 | G90205 | leucyl-tRNA synthe | 503 | 32 | 48.5 | 341 | 2 | A75025 | hypotheical prote |
| 431 | 33 | 50.0 | 964 | 2 | D59404 | plectin isoform p1 | 504 | 32 | 48.5 | 347 | 2 | S12916 | conserved hypotet |
| 432 | 33 | 50.0 | 1020 | 2 | T18260 | 1-phosphatidylinos | 505 | 32 | 48.5 | 348 | 2 | D71937 | probable N-acetylm |
| 433 | 33 | 50.0 | 1039 | 2 | S02711 | cellulase (EC 3.2. | 506 | 32 | 48.5 | 347 | 2 | B64650 | hypotheical prote |
| 434 | 33 | 50.0 | 1052 | 2 | T04439 | hypotheical prote | 507 | 32 | 48.5 | 349 | 2 | A97007 | probable membrane |
| 435 | 33 | 50.0 | 1111 | 2 | A86522 | probable arabinosy | 508 | 32 | 48.5 | 354 | 2 | E81281 | hypotheical prote |
| 436 | 33 | 50.0 | 1136 | 2 | S89278 | dyein heavy chain | 509 | 32 | 48.5 | 355 | 2 | T19016 | hypotheical prote |
| 437 | 33 | 50.0 | 1331 | 2 | A48954 | mannan endo-1,4-be | 510 | 32 | 48.5 | 357 | 2 | D69204 | conserved hypotet |
| 438 | 33 | 50.0 | 1336 | 2 | T18288 | ABC transport prot | 511 | 32 | 48.5 | 357 | 2 | B71348 | probable N-acetylm |
| 439 | 33 | 50.0 | 1339 | 2 | T38991 | conserved hypotet | 512 | 32 | 48.5 | 367 | 2 | B31847 | hypotheical prote |
| 440 | 33 | 50.0 | 1455 | 2 | S43529 | 165K protein, skel | 513 | 32 | 48.5 | 368 | 2 | JT0348 | VSG expression sit |
| 441 | 33 | 50.0 | 1482 | 2 | I49704 | glutamate receptor | 514 | 32 | 48.5 | 369 | 2 | A89411 | protein ZK228.3 [i |
| 442 | 33 | 50.0 | 1482 | 2 | B43274 | N-methyl-D-asparta | 515 | 32 | 48.5 | 371 | 1 | D71201 | hypotheical prote |
| 443 | 33 | 50.0 | 1484 | 2 | S52086 | N-methyl-D-asparta | 516 | 32 | 48.5 | 371 | 2 | T02102 | hypotheical prote |
| 444 | 33 | 50.0 | 1711 | 2 | T31337 | 1,4-beta-glucanase | 517 | 32 | 48.5 | 373 | 2 | AC0199 | conserved hypotet |
| 445 | 33 | 50.0 | 1742 | 2 | T17120 | cellulase (EC 3.2. | 518 | 32 | 48.5 | 378 | 2 | H75213 | serine proteinase |
| 446 | 33 | 50.0 | 2167 | 2 | T34395 | hypotheical prote | 519 | 32 | 48.5 | 390 | 2 | T46028 | hypotheical prote |
| 447 | 33 | 50.0 | 2658 | 2 | A86216 | protein T23G18.2 [| 520 | 32 | 48.5 | 393 | 2 | D81139 | 2-oxoglutarate deh |
| 448 | 33 | 50.0 | 3176 | 2 | CGH03A | collagen alpha 3(V | 521 | 32 | 48.5 | 398 | 2 | A95870 | hypotheical prote |
| 449 | 33 | 50.0 | 4687 | 1 | A39638 | plectin - rat | 522 | 32 | 48.5 | 398 | 2 | B86298 | protein F309.11 [i |
| 450 | 32.5 | 49.2 | 431 | 2 | H86033 | hypotheical prote | 523 | 32 | 48.5 | 403 | 2 | A81882 | probable dihydrol |
| 451 | 32.5 | 49.2 | 431 | 2 | A98187 | hypotheical prote | 524 | 32 | 48.5 | 404 | 2 | C85829 | glycosyl transfera |
| 452 | 32.5 | 49.2 | 581 | 1 | S71170 | phosphoinositide-s | 525 | 32 | 48.5 | 404 | 2 | H90983 | probable glycosyl |
| 453 | 32.5 | 49.2 | 607 | 2 | H64041 | probable long-chain | 526 | 32 | 48.5 | 411 | 2 | AI2939 | conserved hypotet |
| 454 | 32.5 | 49.2 | 639 | 1 | F69280 | iron (II) transpor | 527 | 32 | 48.5 | 411 | 2 | F98342 | hypotheical prote |
| 455 | 32 | 48.5 | 70 | 2 | S35030 | photosystem I chai | 528 | 32 | 48.5 | 413 | 2 | AC2125 | hypotheical prote |
| 456 | 32 | 48.5 | 87 | 2 | S52969 | NADH2 dehydrogenas | 529 | 32 | 48.5 | 421 | 2 | D96641 | hypotheical prote |
| 457 | 32 | 48.5 | 103 | 2 | AD2849 | conserved hypotet | 530 | 32 | 48.5 | 421 | 2 | F85360 | hypotheical prote |
| 458 | 32 | 48.5 | 103 | 2 | B97626 | hypotheical prote | 531 | 32 | 48.5 | 425 | 2 | S85360 | hypotheical prote |
| 459 | 32 | 48.5 | 115 | 2 | T34629 | hypotheical prote | 532 | 32 | 48.5 | 430 | 2 | JC2301 | hypotheical prote |
| 460 | 32 | 48.5 | 116 | 2 | B71060 | hypotheical prote | 533 | 32 | 48.5 | 434 | 2 | T11643 | histone deacetylase |
| 461 | 32 | 48.5 | 130 | 2 | S06817 | lg heavy chain V r | 534 | 32 | 48.5 | 434 | 2 | E96826 | hypotheical prote |
| 462 | 32 | 48.5 | 133 | 2 | C91001 | hypotheical prote | 535 | 32 | 48.5 | 443 | 2 | H85485 | probable transport |
| 463 | 32 | 48.5 | 143 | 2 | D85846 | unknown protein en | 536 | 32 | 48.5 | 443 | 2 | H90634 | probable transport |
| 464 | 32 | 48.5 | 147 | 2 | AC1223 | ethanolamine utili | 537 | 32 | 48.5 | 448 | 2 | E64725 | yaau protein - Esc |
| 465 | 32 | 48.5 | 148 | 2 | AF1576 | ethanolamine utili | 538 | 32 | 48.5 | 448 | 2 | A83775 | hypotheical prote |
| 466 | 32 | 48.5 | 149 | 2 | T35434 | probable integral | 539 | 32 | 48.5 | 466 | 2 | T46054 | hypotheical prote |
| 467 | 32 | 48.5 | 154 | 2 | D82830 | hypotheical prote | 540 | 32 | 48.5 | 472 | 2 | S67470 | 4-aminobutyrate tr |
| | | | | | | | | | | 472 | 2 | B86727 | hypotheical prote |

| | | | | | | | | | | | | | |
|-----|----|------|------|---|--------|---------------------|-----|------|------|------|---|--------|---------------------|
| 541 | 32 | 48.5 | 474 | 2 | A71533 | probable phospholi | 614 | 32 | 48.5 | 1068 | 2 | S01519 | hypothetical prote |
| 542 | 32 | 48.5 | 478 | 2 | H01688 | phospholipase D fa | 615 | 32 | 48.5 | 1075 | 2 | T34223 | hypothetical prote |
| 543 | 32 | 48.5 | 474 | 2 | E89790 | 6-phospho-beta-glu | 616 | 32 | 48.5 | 1112 | 2 | T30202 | probable chitin sy |
| 544 | 32 | 48.5 | 478 | 2 | H82185 | 6-phospho-beta-glu | 617 | 32 | 48.5 | 1116 | 2 | S63397 | probable membrane |
| 545 | 32 | 48.5 | 487 | 2 | D89935 | conserved hypothet | 618 | 32 | 48.5 | 1161 | 2 | H95903 | probable chemotaxi |
| 546 | 32 | 48.5 | 490 | 2 | G85354 | hypothetical prote | 619 | 32 | 48.5 | 1208 | 2 | T27822 | hypothetical prote |
| 547 | 32 | 48.5 | 493 | 2 | A32454 | X-Pro dipeptidase | 620 | 32 | 48.5 | 1211 | 2 | T41702 | probable cation-tr |
| 548 | 32 | 48.5 | 493 | 2 | S72196 | phospholipid trans | 621 | 32 | 48.5 | 1257 | 2 | A88536 | protein B0523.5 li |
| 549 | 32 | 48.5 | 493 | 2 | A53533 | beta 1,3-glucanase | 622 | 32 | 48.5 | 1259 | 4 | GNHUL1 | retrovirus-related |
| 550 | 32 | 48.5 | 499 | 2 | JC6141 | 4-aminobutyrate tr | 623 | 32 | 48.5 | 1275 | 2 | T38588 | reverse transcript |
| 551 | 32 | 48.5 | 500 | 2 | A24281 | 4-aminobutyrate tr | 624 | 32 | 48.5 | 1275 | 2 | S65824 | reverse transcript |
| 552 | 32 | 48.5 | 500 | 2 | JC4022 | 4-aminobutyrate tr | 625 | 32 | 48.5 | 1275 | 2 | B28096 | line-1 protein ORF |
| 553 | 32 | 48.5 | 500 | 2 | I56502 | 4-aminobutyrate tr | 626 | 32 | 48.5 | 1280 | 2 | B34087 | hypothetical prote |
| 554 | 32 | 48.5 | 504 | 2 | E83980 | glycine betaine tr | 627 | 32 | 48.5 | 1515 | 1 | S51863 | cadmium resistance |
| 555 | 32 | 48.5 | 507 | 2 | T48645 | glycine betaine tr | 628 | 32 | 48.5 | 1549 | 2 | S50705 | hypothetical prote |
| 556 | 32 | 48.5 | 507 | 2 | A01336 | glycine betaine tr | 629 | 32 | 48.5 | 1756 | 2 | T02599 | hypothetical prote |
| 557 | 32 | 48.5 | 507 | 2 | A81707 | glycine betaine tr | 630 | 32 | 48.5 | 2870 | 2 | H96974 | cyclic beta 1-2 gl |
| 558 | 32 | 48.5 | 512 | 2 | G69670 | glycine betaine tr | 631 | 31.5 | 47.7 | 110 | 2 | PH1652 | Ig heavy chain v r |
| 559 | 32 | 48.5 | 515 | 2 | T47946 | prolyl aminopeptid | 632 | 31.5 | 47.7 | 121 | 2 | S31104 | Ig heavy chain V6 |
| 560 | 32 | 48.5 | 517 | 2 | G84136 | glycine betaine tr | 633 | 31.5 | 47.7 | 121 | 2 | S24682 | Ig heavy chain V6 |
| 561 | 32 | 48.5 | 520 | 2 | D90014 | hypothetical prote | 634 | 31.5 | 47.7 | 245 | 2 | P91253 | probable DNA modif |
| 562 | 32 | 48.5 | 526 | 2 | C71315 | probable virulence | 635 | 31.5 | 47.7 | 374 | 2 | AC0469 | probable uroporph |
| 563 | 32 | 48.5 | 527 | 2 | G85760 | hypothetical prote | 636 | 31.5 | 47.7 | 477 | 1 | KCMS81 | stromelysin 1 (EC |
| 564 | 32 | 48.5 | 527 | 2 | H90858 | hypothetical prote | 637 | 31.5 | 47.7 | 581 | 2 | T50841 | phosphoinositide-s |
| 565 | 32 | 48.5 | 540 | 2 | G90068 | choline transporte | 638 | 31.5 | 47.7 | 610 | 2 | T22909 | hypothetical prote |
| 566 | 32 | 48.5 | 568 | 2 | D90525 | hypothetical prote | 639 | 31.5 | 47.7 | 1170 | 2 | S52525 | probable membrane |
| 567 | 32 | 48.5 | 569 | 2 | G87432 | methionyl-tRNA syn | 640 | 31 | 47.0 | 49 | 2 | PL0096 | Ig heavy chain V r |
| 568 | 32 | 48.5 | 574 | 2 | S22596 | hypothetical prote | 641 | 31 | 47.0 | 66 | 2 | C82699 | hypothetical prote |
| 569 | 32 | 48.5 | 575 | 2 | S22594 | hypothetical prote | 642 | 31 | 47.0 | 75 | 2 | A82900 | hypothetical prote |
| 570 | 32 | 48.5 | 575 | 2 | S22595 | hypothetical prote | 643 | 31 | 47.0 | 93 | 2 | T27578 | T-cell receptor be |
| 571 | 32 | 48.5 | 578 | 2 | D95400 | probable oxidoredu | 644 | 31 | 47.0 | 100 | 2 | AH1192 | B. subtilis YneR p |
| 572 | 32 | 48.5 | 584 | 2 | T19565 | hypothetical prote | 645 | 31 | 47.0 | 100 | 2 | AF1550 | B. subtilis YneR p |
| 573 | 32 | 48.5 | 587 | 2 | A31776 | lactose permease - | 646 | 31 | 47.0 | 103 | 2 | PH1045 | Ig light chain V r |
| 574 | 32 | 48.5 | 587 | 2 | T22006 | hypothetical prote | 647 | 31 | 47.0 | 104 | 2 | P97839 | Ig heavy chain V r |
| 575 | 32 | 48.5 | 593 | 2 | E70582 | probable bet p prot | 648 | 31 | 47.0 | 106 | 2 | S37454 | hypothetical prote |
| 576 | 32 | 48.5 | 599 | 2 | S67084 | probable membrane | 649 | 31 | 47.0 | 110 | 2 | S54842 | hypothetical prote |
| 577 | 32 | 48.5 | 606 | 2 | G72282 | hypothetical prote | 650 | 31 | 47.0 | 110 | 2 | F82925 | hypothetical prote |
| 578 | 32 | 48.5 | 607 | 2 | S77092 | hypothetical prote | 651 | 31 | 47.0 | 111 | 2 | SH1082 | amyloid precursor |
| 579 | 32 | 48.5 | 613 | 1 | ERADEM | fiber protein - mo | 652 | 31 | 47.0 | 111 | 2 | PH1645 | Ig heavy chain V r |
| 580 | 32 | 48.5 | 614 | 2 | T28930 | hypothetical prote | 653 | 31 | 47.0 | 114 | 2 | S26278 | T cell receptor be |
| 581 | 32 | 48.5 | 620 | 2 | F83976 | cytochrome-c oxida | 654 | 31 | 47.0 | 114 | 2 | S17380 | T cell receptor be |
| 582 | 32 | 48.5 | 625 | 2 | D45335 | cytochrome-c oxida | 655 | 31 | 47.0 | 114 | 2 | S36280 | Ig heavy chain V r |
| 583 | 32 | 48.5 | 631 | 2 | G48874 | probable membrane | 656 | 31 | 47.0 | 114 | 2 | E69137 | hypothetical prote |
| 584 | 32 | 48.5 | 634 | 2 | G82490 | methyl-accepting c | 657 | 31 | 47.0 | 116 | 2 | E71566 | probable S16 ribos |
| 585 | 32 | 48.5 | 661 | 2 | T40056 | nadh-cytochrome p | 658 | 31 | 47.0 | 116 | 2 | D86723 | hypothetical prote |
| 586 | 32 | 48.5 | 662 | 2 | T41215 | probable acetate-C | 659 | 31 | 47.0 | 117 | 2 | AB1378 | conserved hypothet |
| 587 | 32 | 48.5 | 662 | 2 | T48128 | probable reverse t | 660 | 31 | 47.0 | 117 | 2 | AC1747 | conserved hypothet |
| 588 | 32 | 48.5 | 663 | 2 | S90291 | hypothetical prote | 661 | 31 | 47.0 | 118 | 1 | B70021 | arsenate reductase |
| 589 | 32 | 48.5 | 678 | 1 | S29123 | NADPH-ferrihemopro | 662 | 31 | 47.0 | 119 | 1 | AVMST6 | Ig heavy chain V r |
| 590 | 32 | 48.5 | 685 | 2 | C70678 | probable electron | 663 | 31 | 47.0 | 119 | 2 | S37453 | Ig mu chain - huma |
| 591 | 32 | 48.5 | 712 | 2 | S23650 | retrovirus-related | 664 | 31 | 47.0 | 119 | 2 | B33876 | carcinoembryonic a |
| 592 | 32 | 48.5 | 726 | 2 | A87041 | exodeoxyribonuclea | 665 | 31 | 47.0 | 119 | 2 | B72117 | S16 ribosomal prot |
| 593 | 32 | 48.5 | 727 | 2 | T00383 | KIAA0632 protein - | 666 | 31 | 47.0 | 119 | 2 | B86505 | S16 ribosomal prot |
| 594 | 32 | 48.5 | 734 | 1 | S26072 | photosystem I prot | 667 | 31 | 47.0 | 120 | 2 | C25429 | T-cell receptor be |
| 595 | 32 | 48.5 | 737 | 2 | T06839 | probable photosyst | 668 | 31 | 47.0 | 121 | 2 | T27767 | hypothetical prote |
| 596 | 32 | 48.5 | 759 | 2 | E84854 | probable copper am | 669 | 31 | 47.0 | 121 | 2 | T43130 | hypothetical prote |
| 597 | 32 | 48.5 | 776 | 2 | D98354 | oligo alginate lya | 670 | 31 | 47.0 | 121 | 2 | H83687 | hypothetical prote |
| 598 | 32 | 48.5 | 776 | 2 | AC2928 | oligo alginate lya | 671 | 31 | 47.0 | 122 | 2 | F90235 | hypothetical prote |
| 599 | 32 | 48.5 | 843 | 2 | T41237 | conserved hypothet | 672 | 31 | 47.0 | 122 | 2 | S38492 | Ig heavy chain - h |
| 600 | 32 | 48.5 | 848 | 2 | S44732 | b0523.5 protein - | 673 | 31 | 47.0 | 123 | 2 | C36006 | Ig heavy chain V r |
| 601 | 32 | 48.5 | 866 | 2 | H86288 | hypothetical prote | 674 | 31 | 47.0 | 123 | 2 | S24692 | Ig heavy chain V6 |
| 602 | 32 | 48.5 | 866 | 2 | A11486 | phosphoenolpyruvat | 675 | 31 | 47.0 | 124 | 2 | AG0643 | probable lipoprote |
| 603 | 32 | 48.5 | 868 | 2 | A82515 | conserved hypothet | 676 | 31 | 47.0 | 125 | 2 | F85673 | hypothetical prote |
| 604 | 32 | 48.5 | 871 | 2 | H72597 | hypothetical prote | 677 | 31 | 47.0 | 125 | 2 | B90814 | ycfL protein precu |
| 605 | 32 | 48.5 | 893 | 2 | S46442 | nitrate reductase | 678 | 31 | 47.0 | 125 | 2 | E64854 | hypothetical prote |
| 606 | 32 | 48.5 | 905 | 1 | JN0803 | hypothetical prote | 679 | 31 | 47.0 | 125 | 2 | S49604 | Ig heavy chain V r |
| 607 | 32 | 48.5 | 931 | 2 | B75027 | hypothetical prote | 680 | 31 | 47.0 | 128 | 2 | S26790 | Ig heavy chain V r |
| 608 | 32 | 48.5 | 941 | 2 | D82599 | hypothetical prote | 681 | 31 | 47.0 | 128 | 2 | B97737 | hypothetical prote |
| 609 | 32 | 48.5 | 941 | 2 | A82797 | hypothetical prote | 682 | 31 | 47.0 | 129 | 2 | AG0196 | probable lipoprote |
| 610 | 32 | 48.5 | 1002 | 2 | T43236 | carboxypeptidase C | 683 | 31 | 47.0 | 129 | 2 | B82143 | conserved lipoprote |
| 611 | 32 | 48.5 | 1008 | 2 | H72310 | conserved hypothet | 684 | 31 | 47.0 | 133 | 2 | H24092 | T-cell receptor be |
| 612 | 32 | 48.5 | 1016 | 2 | H71460 | probable outer mem | 685 | 31 | 47.0 | 133 | 2 | T24092 | T-cell receptor be |
| 613 | 32 | 48.5 | 1067 | 2 | D96545 | probable DNA polym | 686 | 31 | 47.0 | 140 | 2 | I47208 | Ig heavy chain var |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|--------|---------------------|-----|----|------|-----|---|--------|--------------------|
| 687 | 31 | 47.0 | 140 | 2 | I76667 | pregnancy-specific | 760 | 31 | 47.0 | 301 | 2 | T26550 | hypothetical prote |
| 688 | 31 | 47.0 | 147 | 2 | S60111 | bis(5'-nucleosyl) - | 761 | 31 | 47.0 | 305 | 2 | T20585 | hypothetical prote |
| 689 | 31 | 47.0 | 150 | 2 | T01158 | hypothetical prote | 762 | 31 | 47.0 | 306 | 2 | A88040 | protein p47f6.1 [i |
| 690 | 31 | 47.0 | 154 | 2 | AD0252 | probable integral | 763 | 31 | 47.0 | 309 | 2 | C72589 | hypothetical prote |
| 691 | 31 | 47.0 | 160 | 2 | D70652 | hypothetical prote | 764 | 31 | 47.0 | 317 | 2 | T25003 | hypothetical prote |
| 692 | 31 | 47.0 | 163 | 2 | D81080 | conserved hypotet | 765 | 31 | 47.0 | 317 | 2 | S01412 | hypothetical prote |
| 693 | 31 | 47.0 | 165 | 1 | I51194 | ribosomal protein | 766 | 31 | 47.0 | 317 | 2 | H89893 | hypothetical prote |
| 694 | 31 | 47.0 | 165 | 1 | R3RT10 | ribosomal protein | 767 | 31 | 47.0 | 318 | 2 | B72676 | hypothetical prote |
| 695 | 31 | 47.0 | 165 | 1 | S55918 | ribosomal protein | 768 | 31 | 47.0 | 321 | 2 | G84750 | probable homeodoma |
| 696 | 31 | 47.0 | 165 | 2 | H59404 | ribosomal protein | 769 | 31 | 47.0 | 326 | 2 | A89931 | conserved hypotet |
| 697 | 31 | 47.0 | 166 | 2 | T43301 | ribosomal protein | 770 | 31 | 47.0 | 326 | 2 | F72639 | hypothetical prote |
| 698 | 31 | 47.0 | 174 | 2 | S59848 | ribosomal protein | 771 | 31 | 47.0 | 327 | 2 | AB1211 | glycosyltransferas |
| 699 | 31 | 47.0 | 174 | 2 | F70828 | hypothetical prote | 772 | 31 | 47.0 | 335 | 2 | S44635 | f22b7.7 protein - |
| 700 | 31 | 47.0 | 176 | 2 | T38392 | 60s ribosomal prot | 773 | 31 | 47.0 | 336 | 2 | T31761 | hypothetical prote |
| 701 | 31 | 47.0 | 177 | 2 | AH1669 | probable NAD(P)H o | 774 | 31 | 47.0 | 338 | 2 | T18715 | hypothetical prote |
| 702 | 31 | 47.0 | 180 | 2 | S56056 | ribosomal protein | 775 | 31 | 47.0 | 338 | 2 | T32679 | hypothetical prote |
| 703 | 31 | 47.0 | 180 | 2 | S58767 | streptothricin ace | 776 | 31 | 47.0 | 340 | 2 | T25919 | hypothetical prote |
| 704 | 31 | 47.0 | 180 | 2 | G69222 | molybdenum formylm | 777 | 31 | 47.0 | 345 | 2 | S48517 | SUR4 protein - yea |
| 705 | 31 | 47.0 | 185 | 2 | F69746 | hypothetical prote | 778 | 31 | 47.0 | 355 | 2 | A53770 | growth factor-resp |
| 706 | 31 | 47.0 | 189 | 2 | B84152 | hypothetical prote | 779 | 31 | 47.0 | 362 | 2 | A38545 | hypothetical prote |
| 707 | 31 | 47.0 | 190 | 2 | T37168 | probable tetR-fami | 780 | 31 | 47.0 | 362 | 2 | JQ2037 | hypothetical 41k p |
| 708 | 31 | 47.0 | 191 | 2 | F84932 | hypothetical prote | 781 | 31 | 47.0 | 369 | 2 | S68692 | deoxyhypusine synt |
| 709 | 31 | 47.0 | 198 | 1 | Q0EXC3 | Putative methylase | 782 | 31 | 47.0 | 369 | 2 | T48720 | translation initia |
| 710 | 31 | 47.0 | 198 | 2 | AF0991 | conserved hypotet | 783 | 31 | 47.0 | 375 | 2 | AE0551 | hypothetical prote |
| 711 | 31 | 47.0 | 198 | 2 | B83598 | conserved hypotet | 784 | 31 | 47.0 | 377 | 2 | AE0589 | galactosyltransfer |
| 712 | 31 | 47.0 | 198 | 2 | B91168 | hypothetical prote | 785 | 31 | 47.0 | 377 | 2 | A71450 | hypothetical prote |
| 713 | 31 | 47.0 | 198 | 2 | B86014 | hypothetical prote | 786 | 31 | 47.0 | 379 | 2 | JC4843 | ATP-gated ionchan |
| 714 | 31 | 47.0 | 198 | 2 | F84264 | sulfite oxidase ho | 787 | 31 | 47.0 | 380 | 2 | S61598 | probable membrane |
| 715 | 31 | 47.0 | 203 | 2 | B83606 | hypothetical prote | 788 | 31 | 47.0 | 381 | 2 | S33449 | pituitary adenylat |
| 716 | 31 | 47.0 | 205 | 2 | S17911 | cytochrome-c oxida | 789 | 31 | 47.0 | 382 | 2 | T27801 | hypothetical prote |
| 717 | 31 | 47.0 | 205 | 2 | E64621 | conserved hypotet | 790 | 31 | 47.0 | 387 | 2 | T35436 | probable adenosine |
| 718 | 31 | 47.0 | 205 | 2 | G71891 | hypothetical prote | 791 | 31 | 47.0 | 387 | 2 | E81306 | hypothetical prote |
| 719 | 31 | 47.0 | 211 | 2 | H83209 | hypothetical prote | 792 | 31 | 47.0 | 389 | 2 | H86676 | hypothetical prote |
| 720 | 31 | 47.0 | 213 | 1 | EPBO | phosphatidylcholin | 793 | 31 | 47.0 | 389 | 2 | E90039 | nitrite extrusion |
| 721 | 31 | 47.0 | 214 | 2 | T25466 | hypothetical prote | 794 | 31 | 47.0 | 403 | 2 | AC2271 | precorrin-6γ-depen |
| 722 | 31 | 47.0 | 219 | 2 | AE2449 | hypothetical prote | 795 | 31 | 47.0 | 403 | 2 | H88636 | protein W09G12.8 [|
| 723 | 31 | 47.0 | 220 | 2 | AG0464 | conserved hypotet | 796 | 31 | 47.0 | 409 | 2 | A95854 | hypothetical oxido |
| 724 | 31 | 47.0 | 228 | 2 | B64604 | hypothetical prote | 797 | 31 | 47.0 | 413 | 2 | P95918 | probable aminotrip |
| 725 | 31 | 47.0 | 231 | 2 | A11262 | ABC transporter, A | 798 | 31 | 47.0 | 413 | 2 | S45467 | aminopeptidase Y h |
| 726 | 31 | 47.0 | 231 | 2 | AC1625 | ABC transporter, A | 799 | 31 | 47.0 | 414 | 2 | T22760 | hypothetical prote |
| 727 | 31 | 47.0 | 232 | 2 | D90254 | conserved hypotet | 800 | 31 | 47.0 | 416 | 2 | T46401 | hypothetical prote |
| 728 | 31 | 47.0 | 233 | 2 | T34896 | conserved hypotet | 801 | 31 | 47.0 | 421 | 2 | B81079 | glutamate dehydrog |
| 729 | 31 | 47.0 | 234 | 2 | AF2224 | hypothetical prote | 802 | 31 | 47.0 | 421 | 2 | B81864 | probable glutamate |
| 730 | 31 | 47.0 | 234 | 2 | AH2418 | hypothetical prote | 803 | 31 | 47.0 | 425 | 2 | S69796 | pectate lyase [EC |
| 731 | 31 | 47.0 | 239 | 1 | JC1373 | ribonuclease [EC 3 | 804 | 31 | 47.0 | 425 | 2 | JC7271 | pectate lyase [EC |
| 732 | 31 | 47.0 | 248 | 2 | AB1114 | conserved hypotet | 805 | 31 | 47.0 | 425 | 2 | S28295 | hypothetical prote |
| 733 | 31 | 47.0 | 256 | 2 | T41229 | hypothetical prote | 806 | 31 | 47.0 | 428 | 2 | A35534 | tetracyclorolypol |
| 734 | 31 | 47.0 | 258 | 2 | H70487 | cytochrome-c oxida | 807 | 31 | 47.0 | 433 | 2 | AG0831 | alpha-ketoglutarat |
| 735 | 31 | 47.0 | 261 | 2 | T11839 | cytochrome-c oxida | 808 | 31 | 47.0 | 434 | 2 | H70989 | probable GABA perm |
| 736 | 31 | 47.0 | 261 | 2 | T10992 | cytochrome-c oxida | 809 | 31 | 47.0 | 434 | 2 | T43197 | nucleoporin homolo |
| 737 | 31 | 47.0 | 262 | 1 | OTFF3 | cytochrome-c oxida | 810 | 31 | 47.0 | 436 | 2 | H97270 | thiamine biosynthe |
| 738 | 31 | 47.0 | 262 | 1 | OTFF3Y | cytochrome-c oxida | 811 | 31 | 47.0 | 442 | 2 | S49741 | probable membrane |
| 739 | 31 | 47.0 | 262 | 2 | T45556 | cytochrome-c oxida | 812 | 31 | 47.0 | 446 | 2 | H97091 | chitinase family p |
| 740 | 31 | 47.0 | 262 | 2 | T34378 | hypothetical prote | 813 | 31 | 47.0 | 447 | 2 | C83890 | beta-glucosidase b |
| 741 | 31 | 47.0 | 265 | 1 | OTBY3M | cytochrome-c oxida | 814 | 31 | 47.0 | 450 | 2 | A48969 | beta-glucosidase (|
| 742 | 31 | 47.0 | 265 | 1 | OTB3M | cytochrome-c oxida | 815 | 31 | 47.0 | 450 | 2 | C96947 | PTS cellobiose-ape |
| 743 | 31 | 47.0 | 265 | 1 | OTR23M | cytochrome-c oxida | 816 | 31 | 47.0 | 454 | 2 | AE2105 | hypothetical prote |
| 744 | 31 | 47.0 | 265 | 1 | OTW3M | cytochrome-c oxida | 817 | 31 | 47.0 | 457 | 2 | AC1167 | 6-phospho-beta-glu |
| 745 | 31 | 47.0 | 265 | 1 | S20801 | cytochrome-c oxida | 818 | 31 | 47.0 | 457 | 2 | D71717 | cysteine-tRNA liga |
| 746 | 31 | 47.0 | 265 | 2 | A48304 | cytochrome-c oxida | 819 | 31 | 47.0 | 457 | 2 | G69341 | conserved hypotet |
| 747 | 31 | 47.0 | 265 | 2 | S14123 | cytochrome-c oxida | 820 | 31 | 47.0 | 457 | 2 | T26642 | hypothetical prote |
| 748 | 31 | 47.0 | 265 | 2 | B82716 | ATP synthase, A ch | 821 | 31 | 47.0 | 457 | 2 | E88456 | protein W03A5.3 [i |
| 749 | 31 | 47.0 | 266 | 2 | B82713 | hypothetical prote | 822 | 31 | 47.0 | 459 | 2 | G97713 | cysteine-tRNA liga |
| 750 | 31 | 47.0 | 267 | 2 | G71233 | hypothetical prote | 823 | 31 | 47.0 | 461 | 2 | B82155 | deoxyribodipyrimid |
| 751 | 31 | 47.0 | 272 | 2 | S52012 | cytochrome-c oxida | 824 | 31 | 47.0 | 463 | 2 | D72356 | conserved hypotet |
| 752 | 31 | 47.0 | 272 | 2 | S57460 | cytochrome-c oxida | 825 | 31 | 47.0 | 465 | 2 | G95973 | endo-1,3-1,4-beta- |
| 753 | 31 | 47.0 | 274 | 2 | T33707 | hypothetical prote | 826 | 31 | 47.0 | 465 | 2 | H95369 | EgIC ENDO-1,3-1,4- |
| 754 | 31 | 47.0 | 277 | 2 | A87184 | thiosulfate sulfur | 827 | 31 | 47.0 | 466 | 2 | T44252 | transport protein |
| 755 | 31 | 47.0 | 277 | 2 | G70809 | probable thiosulfa | 828 | 31 | 47.0 | 467 | 2 | JN0616 | pituitary adenylat |
| 756 | 31 | 47.0 | 281 | 2 | B81894 | hypothetical prote | 829 | 31 | 47.0 | 467 | 2 | A99498 | hypothetical prote |
| 757 | 31 | 47.0 | 281 | 2 | G81126 | conserved hypotet | 830 | 31 | 47.0 | 467 | 2 | AF2021 | hypothetical prote |
| 758 | 31 | 47.0 | 284 | 2 | T06159 | probable receptor | 831 | 31 | 47.0 | 469 | 2 | B96947 | beta-glucosidase [|
| 759 | 31 | 47.0 | 288 | 2 | D83731 | ABC transporter (A | 832 | 31 | 47.0 | 470 | 2 | B72567 | hypothetical prote |

833 31 47.0 471 1 S78072 serine-type carbox
 834 31 47.0 473 2 T27227 hypothetical prote
 835 31 47.0 473 2 S64014 probable transport
 836 31 47.0 476 2 A44170 membrane-bound rib
 837 31 47.0 476 2 E27079 phospholipase D ho
 838 31 47.0 476 2 A86545 phospholipase D ty
 839 31 47.0 477 2 E37073 phospho-beta-glucos
 840 31 47.0 483 1 VCBP73 minor coat protein
 841 31 47.0 484 2 A11419 beta-glucosidase h
 842 31 47.0 484 2 A11794 beta-glucosidase h
 843 31 47.0 484 2 T25731 hypothetical prote
 844 31 47.0 487 1 I40654 60K inner membrane
 845 31 47.0 491 2 J50396 phospho-beta-galac
 846 31 47.0 492 2 S46298 catalase (EC 1.11.
 847 31 47.0 492 2 AH2079 alpha-amylase (imp
 848 31 47.0 495 2 S39061 pituitary adenylat
 849 31 47.0 495 2 S36114 pituitary adenylat
 850 31 47.0 496 2 B83591 probable transport
 851 31 47.0 501 2 A90595 cardiolipin synthe
 852 31 47.0 511 2 H86694 prophage p11 prote
 853 31 47.0 511 2 C86798 prophage p13 prote
 854 31 47.0 513 2 S47631 pituitary adenylat
 855 31 47.0 513 2 S58200 probable membrane
 856 31 47.0 519 1 J50725 cytochrome P450 AL
 857 31 47.0 519 1 J50726 cytochrome P450 AL
 858 31 47.0 523 2 S55328 serine-type carbox
 859 31 47.0 523 2 S39060 pituitary adenylat
 860 31 47.0 525 2 JN0902 pituitary adenylat
 861 31 47.0 526 2 T25535 hypothetical prote
 862 31 47.0 526 2 AH0820 conserved hypothet
 863 31 47.0 531 2 S76616 hypothetical prote
 864 31 47.0 535 2 T47790 hypothetical prote
 865 31 47.0 536 2 S63651 cytochrome-c oxida
 866 31 47.0 539 2 E83181 probable MFS trans
 867 31 47.0 540 2 B40901 equine arteritis v
 868 31 47.0 543 2 T20717 hypothetical prote
 869 31 47.0 548 2 E89910 glycine betaine tr
 870 31 47.0 552 2 F94648 hypothetical prote
 871 31 47.0 555 2 T47665 beta-N-acetylhexos
 872 31 47.0 557 2 H95237 transcription regu
 873 31 47.0 557 2 A99702 conserved hypothet
 874 31 47.0 567 2 H87370 major facilitator
 875 31 47.0 567 2 B81408 probable thiol-dis
 876 31 47.0 577 2 S77715 cytochrome c-type
 877 31 47.0 584 2 T27009 hypothetical prote
 878 31 47.0 605 2 G58833 probable pyruvate
 879 31 47.0 607 2 T42399 acetylcholinestera
 880 31 47.0 614 2 A12882 MFS permease [suga
 881 31 47.0 625 2 C75044 threonyl-tRNA synt
 882 31 47.0 625 2 D71116 threonine-tRNA lig
 883 31 47.0 632 2 AE3560 proline/betaine lig
 884 31 47.0 636 2 T37843 probable beta-gluc
 885 31 47.0 638 2 G02068 white homolog - hu
 886 31 47.0 638 2 JC2139 phenylethylamine o
 887 31 47.0 643 2 H83635 conserved hypothet
 888 31 47.0 646 2 JC7777 ATP binding casset
 889 31 47.0 650 2 T24739 hypothetical prote
 890 31 47.0 652 2 C70698 probable nitrate r
 891 31 47.0 652 2 T39409 hypothetical prote
 892 31 47.0 653 2 T49842 related to Na+/H+-
 893 31 47.0 657 2 G97658 hypothetical prote
 894 31 47.0 675 2 S53831 NADH2 dehydrogenas
 895 31 47.0 676 2 E72662 hypothetical prote
 896 31 47.0 684 2 A56102 amine oxidase (cop
 897 31 47.0 692 2 H90045 hypothetical prote
 898 31 47.0 700 2 T32205 hypothetical prote
 899 31 47.0 705 2 T01730 hypothetical prote
 900 31 47.0 706 2 S62933 hypothetical prote
 901 31 47.0 710 2 S63598 cyclomaltodextrin
 902 31 47.0 712 1 ALBSG3 cyclomaltodextrin
 903 31 47.0 712 2 T27165 hypothetical prote
 904 31 47.0 713 1 ALBSG7 cyclomaltodextrin
 905 31 47.0 713 1 ALBSG1 cyclomaltodextrin

906 31 47.0 713 2 A58800 cyclomaltodextrin
 907 31 47.0 713 2 S09196 cyclomaltodextrin
 908 31 47.0 713 2 AE0531 lysine decarboxyla
 909 31 47.0 713 2 T20090 hypothetical prote
 910 31 47.0 714 1 ALBSG6 cyclomaltodextrin
 911 31 47.0 718 1 ALBSGC cyclomaltodextrin
 912 31 47.0 718 1 ALBSMX cyclomaltodextrin
 913 31 47.0 718 1 ALBSMX conserved hypothet
 914 31 47.0 726 2 G83310 conserved hypothet
 915 31 47.0 741 2 H90607 conserved hypothet
 916 31 47.0 741 2 D83633 beta-amyloloid precu
 917 31 47.0 751 2 A49974 amyloid beta (A4)
 918 31 47.0 763 2 A49321 amyloid precursor-
 919 31 47.0 765 2 S42880 probable mannose-1
 920 31 47.0 767 2 E95924 glycosyltransferas
 921 31 47.0 768 2 B97083 inhibition protein
 922 31 47.0 773 2 T46188 hypothetical prote
 923 31 47.0 790 2 G59097 methionine-tRNA li
 924 31 47.0 797 2 T05247 probable heavy-met
 925 31 47.0 804 1 A69309 ribosomal protein
 926 31 47.0 804 2 T25673 ribosomal protein
 927 31 47.0 809 2 S40460 helicase - human h
 928 31 47.0 820 2 T41978 nitrite reductase
 929 31 47.0 822 2 D87325 probable helicase
 930 31 47.0 824 2 T44222 helicase imported
 931 31 47.0 824 2 T44037 hypothetical prote
 932 31 47.0 826 2 G90283 probable alpha-ara
 933 31 47.0 835 2 C97322 hypothetical prote
 934 31 47.0 836 2 T31613 DNA helicase/prima
 935 31 47.0 838 2 S61250 vacuolar assembly
 936 31 47.0 841 2 T09455 hypothetical prote
 937 31 47.0 841 2 B71212 hypothetical prote
 938 31 47.0 851 2 T38497 1-phosphatidylinos
 939 31 47.0 852 2 S25359 proteinase [import
 940 31 47.0 871 2 T49216 DNA helicase/prima
 941 31 47.0 875 1 A36369 gene 55 protein -
 942 31 47.0 875 2 H90371 99.5K DNA helicase
 943 31 47.0 880 2 T42600 outer membrane u
 944 31 47.0 881 1 W2BE55 protein-tyrosine k
 945 31 47.0 881 1 W2BE59 probable mmp12 pro
 946 31 47.0 889 2 AG0859 spore germination
 947 31 47.0 960 1 JN0677 polymorphic membra
 948 31 47.0 968 2 F70746 DNA-directed DNA p
 949 31 47.0 970 2 F64230 alpha-mannosidase
 950 31 47.0 983 2 A81723 collagenase - Clos
 951 31 47.0 984 1 DJNVCP probable DNA-direc
 952 31 47.0 1007 2 T42219 alpha-mannosidase
 953 31 47.0 1021 2 I40805 probable DNA-direc
 954 31 47.0 1021 2 S26985 plasmodium-associ
 955 31 47.0 1028 2 A53449 BIG-1 protein - ra
 956 31 47.0 1028 2 S56229 probable membrane
 957 31 47.0 1029 2 S56229 hypothetical prote
 958 31 47.0 1036 2 H64245 hypothetical prote
 959 31 47.0 1042 2 T29307 probable arabinosy
 960 31 47.0 1082 2 T45096 unknown protein li
 961 31 47.0 1085 2 C96797 cellobiose-phospho
 962 31 47.0 1086 2 AF1662 DNA polymerase III
 963 31 47.0 1091 2 AF2953 probable DNA polyme
 964 31 47.0 1091 2 G98329 major DNA binding
 965 31 47.0 1132 2 T44001 hypothetical prote
 966 31 47.0 1209 2 T16663 hypothetical prote
 967 31 47.0 1307 2 T25563 hypothetical prote
 968 31 47.0 1339 2 JC5508 DNA-directed DNA p
 969 31 47.0 1390 2 T30346 insulin receptor -
 970 31 47.0 1403 2 S64142 hypothetical prote
 971 31 47.0 1475 2 A60026 cell communication
 972 31 47.0 1515 2 T52081 MRP-like ABC trans
 973 31 47.0 1867 2 T38348 probable 1,3-beta-
 974 31 47.0 1900 2 AG2391 serine/threonine k
 975 31 47.0 2358 2 T39569 probable alpha-glu
 976 31 47.0 2371 2 T43432 alpha-glucan synth
 977 31 47.0 2482 2 I48922 cation-independent
 978 31 47.0 2483 1 A49617 insulin-like growt

979 31 47.0 2559 2 T30850 fat facets protein
980 31 47.0 3016 2 S77300 hypothetical prote
981 31 47.0 4598 2 T28667 dynein beta heavy
982 31 47.0 4845 2 T31067 BIR repeat contain
983 30.5 46.2 44 2 A36864 OAC1 protein - Azo
984 30.5 46.2 245 2 A71209 hypothetical prote
985 30.5 46.2 247 2 B75022 hypothetical prote
986 30.5 46.2 307 2 A28771 reaction center pr
987 30.5 46.2 341 2 S40612 myosin-related pro
988 30.5 46.2 416 2 T25036 hypothetical prote
989 30.5 46.2 426 2 C90994 interrupted molybd
990 30.5 46.2 426 2 F85839 probable regulator
991 30.5 46.2 494 2 E70031 hypothetical prote
992 30.5 46.2 546 2 T26568 hypothetical prote
993 30.5 46.2 619 2 T34451 hypothetical prote
994 30.5 46.2 645 2 A75390 NADH2 dehydrogenas
995 30.5 46.2 1015 2 T15830 hypothetical prote
996 30 45.5 32 2 PH1735 Ig heavy chain V r
997 30 45.5 38 2 PL0229 T-cell receptor be
998 30 45.5 42 2 T07248 hypothetical prote
999 30 45.5 44 2 S56313 GUT8-2a protein -
1000 30 45.5 58 2 AF2015 hypothetical prote

ALIGNMENTS

RESULT 1

PH1004
Ig heavy chain V region (clone 165.5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1004
R;Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IGM and IgG anti-DNA antibodies are the products of clonally selective B c
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1004
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-91 <TIL>
A;Cross-references: UNIPARC:UPI0000176ACD
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 77.3%; Score 51; DB 2; Length 91;
Best Local Similarity 72.7%; Pred. No. 0.11;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RETVFWYFDV 11
DB 80 REGCYWYFDV 90

RESULT 2

A30540
Ig heavy chain V region (253.12D3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 16-Aug-1996
C;Accession: A30540
R;Claflin, J.L.; Berry, J.
J. Immunol. 141, 4012-4019, 1988
A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneu
A;Reference number: A30534; MUID:89035545; PMID:3141511
A;Accession: A30540
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-123 <CLA>
A;Cross-references: UNIPARC:UPI0000176C34
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>

Query Match 71.2%; Score 47; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYWYFDV 11
DB 106 FYWYFDV 112

RESULT 3

B49038
Ig lambda chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: B49038
R;Weiss, U.; Zoebelen, R.; Rajewsky, K.
Eur. J. Immunol. 22, 511-517, 1992
A;Title: Accumulation of somatic mutants in the B cell compartment after primary immuniz
A;Reference number: A49038; MUID:92164733; PMID:1537385
A;Accession: B49038
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-31 <WEI>
A;Cross-references: UNIPARC:UPI00001154F6; GB:S85733; NID:9246316; PIDN:AA821560.1; PID:
A;Experimental source: spleen
A;Note: sequence extracted from NCBI backbone (NCBIN:85733, NCBIIP:85761)
C;Keywords: heterotetramer; immunoglobulin

Query Match 66.7%; Score 44; DB 2; Length 31;
Best Local Similarity 85.7%; Pred. No. 0.58;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 FWYFDV 11
DB 25 YWYFDV 31

RESULT 4

C49038
Ig lambda chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: C49038
R;Weiss, U.; Zoebelen, R.; Rajewsky, K.
Eur. J. Immunol. 22, 511-517, 1992
A;Title: Accumulation of somatic mutants in the B cell compartment after primary immuniz
A;Reference number: A49038; MUID:92164733; PMID:1537385
A;Accession: C49038
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-38 <WEI>
A;Cross-references: UNIPARC:UPI00001154F7; GB:S85734; NID:9246318; PIDN:AA821561.1; PID:
A;Experimental source: spleen
A;Note: sequence extracted from NCBI backbone (NCBIN:85734, NCBIIP:85801)
C;Keywords: heterotetramer; immunoglobulin

Query Match 66.7%; Score 44; DB 2; Length 38;
Best Local Similarity 85.7%; Pred. No. 0.71;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYWYFDV 11
DB 32 YWYFDV 38

RESULT 5

E49038
Ig lambda chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: E49038
R;Weiss, U.; Zoebelen, R.; Rajewsky, K.

Eur. J. Immunol. 22, 511-517, 1992
A;Title: Accumulation of somatic mutants in the B cell compartment after primary immunization
A;Reference number: A49038; MUID:92164733; PMID:1537385
A;Accession: E49038
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-56 <WEI>
A;Cross-references: UNIPARC:UPI00001154F9; GB:S85736; NID:g246322; PIDN:AB21563.1; PID:
A;Experimental source: spleen
A;Note: sequence extracted from NCBI backbone (NCBI:85736, NCBIP:85804)
C;Keywords: heterotetramer; immunoglobulin

Query Match 66.7%; Score 44; DB 2; Length 56;
Best Local Similarity 85.7%; Pred. No. 1;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYWYFDV 11
:|||||
Db 50 YYWYFDV 56

RESULT 6

D49038
Ig lambda chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: D49038
R;Weiss, U.; Zoebelen, R.; Rajewsky, K.
Eur. J. Immunol. 22, 511-517, 1992
A;Title: Accumulation of somatic mutants in the B cell compartment after primary immunization
A;Reference number: A49038; MUID:92164733; PMID:1537385
A;Accession: D49038
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-56 <WEI>
A;Cross-references: UNIPARC:UPI00001154F8; GB:S85735; NID:g246320; PIDN:AB21562.1; PID:
A;Experimental source: spleen
A;Note: sequence extracted from NCBI backbone (NCBI:85735, NCBIP:85802)
C;Keywords: heterotetramer; immunoglobulin

Query Match 66.7%; Score 44; DB 2; Length 58;
Best Local Similarity 85.7%; Pred. No. 1.1;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYWYFDV 11
:|||||
Db 52 YYWYFDV 58

RESULT 7

G30539
Ig heavy chain V region (224.7E7) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 16-Aug-1996
C;Accession: G30539
R;Claflin, J.L.; Berry, J.
J. Immunol. 141, 4012-4019, 1988
A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneumoniae
A;Reference number: A30534; MUID:89035545; PMID:3141511
A;Accession: G30539
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-124 <CLA>
A;Cross-references: UNIPARC:UPI0000176D23
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>

Query Match 66.7%; Score 44; DB 2; Length 124;
Best Local Similarity 85.7%; Pred. No. 2.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYWYFDV 11

Db 107 YYWYFDV 113
:|||||

RESULT 8

F30539
Ig heavy chain V region (224.4B11) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 16-Aug-1996
C;Accession: F30539
R;Claflin, J.L.; Berry, J.
J. Immunol. 141, 4012-4019, 1988
A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneumoniae
A;Reference number: A30534; MUID:89035545; PMID:3141511
A;Accession: F30539
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-124 <CLA>
A;Cross-references: UNIPARC:UPI0000176D27
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>

Query Match 66.7%; Score 44; DB 2; Length 124;
Best Local Similarity 85.7%; Pred. No. 2.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYWYFDV 11
:|||||
Db 107 YYWYFDV 113

RESULT 9

H30539
Ig heavy chain V region (252.5E10) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 16-Aug-1996
C;Accession: H30539
R;Claflin, J.L.; Berry, J.
J. Immunol. 141, 4012-4019, 1988
A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneumoniae
A;Reference number: A30534; MUID:89035545; PMID:3141511
A;Accession: H30539
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-124 <CLA>
A;Cross-references: UNIPARC:UPI0000176D22
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>

Query Match 66.7%; Score 44; DB 2; Length 124;
Best Local Similarity 85.7%; Pred. No. 2.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYWYFDV 11
:|||||
Db 107 YYWYFDV 113

RESULT 10

T40165
translation elongation factor eEF-1 alpha [similarity] - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
C;Accession: T40165; T39977
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Lelaure, V.; Galibert, F.
submitted to the EMBL Data Library, October 1998
A;Reference number: Z21908
A;Accession: T40165
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-592 <WOO>

A;Cross-references: UNIPROT:O74774; UNIPARC:UPI000006C873; EMBL:AL033385; PIDN:CAA21884.
A;Experimental source: strain 972h-; cosmid c2G5
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Lelaure, V.; Galibert, F.
submitted to the EMBL Data Library, October 1998
A;Accession: T39977
A;Reference number: Z21896
A;Molecule type: DNA
A;Residues: 347-592 <LYN>
A;Cross-references: UNIPARC:UPI0000169078; EMBL:AL031853; PIDN:CAA21259.1; GSPDB:GN00067
C;Genetics:
A;Gene: SPDB:SPBC2G5.08
A;Map position: 2
A;Introns: 14/1; 32/1
C;Superfamily: translation elongation factor Tu homology
F;178-326/Domain: translation elongation factor Tu homology <ETU>

Query Match 66.7%; Score 44; DB 2; Length 592;
Best Local Similarity 70.0%; Pred. No. 10;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 ETVFYWYFDV 11
:::|||||
DB 57 DTWYIYFDV 66

RESULT 11
PH1006
Ig heavy chain V region (clone 202.33) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1006
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B c
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1006
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-108 <TIL>
A;Cross-references: UNIPARC:UPI0000176D16
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;10-93/Domain: immunoglobulin homology <IMM>

Query Match 63.6%; Score 42; DB 2; Length 108;
Best Local Similarity 87.5%; Pred. No. 4.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 VFYWYFDV 11
:|||||
DB 100 VGYWYFDV 107

RESULT 12
S13687
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-May-1997
C;Accession: S13687
R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Houghton, G.; Clarke, S.H.
Eur. J. Immunol. 19, 1289-1295, 1989
A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl
A;Reference number: S13685; MUID:89338557; PMID:2503389
A;Accession: S13687
A;Molecule type: mRNA
A;Residues: 1-111 <PEN>
A;Cross-references: UNIPARC:UPI0000176902; EMBL:X53340
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>

Query Match 63.6%; Score 42; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YWYFDV 11
:|||||
DB 82 YWYFDV 87

RESULT 13
S26744
Ig heavy chain J region JH1 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 25-Feb-1994 #sequence_revision 24-Oct-1998 #text_change 31-Dec-2004
C;Accession: S26744
R;Solín, M.L.; Kaartinen, M.
Immunogenetics 36, 306-313, 1992
A;Title: Allelic polymorphism of mouse Igh-J locus, which encodes immunoglobulin heavy c
A;Reference number: S26744; MUID:92355114; PMID:1644448
A;Accession: S26744
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-17 <SOL>
A;Cross-references: UNIPROT:Q924P5; UNIPROT:Q924R3; UNIPROT:Q91V67; UNIPARC:UPI0000176D
C;Superfamily: immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin

Query Match 62.1%; Score 41; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YWYFDV 11
:|||||
DB 1 YWYFDV 6

RESULT 14
S13689
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-May-1997
C;Accession: S13689
R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Houghton, G.; Clarke, S.H.
Eur. J. Immunol. 19, 1289-1295, 1989
A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl
A;Reference number: S13685; MUID:89338557; PMID:2503389
A;Accession: S13689
A;Molecule type: mRNA
A;Residues: 1-91 <PEN>
A;Cross-references: UNIPARC:UPI0000176903; EMBL:X53342
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin

Query Match 62.1%; Score 41; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YWYFDV 11
:|||||
DB 82 YWYFDV 87

RESULT 15
S13692
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-May-1997
C;Accession: S13692
R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Houghton, G.; Clarke, S.H.
Eur. J. Immunol. 19, 1289-1295, 1989
A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl
A;Reference number: S13685; MUID:89338557; PMID:2503389
A;Accession: S13692
A;Molecule type: mRNA

A;Residues: 1-101 <PEN>
A;Cross-references: UNIPARC:UPI0000176D57; EMBL:X53345
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 62.1%; Score 41; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YWYFDV 11

Db 85 YWYFDV 90

RESULT 16

PH1002

Ig heavy chain V region (clone 165.45) - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1002
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

A;Title: Both Igm and Igg anti-DNA antibodies are the products of clonally selective B c
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1002

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-106 <TIL>

A;Cross-references: UNIPARC:UPI0000176D13

A;Experimental source: B cell, strain [NZB x NZW]F1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 62.1%; Score 41; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YWYFDV 11

Db 100 YWYFDV 105

RESULT 17

PH0987

Ig heavy chain V region (clone 163.47) - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH0987
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

A;Title: Both Igm and Igg anti-DNA antibodies are the products of clonally selective B c
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH0987

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-107 <TIL>

A;Cross-references: UNIPARC:UPI0000176D07

A;Experimental source: B cell, strain [NZB x NZW]F1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 62.1%; Score 41; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YWYFDV 11

Db 101 YWYFDV 106

RESULT 18

S13688

Ig heavy chain V region - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 30-May-1997

C;Accession: S13688

R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.

Eur. J. Immunol. 19, 1289-1295, 1989

A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl

A;Reference number: S13685; MUID:89338557; PMID:2503389

A;Accession: S13688

A;Molecule type: mRNA

A;Residues: 1-110 <PEN>

A;Cross-references: UNIPARC:UPI0000176904; EMBL:X53341

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;10-93/Domain: immunoglobulin homology <IMM>

Query Match 62.1%; Score 41; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YWYFDV 11

Db 98 YWYFDV 103

RESULT 19

S13693

Ig heavy chain V region - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 30-May-1997

C;Accession: S13693

R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.

Eur. J. Immunol. 19, 1289-1295, 1989

A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl

A;Reference number: S13685; MUID:89338557; PMID:2503389

A;Accession: S13693

A;Molecule type: mRNA

A;Residues: 1-111 <PEN>

A;Cross-references: UNIPARC:UPI0000176E3D; EMBL:X53346

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 62.1%; Score 41; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YWYFDV 11

Db 102 YWYFDV 107

RESULT 20

S26463

Ig heavy chain V region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C;Accession: S26463

R;Kavaler, J.

submitted to the EMBL Data Library, April 1991

A;Reference number: S26459

A;Accession: S26463

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-111 <KAV>

A;Cross-references: UNIPARC:UPI0000115F67; EMBL:X59113; NID:951922; PIDN:CAA41839.1; PID

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 62.1%; Score 41; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 6.3;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YWYFDV 11
|||||

Db 96 YWYFDV 101

RESULT 21
S13686
IG heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-May-1997
C;Accession: S13686
R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.
Eur. J. Immunol. 19, 1289-1295, 1989
A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to clonal selection
A;Reference number: S13685; MUID:89338557; PMID:2503389
A;Accession: S13686
A;Molecule type: mRNA
A;Residues: 1-112 <PEN>
A;Cross-references: UNIPARC:UPI0000176901; EMBL:X53339
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 62.1%; Score 41; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YWYFDV 11
|||||

Db 103 YWYFDV 108

RESULT 22
S26327
IG heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
C;Accession: S26327
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26327
A;Molecule type: mRNA
A;Residues: 1-112 <STA>
A;Cross-references: UNIPARC:UPI00001769AD; EMBL:X59192
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-91/Domain: immunoglobulin homology <IMM>

Query Match 62.1%; Score 41; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YWYFDV 11
|||||

Db 96 YWYFDV 101

RESULT 23
S13690
IG heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C;Accession: S13690
R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.
Eur. J. Immunol. 19, 1289-1295, 1989
A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to clonal selection
A;Reference number: S13685; MUID:89338557; PMID:2503389
A;Accession: S13690
A;Molecule type: mRNA

A;Residues: 1-112 <PEN>
A;Cross-references: UNIPARC:UPI000017685P; EMBL:X53343
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 62.1%; Score 41; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YWYFDV 11
|||||

Db 103 YWYFDV 108

RESULT 24
PH1022
IG heavy chain V region (clone 202.17) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1022
R;Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1022
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-112 <TIL>
A;Cross-references: UNIPARC:UPI0000176CEE
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 62.1%; Score 41; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YWYFDV 11
|||||

Db 106 YWYFDV 111

RESULT 25
S13685
IG heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 30-May-1997
C;Accession: S13685
R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.
Eur. J. Immunol. 19, 1289-1295, 1989
A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to clonal selection
A;Reference number: S13685; MUID:89338557; PMID:2503389
A;Accession: S13685
A;Molecule type: mRNA
A;Residues: 1-112 <PEN>
A;Cross-references: UNIPARC:UPI0000176900; EMBL:X53338
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 62.1%; Score 41; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YWYFDV 11
|||||

Db 103 YWYFDV 108

RESULT 26
PH1018

Ig heavy chain V region (clone 17s.130) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PH1018
 R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IGG anti-DNA antibodies are the products of clonally selective B cells
 A:Reference number: PH0971; MUID:92381444; PMID:1512540
 A:Accession: PH1018
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-113 <TIL>
 A:Cross-references: UNIPARC:UPI0000176CEA
 A:Experimental source: B cell, strain [NZB x NZW]F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 62.1%; Score 41; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 6.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YWYFDV 11
 |||||
 Db 107 YWYFDV 112

RESULT 27
 SI3694
 Ig heavy chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: SI3694
 R:Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.
 Eur. J. Immunol. 19, 1289-1295, 1989
 A:Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to clonal selection
 A:Reference number: SI3685; MUID:89338557; PMID:2503389
 A:Accession: SI3694
 A:Molecule type: mRNA
 A:Residues: 1-115 <PEN>
 A:Cross-references: UNIPARC:UPI0000113776; EMBL:X53347; NID:g55240; PIDN:CAA37433.1; PIDN:CAA37430.1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 62.1%; Score 41; DB 2; Length 115;
 Best Local Similarity 100.0%; Pred. No. 6.6;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YWYFDV 11
 |||||
 Db 102 YWYFDV 107

RESULT 28
 SI3691
 Ig heavy chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: SI3691
 R:Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.
 Eur. J. Immunol. 19, 1289-1295, 1989
 A:Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to clonal selection
 A:Reference number: SI3685; MUID:89338557; PMID:2503389
 A:Accession: SI3691
 A:Molecule type: mRNA
 A:Residues: 1-116 <PEN>
 A:Cross-references: UNIPARC:UPI0000113773; EMBL:X53344; NID:g55235; PIDN:CAA37430.1; PIDN:CAA37430.1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 62.1%; Score 41; DB 2; Length 116;
 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 6.6;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YWYFDV 11
 |||||
 Db 102 YWYFDV 107

RESULT 29
 MHMSJ5
 Ig heavy chain V region (J558) - mouse (tentative sequence)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
 C:Accession: A26242
 R:Schilling, J.; Cleavinger, B.; Davie, J.M.; Hood, L.
 Nature 283, 35-40, 1980
 A:Title: Amino acid sequence of homogeneous antibodies to dextran and DNA rearrangements
 A:Reference number: A26242; MUID:80078170; PMID:6765983
 A:Accession: A26242
 A:Molecule type: protein
 A:Residues: 1-117 <SCH>
 A:Cross-references: UNIPROT:P01757; UNIPARC:UPI00000270F2
 A:Note: the sequences of 10 hybridoma proteins that also bind dextran differ from that of the J558 parent cell line
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; hybridoma; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:22-96/Disulfide bonds: #status predicted

Query Match 62.1%; Score 41; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YWYFDV 11
 |||||
 Db 101 YWYFDV 106

RESULT 30
 D30556
 Ig heavy chain V region (5G4) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 23-Feb-1989 #sequence_revision 23-Feb-1989 #text_change 16-Aug-1996
 C:Accession: D30556
 R:Clafilin, J.L.; Berry, J.; Flaherty, D.; Dunnick, W.
 J. Immunol. 139, 3060-3068, 1987
 A:Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced with phosphocholine
 A:Reference number: A30556; MUID:87196439; PMID:3106498
 A:Accession: D30556
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-121 <CLA>
 A:Cross-references: UNIPARC:UPI0000176C3B
 A:Note: the sequence was determined from the differentiated gene
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:13-98/Domain: immunoglobulin homology <IMM>

Query Match 62.1%; Score 41; DB 2; Length 121;
 Best Local Similarity 100.0%; Pred. No. 6.9;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YWYFDV 11
 |||||
 Db 105 YWYFDV 110

RESULT 31
 B30515
 Ig heavy chain V region (5-1E4) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Nov-1988 #sequence_revision 03-Aug-1992 #text_change 16-Aug-1996
 C:Accession: B30515

R;Feeney, A.J.; Clarke, S.H.; Mosier, D.E.

J. Immunol. 141, 1267-1272, 1988

A;Title: Specific H chain functional diversity may be required for non-T15 antibodies to

A;Reference number: A30515; MUID:88285740; PMID:3135325

A;Accession: E30515

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-122 <FEA>

A;Cross-references: UNIPARC:UPI0000176C46

A;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;14-99/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 62.1%; Score 41; DB 2; Length 122;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YWYFDV 11

|||||

Db 106 YWYFDV 111

RESULT 32

AVMS13

Ig heavy chain V region (HPCG13) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004

A;Accession: E93256

R;Gearhart, P.J.; Johnson, N.D.; Douglas, R.; Hood, L.

Nature 291, 29-34, 1981

A;Title: IgG antibodies to phosphorylcholine exhibit more diversity than their IgM count

A;Reference number: A93256; MUID:81197602; PMID:7231520

A;Accession: E93256

A;Molecule type: protein

A;Residues: 1-123 <GEA>

A;Cross-references: UNIPROT:P01793; UNIPARC:UPI0000027116

A;Note: the possibility that some of the diversity seen in sequences of phosphorylcholin

C;Comment: This hybridoma protein binds phosphorylcholine.

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; hybridoma; immunoglobulin

F;15-100/Domain: immunoglobulin homology <IMM>

F;22-98/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 62.1%; Score 41; DB 1; Length 123;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YWYFDV 11

|||||

Db 107 YWYFDV 112

RESULT 33

AVMSH8

Ig heavy chain V region (HPCG8) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004

A;Accession: E93256

R;Gearhart, P.J.; Johnson, N.D.; Douglas, R.; Hood, L.

Nature 291, 29-34, 1981

A;Title: IgG antibodies to phosphorylcholine exhibit more diversity than their IgM count

A;Reference number: A93256; MUID:81197602; PMID:7231520

A;Accession: E93256

A;Molecule type: protein

A;Residues: 1-123 <GEA>

A;Cross-references: UNIPROT:P01793; UNIPARC:UPI0000027115

A;Note: the possibility that some of the diversity seen in sequences of phosphorylcholin

C;Comment: This hybridoma protein binds phosphorylcholine.

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; hybridoma; immunoglobulin

F;15-100/Domain: immunoglobulin homology <IMM>

F;22-98/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 62.1%; Score 41; DB 1; Length 123;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YWYFDV 11

|||||

Db 107 YWYFDV 112

RESULT 34

AVMS75

Ig heavy chain VH1 regions (TEPC 15, S107, H8, HPCW1, HPCW2, 224.2B8, 224.2G3, 25

C;Species: Mus musculus (house mouse)

C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004

A;Accession: A93804; A90795; A94474; A94449; A93256; C30539; A02070; A90.

R;Rudikoff, S.; Potter, M.

Proc. Natl. Acad. Sci. U.S.A. 73, 2109-2112, 1976

A;Title: Size differences among immunoglobulin heavy chains from phosphorylcholine-bindin

A;Reference number: A93804; MUID:76222762; PMID:819932

A;Contents: TEPC 15

A;Accession: A93804

A;Molecule type: protein

A;Residues: 1-123 <RUD>

A;Cross-references: UNIPROT:P01787; UNIPARC:UPI000002710F

R;Early, P.; Huang, H.; Davis, M.; Calame, K.; Hood, L.

Cell 19, 981-992, 1980

A;Title: An immunoglobulin heavy chain variable region gene is generated from three segme

A;Reference number: A90795; MUID:80199926; PMID:6769593

A;Contents: S107

A;Accession: A90795

A;Molecule type: DNA

A;Residues: 1-101 <EAR>

A;Cross-references: UNIPARC:UPI0000173733

A;Note: sequence determined from the germline H107 gene

R;Rudikoff, S.; Barstad, P.; Potter, M.; Hood, L.

unpublished results, cited by Hood, L., Campbell, J.H., and Elgin, S.C.R., Annu. Rev. Ger

A;Reference number: A94474

A;Contents: S107

A;Accession: A94474

A;Molecule type: protein

A;Residues: 1-123 <RU2>

A;Cross-references: UNIPARC:UPI000002710F

R;Barstad, P.

Ph.D. thesis, California Institute of Technology, Pasadena, 1975, cited by Hood, L., Cam

A;Reference number: A94449

A;Contents: H8

A;Accession: A94449

A;Molecule type: protein

A;Residues: 1-104,'B',106-123 <BAR>

A;Cross-references: UNIPARC:UPI0000027110

R;Gearhart, P.J.; Johnson, N.D.; Douglas, R.; Hood, L.

Nature 291, 29-34, 1981

A;Title: IgG antibodies to phosphorylcholine exhibit more diversity than their IgM count

A;Reference number: A93256; MUID:81197602; PMID:7231520

A;Accession: A93256

A;Molecule type: protein

A;Residues: 1-123 <GEA>

A;Cross-references: UNIPARC:UPI000002710F

A;Experimental source: hybridoma proteins HPCW1, HPCW2, HPCW3

R;Claflin, J.L.; Berry, J.

J. Immunol. 141, 4012-4019, 1988

A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneu

A;Reference number: A30534; MUID:89035545; PMID:3141511

A;Accession: C30539

A;Status: nucleic acid

A;Molecule type: mRNA

A;Residues: 1-123 <CLA>

A;Cross-references: UNIPARC:UPI000002710F

A;Experimental source: hybridoma proteins 224.2B8, 224.2G3

A;Accession: I30539

A;Status: nucleic acid

A;Molecule type: mRNA

A;Residues: 1-123 <CL2>

A;Cross-references: UNIPARC:UPI000002710F
A;Experimental source: hybridoma proteins 252.5E11, 253.12G5
A;Accession: B30539
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-121 <CL3>
A;Cross-references: UNIPARC:UPI0000173734
A;Experimental source: hybridoma protein 174.2E11
C;Comment: These chains were isolated from myeloma and hybridoma proteins that bind phos
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; hybridoma; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>
F;22-98/Disulfide bonds: #status predicted

Query Match 62.1%; Score 41; DB 1; Length 123;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YWYFDV 11
Db 107 YWYFDV 112

RESULT 35
PL0017
Ig heavy chain V-D-J region (P28) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Aug-1996
C;Accession: PL0017
R;Chien, N.C.; Pollock, R.R.; Desaynard, C.; Scharff, M.D.
J. Exp. Med. 167, 954-973, 1988
A;Title: Point mutations cause the somatic diversification of IgM and IgG2a antiphospho
A;Reference number: JL0029; MUID:88171315; PMID:3127529
A;Accession: PL0017
A;Molecule type: mRNA
A;Residues: 1-123 <CHI>
A;Cross-references: UNIPARC:UPI0000176C41
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-101/Domain: V region (fragment) <VRE>
F;15-100/Domain: immunoglobulin homology <IMM>
F;102-106/Domain: D region <DRE>
F;107-123/Domain: J region (fragment) <JRE>

Query Match 62.1%; Score 41; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YWYFDV 11
Db 107 YWYFDV 112

RESULT 36
B30540
Ig heavy chain V region (253.15D10) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 16-Aug-1996
C;Accession: B30540
R;Claflin, J.L.; Berry, J.
J. Immunol. 141, 4012-4019, 1988
A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneu
A;Reference number: A30534; MUID:89035545; PMID:3141511
A;Accession: B30540
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-123 <CLA>
A;Cross-references: UNIPARC:UPI0000176D24
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>

Query Match 62.1%; Score 41; DB 2; Length 123;

Best Local Similarity 100.0%; Pred. No. 7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YWYFDV 11
Db 107 YWYFDV 112

RESULT 37
B30556
Ig heavy chain V region (2B2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Feb-1989 #sequence_revision 23-Feb-1989 #text_change 16-Aug-1996
C;Accession: B30556
R;Claflin, J.L.; Berry, J.; Flaherty, D.; Dunnick, W.
J. Immunol. 138, 3060-3068, 1987
A;Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced wit
A;Reference number: A30556; MUID:87196439; PMID:3106498
A;Accession: B30556
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-123 <CLA>
A;Cross-references: UNIPARC:UPI0000176C3C
A;Note: the sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>

Query Match 62.1%; Score 41; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YWYFDV 11
Db 107 YWYFDV 112

RESULT 38
D30539
Ig heavy chain V region (224.2B11) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 16-Aug-1996
C;Accession: D30539
R;Claflin, J.L.; Berry, J.
J. Immunol. 141, 4012-4019, 1988
A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneu
A;Reference number: A30534; MUID:89035545; PMID:3141511
A;Accession: D30539
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-123 <CLA>
A;Cross-references: UNIPARC:UPI0000176D29
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>

Query Match 62.1%; Score 41; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YWYFDV 11
Db 107 YWYFDV 112

RESULT 39
B30560
Ig heavy chain V region (28.4.10A) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 23-Jul-1999
C;Accession: B30560
R;Matsuda, T.; Kabat, E.A.
J. Immunol. 142, 863-870, 1989

A;Title: Variable region cDNA sequences and antigen binding specificity of mouse monoclonal antibody 1A10 (MOPC 511).
A;Reference number: A30560; MUID:89110062; PMID:2464028
A;Accession: B30560
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-123 <MAT>
A;Cross-references: UNIPARC:UPI0000114E20; GB:M24269; NID:g195619; PIDN:AAA38373.1; PID:195619
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 62.1%; Score 41; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YWYFDV 11
Db 107 YWYFDV 112

RESULT 40
A;Title: Ig heavy chain V region (M511) - mouse (tentative sequence)
A;Reference number: A93857; MUID:81054880; PMID:6776528
A;Accession: B93857
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-124 <ROB>
A;Cross-references: UNIPARC:UPI0000173735
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>
F;22-98/Disulfide bonds: #status predicted

Query Match 62.1%; Score 41; DB 1; Length 124;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YWYFDV 11
Db 108 YWYFDV 113

RESULT 41
A;Title: Ig heavy chain precursor V-D-J region (clone pCP12) - mouse (fragment)
A;Reference number: A93857; MUID:81054880; PMID:6776528
A;Accession: B93857
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-137 <REI>
A;Cross-references: UNIPARC:UPI0000115093; EMBL:Y00743; NID:g52483; PIDN:CAA68712.1; PID:115093
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region pCP12 #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
F;118-120/Domain: D region #status predicted <DRE>
F;121-137/Domain: J region #status predicted <JRE>

A;Title: cytochrome-c oxidase (EC 1.9.3.1) chain III - Trypanosoma brucei mitochondrion (fragment)
A;Reference number: A28782; MUID:88210466; PMID:2452697
A;Accession: A28782
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-181 <FEA>
A;Cross-references: UNIPROT:Q35993; UNIPARC:UPI00001751A6
C;Superfamily: cytochrome-c oxidase chain III
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane;
F;1-181/Domain: cytochrome-c oxidase chain III

Query Match 62.1%; Score 41; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VFYWF 9
Db 32 VFYWF 37

RESULT 43
A;Title: cytochrome-c oxidase (EC 1.9.3.1) chain III - Leishmania tarentolae mitochondrion (fragment)
A;Reference number: A22848; MUID:85079995; PMID:6096360
A;Accession: G22848
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-284
A;Cross-references: UNIPROT:P14546; UNIPARC:UPI00001280D7; GB:M10126
C;Superfamily: cytochrome-c oxidase chain III
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane;
F;1-284/Domain: cytochrome-c oxidase chain III

Query Match 62.1%; Score 41; DB 2; Length 284;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VFYWF 9
Db 135 VFYWF 140

RESULT 44
A;Title: cytochrome-c oxidase (EC 1.9.3.1) chain III - Crithidia fasciculata mitochondrion (fragment)
A;Reference number: A25877; MUID:85079995; PMID:6096360
A;Accession: G22848
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-284
A;Cross-references: UNIPROT:P14546; UNIPARC:UPI00001280D7; GB:M10126
C;Superfamily: cytochrome-c oxidase chain III
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane;
F;1-284/Domain: cytochrome-c oxidase chain III

R;Sloof, P.; van den Burg, J.; Voogd, A.; Benne, R.
Nucleic Acids Res. 15, 51-65, 1987

A;Title: The nucleotide sequence of a 3.2 kb segment of mitochondrial maxicircle DNA from
cytochrome b gene and a possible frameshift gene; further evidence for the use of unusual
A;Reference number: A25877; MUID:87146364; PMID:3029678

A;Accession: A25877
A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-287 <SLO>

A;Cross-references: UNIPARC:UPI00001751A5

C;Genetics:

A;Genome: mitochondrion

A;Genetic code: SGC6

C;Superfamily: cytochrome-c oxidase chain III

C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 62.1%; Score 41; DB 2; Length 287;
Best Local Similarity 100.0%; Pred. No. 16;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VFYWF 9

Db 138 VFYWF 143

RESULT 45

E82848

alpha-ketoglutarate permease symporter XF0087 [imported] - Xylella fastidiosa (strain 9a

C;Species: Xylella fastidiosa

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: E82848

R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: A82515; MUID:20365717; PMID:10910347

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: E82848

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-435 <STM>

A;Cross-references: UNIPROT:Q9PH59; UNIPARC:UPI00000C22C8; GB:AE003863; GB:AE003849; NID

A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H

as-Neto, E.; Docena, C.; El-Dorfy, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Mazino, C.L.; Marques, M.V.; Martins, E

A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

. F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A;Authors: da Silva, A.C.R.; da Silva, P.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tshunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A;Reference number: A59328

A;Contents: annotation

C;Genetics:

A;Gene: XF0087

C;Superfamily: citrate utilization determinant

Query Match 62.1%; Score 41; DB 2; Length 435;

Best Local Similarity 85.7%; Pred. No. 24;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ETVFYWF 8

Db 403 ETVFFWF 409

RESULT 46

A25941

Ig heavy chain J-H1 region - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999

C;Accession: A25941; JH0666

R;Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, S.; Waldmann, H.

Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986

A;Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse antibody

A;Reference number: A25941; MUID:86287397; PMID:3016742

A;Accession: A25941

A;Molecule type: DNA

A;Residues: 1-18 <BRU>

A;Cross-references: UNIPARC:UPI0000114C27; GB:M13798; NID:g204707; PIDN:AAA41371.1; PID:

R;Lang, P.; Mocikat, R.

Gene 102, 261-264, 1991

A;Title: Immunoglobulin heavy-chain joining genes in the rat: comparison with mouse and

A;Reference number: JH0666; MUID:91340162; PMID:1908401

A;Accession: JH0666

A;Molecule type: DNA

A;Residues: 1-18 <LAN>

A;Cross-references: UNIPARC:UPI0000114C27; EMBL:X56791

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 60.6%; Score 40; DB 2; Length 18;

Best Local Similarity 83.3%; Pred. No. 1.6;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FYWYFD 10

Db 1 YYWYFD 6

RESULT 47

T37538

hypothetical protein SPAC11E3.10 - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: T37538

R;Murphy, L.; Harziz, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.

submitted to the EMBL Data Library, August 1997

A;Reference number: Z21721

A;Accession: T37538

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-162 <MUR>

A;Cross-references: UNIPROT:O13689; UNIPARC:UPI000013AA46; EMBL:Z98595; PIDN:CAB11189.2;

A;Experimental source: strain 972h-; cosmid c11E3

C;Genetics:

A;Gene: SPDB:SPAC11E3.10

A;Map position: 1

A;Introns: 21/2; 29/2; 91/3; 101/3

Query Match 60.6%; Score 40; DB 2; Length 162;

Best Local Similarity 75.0%; Pred. No. 13;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 VFYWFYFDV 11

Db 55 VFYWFYFDL 62

RESULT 48

AE3196

conserved hypothetical protein Atus299 [imported] - Agrobacterium tumefaciens (strain CS

C;Species: Agrobacterium tumefaciens

C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 02-Jun-2003

C;Accession: AE3196

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUID:2160850; PMID:11743193

A;Accession: AE3196
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-364 <KUR>
A;Cross-references: UNIPARC:UPI00000D158A; GB:AE008687; PIDN:AAL45987.1; PID:gl7743741;
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu5299
A;Genome: plasmid
C;Superfamily: uncharacterized conserved protein

Query Match 60.6%; Score 40; DB 2; Length 364;
Best Local Similarity 83.3%; Pred. No. 29;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YWYFDV 11
|
Db 44 YWYFDI 49

RESULT 49

G89009
Protein R08F11.5 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: G89009
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biological processes
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.elegans/
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 283, 2103, 1999
A;Accession: G89009
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-381 <STO>
A;Cross-references: UNIPROT:O01880; UNIPARC:UPI00000805EF; GB:chr_V; PIDN:AAB54247.1; PID:gl7743741
C;Genetics:
A;Gene: R08F11.5
A;Map position: 5

Query Match 60.6%; Score 40; DB 2; Length 381;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ETVFYWYFD 10
|
Db 21 EESFYWYFN 29

RESULT 50

A83616
dicarboxylic acid transporter PcaT PA0229 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: A83616
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Brinkman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83616
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-432 <STO>
A;Cross-references: UNIPROT:Q9T6Q9; UNIPARC:UPI00000C4FAC; GB:AE004461; GB:AE004091; NID:gl7743741
A;Experimental source: strain PA01
C;Genetics:
A;Gene: pcaT; PA0229
C;Superfamily: citrate utilization determinant

Query Match 60.6%; Score 40; DB 2; Length 432;

Best Local Similarity 85.7%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ETVFYWY 8
|
Db 398 ENVFYWY 404

Search completed: February 23, 2006, 09:51:54
Job time : 25.5692 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 09:29:53 ; Search time 94.7692 Seconds
(without alignments)
81.892 Million cell updates/sec

Title: US-10-723-872-26
Perfect score: 66
Sequence: 1 RETVFWYFDV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

Database :

UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 45 | 68.2 | 635 | 2 | Q4IQ63 gibberella |
| 2 | 44 | 66.7 | 108 | 2 | Q6H025 sulfolobus |
| 3 | 44 | 66.7 | 197 | 2 | Q4N322 MICC |
| 4 | 43 | 65.2 | 222 | 2 | Q90303 9VIRU |
| 5 | 43 | 65.2 | 244 | 2 | Q8BV32 MOUSE |
| 6 | 43 | 65.2 | 244 | 2 | Q9DCS1 MOUSE |
| 7 | 42 | 63.6 | 251 | 2 | Q9ENN7 9PICO |
| 8 | 42 | 63.6 | 437 | 2 | Q8XTN1 RALSO |
| 9 | 42 | 63.6 | 617 | 2 | Q569B3 RAT |
| 10 | 41 | 62.1 | 34 | 2 | Q4XG06 PLACH |
| 11 | 41 | 62.1 | 111 | 2 | Q7GHK8 9TRYP |
| 12 | 41 | 62.1 | 117 | 1 | HV13 MOUSE |
| 13 | 41 | 62.1 | 122 | 1 | HV21 MOUSE |
| 14 | 41 | 62.1 | 123 | 1 | HV18 MOUSE |
| 15 | 41 | 62.1 | 123 | 1 | HV19 MOUSE |
| 16 | 41 | 62.1 | 123 | 1 | HV23 MOUSE |
| 17 | 41 | 62.1 | 123 | 1 | HV24 MOUSE |
| 18 | 41 | 62.1 | 144 | 2 | Q924P5 MOUSE |
| 19 | 41 | 62.1 | 276 | 2 | Q4UB94 THEAN |
| 20 | 41 | 62.1 | 284 | 1 | COX3 LEITA |
| 21 | 41 | 62.1 | 287 | 2 | Q34935 LEITA |
| 22 | 41 | 62.1 | 288 | 2 | Q33549 9TRYP |
| 23 | 41 | 62.1 | 288 | 2 | Q35993 trypanosoma |
| 24 | 41 | 62.1 | 305 | 2 | Q5X2F2 LEIGH |
| 25 | 41 | 62.1 | 305 | 2 | Q5ZS20 LEIGH |
| 26 | 41 | 62.1 | 429 | 1 | SVN THEVO |
| 27 | 41 | 62.1 | 435 | 2 | Q87F73 XYLEFT |
| 28 | 41 | 62.1 | 435 | 2 | Q8PH59 XYLFA |
| 29 | 41 | 62.1 | 463 | 2 | Q87JUR8 VIBPA |
| 30 | 41 | 62.1 | 467 | 2 | Q9G0U3 LEIGH |
| 31 | 41 | 62.1 | 467 | 2 | Q4VK76 pectobacter |

| | | | | | |
|-----|------|------|------|---|--------------|
| 32 | 41 | 62.1 | 467 | 2 | Q6D9F4 ERWCT |
| 33 | 41 | 62.1 | 468 | 2 | Q6QGY5 PECCC |
| 34 | 41 | 62.1 | 470 | 2 | Q7TMK1 MOUSE |
| 35 | 41 | 62.1 | 475 | 2 | Q6MZ06 HUMAN |
| 36 | 41 | 62.1 | 480 | 2 | Q91XE1 MOUSE |
| 37 | 41 | 62.1 | 480 | 2 | Q63MC5 BURPS |
| 38 | 41 | 62.1 | 480 | 2 | Q62BC6 BURMA |
| 39 | 41 | 62.1 | 480 | 2 | Q6NND0 DROME |
| 40 | 41 | 62.1 | 480 | 2 | Q9VA05 DROME |
| 41 | 40.5 | 61.4 | 287 | 2 | Q9EMR6 AMEPV |
| 42 | 40 | 60.6 | 62 | 2 | Q4XRH5 PLACH |
| 43 | 40 | 60.6 | 127 | 2 | Q59YX1 CANAL |
| 44 | 40 | 60.6 | 133 | 2 | Q7V077 PROMP |
| 45 | 40 | 60.6 | 162 | 1 | YDYA SCHPO |
| 46 | 40 | 60.6 | 213 | 2 | Q4KA56 PSEF5 |
| 47 | 40 | 60.6 | 231 | 2 | Q9MT27 NASPA |
| 48 | 40 | 60.6 | 231 | 2 | Q7NBS0 MYCGA |
| 49 | 40 | 60.6 | 348 | 2 | Q4WV37 ASPFU |
| 50 | 40 | 60.6 | 364 | 2 | Q8KKU1 RHET |
| 51 | 40 | 60.6 | 364 | 2 | Q8UK25 AGRT5 |
| 52 | 40 | 60.6 | 381 | 2 | Q01888 CAEEL |
| 53 | 40 | 60.6 | 429 | 1 | SVN THEAC |
| 54 | 40 | 60.6 | 432 | 2 | Q9I6Q9 FSEAE |
| 55 | 40 | 60.6 | 442 | 2 | Q9MSY8 NASPA |
| 56 | 40 | 60.6 | 476 | 2 | Q4VMU7 XENLA |
| 57 | 40 | 60.6 | 539 | 2 | Q5SMV1 ORYSA |
| 58 | 40 | 60.6 | 550 | 1 | PUTX EMENI |
| 59 | 40 | 60.6 | 552 | 2 | Q5BCJ8 EMENI |
| 60 | 40 | 60.6 | 629 | 2 | Q9Y819 SCHPO |
| 61 | 40 | 60.6 | 783 | 2 | Q8WZY8 NEUCR |
| 62 | 40 | 60.6 | 793 | 2 | Q7RWZ1 NEUCR |
| 63 | 40 | 60.6 | 946 | 2 | Q6LP07 PHOPR |
| 64 | 39 | 59.1 | 29 | 2 | Q4X9B5 PLACH |
| 65 | 39 | 59.1 | 29 | 2 | Q6I9I1 MOUSE |
| 66 | 39 | 59.1 | 49 | 2 | Q7IWI1 LISMF |
| 67 | 39 | 59.1 | 75 | 2 | F89294 GVXN |
| 68 | 39 | 59.1 | 157 | 2 | Q4FYG8 LEIMA |
| 69 | 39 | 59.1 | 196 | 2 | Q7UK94 RHOPA |
| 70 | 39 | 59.1 | 212 | 2 | Q5LMW7 SILPO |
| 71 | 39 | 59.1 | 296 | 2 | Q6D370 ERWCT |
| 72 | 39 | 59.1 | 313 | 2 | Q8R7K6 THETN |
| 73 | 39 | 59.1 | 336 | 2 | Q4RJA5 TETNG |
| 74 | 39 | 59.1 | 397 | 2 | Q7PK40 ANOGA |
| 75 | 39 | 59.1 | 397 | 2 | Q8GIH2 BRUSU |
| 76 | 39 | 59.1 | 397 | 2 | Q8YGE9 BRUME |
| 77 | 39 | 59.1 | 440 | 2 | Q54US8 DICDI |
| 78 | 39 | 59.1 | 456 | 2 | Q4ITI9 AZOVI |
| 79 | 39 | 59.1 | 469 | 2 | Q9PZ03 GVXN |
| 80 | 39 | 59.1 | 481 | 2 | Q8FHE1 ECOL6 |
| 81 | 39 | 59.1 | 483 | 2 | Q61GF2 CAEBR |
| 82 | 39 | 59.1 | 497 | 2 | Q9SQN2 ARATH |
| 83 | 39 | 59.1 | 521 | 2 | Q4H184 NASPA |
| 84 | 39 | 59.1 | 533 | 2 | Q9AZX4 9CAUD |
| 85 | 39 | 59.1 | 533 | 2 | Q9CGP4 LACLA |
| 86 | 39 | 59.1 | 555 | 2 | Q88SR7 LACPL |
| 87 | 39 | 59.1 | 556 | 2 | Q87548 BACFI |
| 88 | 39 | 59.1 | 585 | 2 | Q6KSK7 ORYSA |
| 89 | 39 | 59.1 | 749 | 2 | F73218 SINY3 |
| 90 | 39 | 59.1 | 844 | 2 | Q9JH67 9VIRU |
| 91 | 39 | 59.1 | 855 | 2 | Q8ZVP9 PYRAE |
| 92 | 39 | 59.1 | 1153 | 2 | Q7PAP8 RICSI |
| 93 | 39 | 59.1 | 1153 | 2 | Q92JC1 RICCN |
| 94 | 39 | 59.1 | 1154 | 2 | Q68XK6 RICTY |
| 95 | 39 | 59.1 | 1155 | 2 | Q4UNB4 RICFE |
| 96 | 39 | 59.1 | 1155 | 2 | Q9ZE40 RICPR |
| 97 | 39 | 59.1 | 1608 | 2 | Q54VR7 DICDI |
| 98 | 38 | 57.6 | 98 | 2 | Q8DQJ2 STRR6 |
| 99 | 38 | 57.6 | 116 | 2 | Q9UL89 HUMAN |
| 100 | 38 | 57.6 | 120 | 2 | Q4YRH2 PLABE |
| 101 | 38 | 57.6 | 215 | 2 | Q8DRK9 FSEPK |
| 102 | 38 | 57.6 | 225 | 2 | Q08377 MYCTU |
| 103 | 38 | 57.6 | 225 | 2 | Q7VEZ1 MYCBO |
| 104 | 38 | 57.6 | 240 | 2 | Q8D312 WIGBR |

| | |
|--------|--------------|
| Q6D9F4 | erwinia car |
| Q6QGY5 | pectobacter |
| Q7TMK1 | mus musculus |
| Q6MZ06 | homo sapien |
| Q91XE1 | mus musculus |
| Q63MC5 | burkholderi |
| Q62BC6 | burkholderi |
| Q6NND0 | drosohila |
| Q9VA05 | drosohila |
| Q9EMR6 | anaeacta moo |
| Q4XRH5 | plasmidium |
| Q59YX1 | candida alb |
| Q7V077 | prochloro |
| Q13689 | schizosacch |
| Q4KA56 | pseudomonas |
| Q9MT27 | apodolirion |
| Q7NBS0 | mycoplasma |
| Q4WV37 | aspergillus |
| Q8KKU1 | rhizobium e |
| Q8UK25 | agrobacteri |
| Q01888 | caenorhabdi |
| Q8K87 | thermoplasma |
| Q9I6Q9 | pseudomonas |
| Q9MSY8 | ungernia fl |
| Q4VMU7 | xenopus lae |
| Q5SMV1 | oryza sativ |
| P18696 | emeritella |
| Q5BCJ8 | aspergillus |
| Q9Y819 | schizosacch |
| Q8WZY8 | neurospora |
| Q7RWZ1 | neurospora |
| Q6LP07 | photobacter |
| Q4X9B5 | plasmidium |
| Q6I9I1 | mus musculus |
| Q7IWI1 | listeria mo |
| P89294 | xestia c-ni |
| Q4FYG8 | leishmania |
| Q7UK94 | rhodopirell |
| Q5LMW7 | silicibacte |
| Q6D370 | erwinia car |
| Q8R7K6 | thermoanaer |
| Q4RJA5 | tetradodon n |
| Q7PK40 | anophella su |
| Q8GIH2 | brucella su |
| Q8YGE9 | brucella me |
| Q54US8 | dictyosteli |
| Q4ITI9 | azotobacter |
| Q9PZ03 | xestia c-ni |
| Q8FHE1 | escherichia |
| Q61GF2 | caenorhabdi |
| Q9SQN2 | arabidopsis |
| Q4H184 | romulea mon |
| Q9AZX4 | bacterioph |
| Q9CGP4 | lactococcus |
| Q88SR7 | lactobacill |
| Q87548 | bacillus fi |
| Q6KSK7 | oryza sativ |
| P73218 | synecocyst |
| Q9JH67 | ovine astro |
| Q8ZVP9 | pyrobaculum |
| Q7PAP8 | rickettsia |
| Q92JC1 | rickettsia |
| Q68XK6 | rickettsia |
| Q4UNB4 | rickettsia |
| Q9ZE40 | rickettsia |
| Q54VR7 | dictyosteli |
| Q8DQJ2 | streptococ |
| Q9UL89 | homo sapien |
| Q4YRH2 | plasmidium |
| Q8DRK9 | pseudomonas |
| Q08377 | mycobacteri |
| Q7VEZ1 | mycobacteri |
| Q8D312 | wiggleswort |

| | | | | | | | | | | | | | |
|-----|----|------|------|---|---------------|---------------------|-----|----|------|------|---|--------------|--------------------|
| 105 | 38 | 57.6 | 242 | 2 | Q8WL10_9CHLO | O8w110 ankistodes | 178 | 37 | 56.1 | 226 | 2 | Q56RS4_DROAI | Q56rs4 drosophila |
| 106 | 38 | 57.6 | 256 | 2 | Q9PNV1_CAMJE | Q9pnv1 campylobact | 179 | 37 | 56.1 | 238 | 2 | Q911R4_PSEAE | Q911r4 pseudomonas |
| 107 | 38 | 57.6 | 266 | 2 | Q7MT39_PAGRT1 | Q7mt39 porphyromon | 180 | 37 | 56.1 | 242 | 2 | Q67NV8_SYMTH | Q67nv8 symbiobacte |
| 108 | 38 | 57.6 | 304 | 2 | Q8U1H7_AGRG1 | Q8u1h7 agrobacteri | 181 | 37 | 56.1 | 247 | 2 | Q7S1B7_NEUCR | Q7s1b7 neutrospora |
| 109 | 38 | 57.6 | 313 | 2 | Q7D1P6_AGRG1 | Q7d1p6 agrobacteri | 182 | 37 | 56.1 | 271 | 2 | Q7NC30_MYCGA | Q7nc30 mycoplasma |
| 110 | 38 | 57.6 | 328 | 2 | Q53847_SPICT | Q53847 spioplasma | 183 | 37 | 56.1 | 272 | 2 | Q6WMW6_DROLT | Q6wmw6 drosophila |
| 111 | 38 | 57.6 | 357 | 2 | Q8U6E8_AGRG1 | Q8u6e8 agrobacteri | 184 | 37 | 56.1 | 278 | 1 | ADHR_DROPE | ADHR drosophila |
| 112 | 38 | 57.6 | 388 | 2 | Q5E418_VIBF1 | Q5e418 vibrio fisc | 185 | 37 | 56.1 | 278 | 1 | ADHR_DROPS | ADHR drosophila |
| 113 | 38 | 57.6 | 392 | 2 | Q6DAK9_ERWCT | Q6dak9 erwinia car | 186 | 37 | 56.1 | 279 | 1 | ADHR_DROGU | ADHR drosophila |
| 114 | 38 | 57.6 | 393 | 1 | YHDX_ECOLI | F45767 escherichia | 187 | 37 | 56.1 | 279 | 1 | ADHR_DROMD | ADHR drosophila |
| 115 | 38 | 57.6 | 393 | 2 | Q8X5G4_ECO57 | Q8x5g4 escherichia | 188 | 37 | 56.1 | 279 | 1 | ADHR_DROSD | ADHR drosophila |
| 116 | 38 | 57.6 | 397 | 2 | Q8SQO8_ENCCU | Q8sqo8 escherichia | 188 | 37 | 56.1 | 279 | 1 | ADHR_DROSD | ADHR drosophila |
| 117 | 38 | 57.6 | 398 | 2 | Q4IH34_GIBZEA | Q4ih34 gibberellito | 189 | 37 | 56.1 | 281 | 1 | ADHR_DROAM | ADHR drosophila |
| 118 | 38 | 57.6 | 399 | 2 | Q7AAE5_ECO57 | Q7aae5 escherichia | 190 | 37 | 56.1 | 288 | 2 | Q79350_HERME | Q79350 herpetomona |
| 119 | 38 | 57.6 | 399 | 2 | Q8PD23_ECOL6 | Q8pd23 escherichia | 191 | 37 | 56.1 | 288 | 2 | Q79351_HERMU | Q79351 herpetomona |
| 120 | 38 | 57.6 | 401 | 2 | Q8TF97_VIBPA | Q8tf97 vibrio para | 192 | 37 | 56.1 | 288 | 2 | Q79354_9TRYP | Q79354 herpetomona |
| 121 | 38 | 57.6 | 401 | 2 | Q8D9A0_VIBVU | Q8d9a0 vibrio vuln | 193 | 37 | 56.1 | 288 | 2 | Q6SGW8_9BACT | Q6sgw8 uncultured |
| 122 | 38 | 57.6 | 401 | 2 | Q7ML71_VIBVY | Q7ml71 vibrio vuln | 194 | 37 | 56.1 | 314 | 2 | Q5FKI8_LACAC | Q5fki8 lactobacill |
| 123 | 38 | 57.6 | 403 | 2 | Q6LO44_PHOPR | Q6lo44 photobacter | 195 | 37 | 56.1 | 329 | 2 | Q5EGM1_CYTJO | Q5egm1 cytophaga j |
| 124 | 38 | 57.6 | 419 | 2 | Q5ILJ1_POLPA | Q5ilj1 polyphondy | 196 | 37 | 56.1 | 329 | 2 | Q5EGM2_CYTJO | Q5egm2 cytophaga j |
| 125 | 38 | 57.6 | 419 | 2 | AGN1_SCHPO | Q13716 schizosacch | 197 | 37 | 56.1 | 332 | 2 | Q4HJK7_CAMLA | Q4hjk7 campylobact |
| 126 | 38 | 57.6 | 435 | 2 | Q21049_DICDI | O21049 dictyosteli | 198 | 37 | 56.1 | 347 | 1 | C5AH_MOUSE | F30993 mus musculu |
| 127 | 38 | 57.6 | 450 | 2 | Q62EG0_BURMA | Q62eg0 burkholderi | 199 | 37 | 56.1 | 348 | 2 | Q51ER6_ENTHI | Q51er6 entamoeba h |
| 128 | 38 | 57.6 | 450 | 2 | Q63P83_BURPS | Q63p83 burkholderi | 200 | 37 | 56.1 | 362 | 2 | Q930T5_RHIME | Q930t5 rhizobium m |
| 129 | 38 | 57.6 | 470 | 2 | Q6JAF8_DICVI | Q6jaf8 dictyocaulu | 201 | 37 | 56.1 | 380 | 2 | Q5TP31_ANOGA | Q5tp31 anopheles g |
| 130 | 38 | 57.6 | 470 | 2 | Q6JAF8_DICVI | Q6jaf8 dictyocaulu | 202 | 37 | 56.1 | 386 | 2 | Q4YQ22_PLABE | Q4yq22 plasmodium |
| 131 | 38 | 57.6 | 474 | 1 | EGL2_BAGSU | Q97k37 clostridium | 203 | 37 | 56.1 | 392 | 2 | Q4RP04_TETNG | Q4rp04 tetraodon n |
| 132 | 38 | 57.6 | 477 | 1 | Q9LBY1_ARATH | F42403 bacillus su | 204 | 37 | 56.1 | 397 | 2 | Q5FWR1_XENTR | Q5fwr1 xenopus tro |
| 133 | 38 | 57.6 | 480 | 2 | Q86291_LACPL | Q9ley1 arabisodpis | 205 | 37 | 56.1 | 401 | 2 | Q9KS98_VIBCH | Q9ks98 vibrio chol |
| 134 | 38 | 57.6 | 480 | 2 | Q88291_LACPL | Q86291 lactobacill | 206 | 37 | 56.1 | 402 | 2 | Q4NGW9_9MICC | Q4ngw9 arthrobacte |
| 135 | 38 | 57.6 | 482 | 2 | Q4H304_CIOIN | O88aa8 lactobacill | 207 | 37 | 56.1 | 412 | 2 | Q4Y4F6_PLACH | Q4y4f6 plasmodium |
| 136 | 38 | 57.6 | 492 | 2 | Q6JAF7_DICVI | O4h304 ciona intes | 208 | 37 | 56.1 | 416 | 2 | Q6KHU9_MYCWO | Q6khu9 mycoplasma |
| 137 | 38 | 57.6 | 521 | 2 | Q5B797_EMENI | O6jaf7 dictyocaulu | 209 | 37 | 56.1 | 426 | 1 | YHFN_BACSU | P40769 bacillus su |
| 138 | 38 | 57.6 | 544 | 2 | Q5B797_EMENI | Q5b79 aspergillus | 210 | 37 | 56.1 | 426 | 2 | Q6DIC6_ERWCT | Q6dic6 erwinia car |
| 139 | 38 | 57.6 | 588 | 2 | Q410G1_GIBZE | O410g1 gibberella | 211 | 37 | 56.1 | 432 | 1 | KGTP_ECOLI | F17448 escherichia |
| 140 | 38 | 57.6 | 632 | 2 | Q5JZ54_ARATH | O22717 arabisodpis | 212 | 37 | 56.1 | 432 | 2 | Q7AB19_ECO57 | Q7ab19 escherichia |
| 141 | 38 | 57.6 | 653 | 2 | Q5JZ54_ARATH | Q93z54 arabisodpis | 213 | 37 | 56.1 | 432 | 2 | Q8X9P3_ECO57 | Q8x9p3 escherichia |
| 142 | 38 | 57.6 | 657 | 2 | Q4UKL1_AGRG1 | O5jz54 pyrococcus | 214 | 37 | 56.1 | 434 | 2 | Q67YF0_ARATH | Q67yf0 arabisodpis |
| 143 | 38 | 57.6 | 688 | 2 | Q4WTV1_ASPFU | O8uk11 agrobacteri | 215 | 37 | 56.1 | 434 | 2 | Q41RBL_9BURK | Q41rb1 burkholderi |
| 144 | 38 | 57.6 | 689 | 2 | Q9CINI_PENMA | Q9cni1 penicillium | 216 | 37 | 56.1 | 434 | 2 | Q63TZ2_BURPS | Q63tz2 burkholderi |
| 145 | 38 | 57.6 | 692 | 1 | STEA_EMENI | Q4wtv1 aspergillus | 217 | 37 | 56.1 | 436 | 1 | THIC_CLOPE | Q8xm9 clostridium |
| 146 | 38 | 57.6 | 692 | 2 | Q5BAZ0_EMENI | Q70yv7 colletotric | 218 | 37 | 56.1 | 458 | 2 | Q8TVI3_METKA | Q8tv13 methanopyru |
| 147 | 38 | 57.6 | 695 | 2 | Q8NKD8_GIBZE | Q74252 emericella | 219 | 37 | 56.1 | 463 | 2 | Q8FF02_ECOL6 | Q8ff02 escherichia |
| 148 | 38 | 57.6 | 695 | 2 | Q4I648_GIBZE | O5baz0 aspergillus | 220 | 37 | 56.1 | 464 | 2 | Q6D617_ERWCT | Q6d617 erwinia car |
| 149 | 38 | 57.6 | 697 | 2 | Q8NK75_GLOLA | O8nk48 gibberella | 221 | 37 | 56.1 | 467 | 2 | Q4X016_ASPFU | Q4x016 aspergillus |
| 150 | 38 | 57.6 | 705 | 2 | Q70Y17_COLLN | O8nk75 glomerella | 222 | 37 | 56.1 | 477 | 2 | Q8EVV3_MYCPE | Q8evv3 mycoplasma |
| 151 | 38 | 57.6 | 715 | 2 | Q96UQ9_MAGGR | Q70yv7 colletotric | 223 | 37 | 56.1 | 479 | 2 | Q67QV4_SYMTH | Q67qv4 symbiobacte |
| 152 | 38 | 57.6 | 734 | 2 | Q6BZD4_DEBHA | Q96uq9 magnaporthe | 224 | 37 | 56.1 | 484 | 2 | Q5SMV5_ORYSA | Q5smv5 oryza sativ |
| 153 | 38 | 57.6 | 785 | 1 | ISP4_SCHPO | Q6bzd4 debaryomyce | 225 | 37 | 56.1 | 487 | 2 | Q7MBA5_PHOLL | Q7mba5 photorhabdu |
| 154 | 38 | 57.6 | 843 | 2 | Q5KVV3_CRYNE | P40900 schizosacch | 226 | 37 | 56.1 | 487 | 2 | Q5BK15_RAT | Q5bk15 rattus norv |
| 155 | 38 | 57.6 | 843 | 2 | Q5KVV3_CRYNE | Q55vv3 cryptococcu | 227 | 37 | 56.1 | 499 | 2 | Q6P3J0_BRARE | Q6p3j0 brachydanio |
| 156 | 38 | 57.6 | 1032 | 2 | Q4PCQ6_USTNA | Q5k45 cryptococcu | 228 | 37 | 56.1 | 502 | 2 | Q820T6_ENTFA | Q820t6 enterococcu |
| 157 | 38 | 57.6 | 1189 | 2 | Q88Y49_LACPL | Q4p9q6 ustilago ma | 229 | 37 | 56.1 | 506 | 2 | Q7XXJ9_ORYSA | Q7xxj9 oryza sativ |
| 158 | 38 | 57.6 | 1450 | 1 | MPSF_CHICK | O88y49 lactobacill | 230 | 37 | 56.1 | 530 | 2 | Q5B8D5_EMENI | Q5b8d5 aspergillus |
| 159 | 37 | 56.8 | 305 | 2 | Q56074_9FLAV | O2173 gallus gall | 231 | 37 | 56.1 | 532 | 2 | Q6FUS1_CANGA | Q6fus1 candida gla |
| 160 | 37 | 56.8 | 305 | 2 | Q67989_RHOOP | O56074 hepatitis g | 232 | 37 | 56.1 | 548 | 2 | Q4WBG4_ASPFU | Q4wbq4 aspergillus |
| 161 | 37 | 56.1 | 112 | 2 | Q8Z177_PYRAE | O67989 rhodococcus | 233 | 37 | 56.1 | 564 | 2 | Q8AAV7_BACTN | Q8aav7 bacteroides |
| 162 | 37 | 56.1 | 117 | 2 | Q61VE4_STRDR | Q8zy77 pyrobaculum | 234 | 37 | 56.1 | 566 | 2 | Q5ATV8_EMENI | Q5atv8 aspergillus |
| 163 | 37 | 56.1 | 121 | 2 | Q6BYT1_SCHJA | Q61ve4 strongyloce | 235 | 37 | 56.1 | 569 | 2 | Q55F76_DICDI | Q55f76 dictyosteli |
| 164 | 37 | 56.1 | 132 | 2 | Q6CB81_YARLI | O5byt1 schistosoma | 236 | 37 | 56.1 | 591 | 2 | Q4P7G6_USTMA | Q4p7g6 ustilago ma |
| 165 | 37 | 56.1 | 141 | 2 | Q33563_9TRYP | Q6cb81 yarrowia li | 237 | 37 | 56.1 | 598 | 2 | Q568Y0_RAT | Q568y0 rattus norv |
| 166 | 37 | 56.1 | 143 | 2 | Q91V67_MOUSE | Q33563 trypanosoma | 238 | 37 | 56.1 | 621 | 2 | Q9FTF3_ORYSA | Q9ftf3 oryza sativ |
| 167 | 37 | 56.1 | 160 | 2 | Q9Q278_9HYST | Q91v67 mus musculu | 239 | 37 | 56.1 | 629 | 2 | Q4WEU2_ASPFU | Q4weu2 aspergillus |
| 168 | 37 | 56.1 | 167 | 2 | Q85SK4_9TRYP | Q9q278 cavia ep. p | 240 | 37 | 56.1 | 663 | 2 | Q5ZE78_ORYSA | Q5ze78 oryza sativ |
| 169 | 37 | 56.1 | 182 | 2 | Q64W16_BACFR | Q85sk4 trypanosoma | 241 | 37 | 56.1 | 666 | 2 | Q41KS3_GIBZE | Q41ks3 gibberella |
| 170 | 37 | 56.1 | 188 | 2 | Q8TFG8_SCHPO | Q64w16 bacteroides | 242 | 37 | 56.1 | 673 | 2 | Q7SAG1_ASHGO | Q7sag1 ashbya goss |
| 171 | 37 | 56.1 | 189 | 1 | APOD_RAT | O8tfg8 schizosacch | 243 | 37 | 56.1 | 695 | 2 | Q419L8_GIBZE | Q419l8 gibberella |
| 172 | 37 | 56.1 | 199 | 2 | Q8ASC9_BACTN | P23593 rattus norv | 244 | 37 | 56.1 | 731 | 2 | Q73MG2_TREDE | Q73mg2 treponema d |
| 173 | 37 | 56.1 | 207 | 2 | Q5LXN9_SILPO | Q23593 rattus norv | 245 | 37 | 56.1 | 733 | 1 | HEXA_BLADI | Q17127 blaberus di |
| 174 | 37 | 56.1 | 219 | 2 | Q98CA4_RHIL0 | O5lxn9 silicibacte | 246 | 37 | 56.1 | 746 | 2 | Q54N84_DICDI | Q54n84 dictyosteli |
| 175 | 37 | 56.1 | 220 | 2 | Q98326_9TRYP | Q98ca4 rhizobium l | 247 | 37 | 56.1 | 770 | 1 | A4_CAVPO | Q60495 c amyloid b |
| 176 | 37 | 56.1 | 222 | 2 | Q8WFX6_9CHLO | Q98326 trypanosoma | 248 | 37 | 56.1 | 806 | 2 | Q7NKI9_GLOVI | Q7nki9 gloobacter |
| 177 | 37 | 56.1 | 224 | 2 | Q4S256_TETNG | O8wfx6 chlamydomon | 249 | 37 | 56.1 | 961 | 2 | P91184_CAEEL | P91184 caenorhabdi |
| | | | | | | Q4s256 tetraodon n | 250 | 37 | 56.1 | 1021 | 2 | Q9XUV2_CAEEL | Q9xuv2 caenorhabdi |

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|-----|------|------|------|---|--------|-------|--------|--------------|
| 251 | 37 | 56.1 | 1307 | 2 | Q4S2T9 | TETNG | Q4S2t9 | tetraodon n |
| 252 | 37 | 56.1 | 1714 | 1 | SYEP | DROME | P28668 | drosophila |
| 253 | 37 | 56.1 | 1750 | 2 | Q8X0H2 | NEUCR | Q8x0h2 | neuropora |
| 254 | 36.5 | 55.3 | 797 | 2 | Q5SSD4 | HUMAN | Q5ssd4 | homo sapien |
| 255 | 36.5 | 55.3 | 797 | 2 | Q6B7S5 | HUMAN | Q6b7s5 | homo sapien |
| 256 | 36.5 | 55.3 | 968 | 2 | Q6TW58 | METKA | Q6tw58 | methanopyru |
| 257 | 36.5 | 55.3 | 1011 | 1 | M3K6 | HUMAN | Q5S382 | homo sapien |
| 258 | 36.5 | 55.3 | 1148 | 2 | Q5SSD5 | HUMAN | Q5ssd5 | homo sapien |
| 259 | 36.5 | 55.3 | 1192 | 2 | Q59HF4 | HUMAN | Q59hf4 | homo sapien |
| 260 | 36.5 | 55.3 | 1288 | 2 | Q75PK3 | HUMAN | Q75pk3 | homo sapien |
| 261 | 36.5 | 55.3 | 2153 | 2 | Q5YMP8 | NOCFA | Q5ymf8 | nocardia fa |
| 262 | 36 | 54.5 | 47 | 2 | Q4X534 | PLACH | Q4x534 | plasmodium |
| 263 | 36 | 54.5 | 76 | 1 | A4 | MACMU | P29216 | macaca mula |
| 264 | 36 | 54.5 | 81 | 1 | LCR29 | ARATH | P82744 | arabidopsis |
| 265 | 36 | 54.5 | 114 | 2 | Q5RG56 | HUMAN | Q5rgs6 | homo sapien |
| 266 | 36 | 54.5 | 123 | 1 | HV22 | MOUSE | P01791 | mus musculus |
| 267 | 36 | 54.5 | 131 | 2 | Q5M0E7 | STR11 | Q5m0e7 | streptococc |
| 268 | 36 | 54.5 | 131 | 2 | Q5M424 | STR12 | Q5m424 | streptococc |
| 269 | 36 | 54.5 | 133 | 2 | Q4YJ02 | PLABE | Q4yjd2 | plasmodium |
| 270 | 36 | 54.5 | 146 | 2 | Q727C5 | DESVH | Q727c5 | desulfovibr |
| 271 | 36 | 54.5 | 174 | 1 | STA | ECOLI | P13018 | escherichia |
| 272 | 36 | 54.5 | 174 | 2 | Q7A2E7 | ACIBA | Q7aze7 | acinetobact |
| 273 | 36 | 54.5 | 174 | 2 | Q75Q08 | ECOLI | Q75q08 | escherichia |
| 274 | 36 | 54.5 | 174 | 2 | Q8GL35 | SHISO | Q8gl35 | shigella so |
| 275 | 36 | 54.5 | 174 | 2 | Q5XUN9 | PROMI | Q5xun9 | proteus mir |
| 276 | 36 | 54.5 | 174 | 2 | Q6AW76 | 9ENTR | Q6aw76 | salmonella |
| 277 | 36 | 54.5 | 174 | 2 | Q4QZB7 | MORMO | Q4qzb7 | morganella |
| 278 | 36 | 54.5 | 174 | 2 | Q75Q96 | ECOLI | Q75qp6 | escherichia |
| 279 | 36 | 54.5 | 174 | 2 | Q75Q02 | SALEN | Q75qq2 | salmonella |
| 280 | 36 | 54.5 | 174 | 2 | Q75NR5 | SHISO | Q75nr5 | shigella so |
| 281 | 36 | 54.5 | 174 | 2 | Q7AJ11 | ECOLI | Q7aj11 | escherichia |
| 282 | 36 | 54.5 | 174 | 2 | Q4JJ97 | 9BURK | Q4jj97 | burkholderia |
| 283 | 36 | 54.5 | 174 | 2 | Q4H456 | VIBCH | Q4h456 | vibrio chol |
| 284 | 36 | 54.5 | 181 | 2 | Q4CBH5 | YARLI | Q4cbh5 | yarrowia li |
| 285 | 36 | 54.5 | 182 | 2 | Q4ZVK9 | PSESY | Q4zvk9 | pseudomonas |
| 286 | 36 | 54.5 | 184 | 2 | Q87Y72 | PSESM | Q87yt2 | pseudomonas |
| 287 | 36 | 54.5 | 185 | 2 | Q4MX95 | BACCE | Q4mx95 | bacillus ce |
| 288 | 36 | 54.5 | 185 | 2 | Q6HG05 | BACHK | Q6hg05 | bacillus th |
| 289 | 36 | 54.5 | 186 | 1 | ISP2 | RALSO | Q8xyl2 | raistonia s |
| 290 | 36 | 54.5 | 206 | 2 | Q8UCF0 | AGRT5 | Q8ucf0 | agrobacteri |
| 291 | 36 | 54.5 | 208 | 2 | Q2U3S8 | RHIME | Q2u3s8 | rhizobium m |
| 292 | 36 | 54.5 | 228 | 2 | Q6DHC8 | BRARE | Q6dnc8 | brachydania |
| 293 | 36 | 54.5 | 231 | 2 | Q787H6 | THEVO | Q787h6 | thermoplasm |
| 294 | 36 | 54.5 | 233 | 2 | Q729K9 | DESVH | Q729k9 | desulfovibr |
| 295 | 36 | 54.5 | 239 | 2 | Q7VNR0 | HAEDU | Q7vne0 | haemophilus |
| 296 | 36 | 54.5 | 243 | 2 | Q4Z5W6 | PLABE | Q4z5w6 | plasmodium |
| 297 | 36 | 54.5 | 246 | 2 | Q4NG66 | 9NICC | Q4ng66 | arthrobacte |
| 298 | 36 | 54.5 | 259 | 2 | P90989 | CABEL | P90989 | caenorhabdi |
| 299 | 36 | 54.5 | 259 | 2 | Q7CWT7 | AGRT5 | Q7cwt7 | agrobacteri |
| 300 | 36 | 54.5 | 264 | 2 | Q4L3C5 | STAHL | Q4l3c5 | staphylococ |
| 301 | 36 | 54.5 | 303 | 2 | Q932N5 | STAAM | Q932n5 | staphylococ |
| 302 | 36 | 54.5 | 313 | 2 | Q4YI52 | PLABE | Q4yi52 | plasmodium |
| 303 | 36 | 54.5 | 314 | 2 | Q899Z1 | CLOTE | Q899z1 | clostridium |
| 304 | 36 | 54.5 | 320 | 2 | Q7UFT7 | RAT | Q7uft7 | rattus norv |
| 305 | 36 | 54.5 | 321 | 2 | Q8AAU5 | BACTN | Q8aaus | bacteroides |
| 306 | 36 | 54.5 | 322 | 2 | Q8VGV5 | MOUSE | Q8vgv5 | mus musculus |
| 307 | 36 | 54.5 | 328 | 2 | Q4XKG6 | PLACH | Q4xkg6 | plasmodium |
| 308 | 36 | 54.5 | 332 | 2 | Q4HG46 | CAMCO | Q4hng6 | campylobact |
| 309 | 36 | 54.5 | 332 | 2 | Q4HPJ1 | CAMUP | Q4hpj1 | campylobact |
| 310 | 36 | 54.5 | 332 | 2 | Q5HS19 | CAMJR | Q5hs19 | campylobact |
| 311 | 36 | 54.5 | 332 | 2 | Q9PMA3 | CAMJE | Q9pma3 | campylobact |
| 312 | 36 | 54.5 | 339 | 2 | Q5B8K5 | EMENI | Q5b8k5 | aspergillus |
| 313 | 36 | 54.5 | 342 | 2 | Q719E3 | VITRI | Q719e3 | vitis ripar |
| 314 | 36 | 54.5 | 349 | 2 | Q21684 | CABEL | Q21684 | caenorhabdi |
| 315 | 36 | 54.5 | 352 | 2 | Q6P0P4 | HUMAN | Q6p0p4 | homo sapien |
| 316 | 36 | 54.5 | 365 | 1 | GP142 | MOUSE | Q7tqn9 | mus musculus |
| 317 | 36 | 54.5 | 370 | 2 | Q7RMC6 | PLAYO | Q7rmc6 | plasmodium |
| 318 | 36 | 54.5 | 381 | 2 | Q4FM25 | 9RICK | Q4fm25 | candidateus |
| 319 | 36 | 54.5 | 383 | 1 | PLEA1 | MOUSE | Q8bul6 | mus musculus |
| 320 | 36 | 54.5 | 383 | 2 | Q5RG54 | HUMAN | Q5rgs4 | homo sapien |
| 321 | 36 | 54.5 | 383 | 2 | Q5R7T7 | PONPY | Q5r7t7 | pongo pygma |
| 322 | 36 | 54.5 | 397 | 2 | Q5E4R2 | VIBF1 | Q5e4r2 | vibrio fisci |
| 323 | 36 | 54.5 | 398 | 2 | Q9YS31 | 9ALPH | Q9ys31 | suid herpes |

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|-----|----|------|-----|---|--------|--------|--------|-------------|-------------|
| 324 | 36 | 54.5 | 400 | 2 | Q5PP78 | 9ALPH | Q5pp78 | suid herpes | |
| 325 | 36 | 54.5 | 400 | 2 | Q8B3S6 | 9ALPH | Q8b3s6 | suid herpes | |
| 326 | 36 | 54.5 | 400 | 2 | Q8B445 | 9ALPH | Q8b445 | suid herpes | |
| 327 | 36 | 54.5 | 400 | 2 | Q91W02 | PRVKA | Q91w02 | pseudorabie | |
| 328 | 36 | 54.5 | 402 | 1 | VGLD | PRVRI | P07645 | pseudorabie | |
| 329 | 36 | 54.5 | 402 | 2 | Q80JB5 | 9ALPH | Q80jb5 | suid herpes | |
| 330 | 36 | 54.5 | 402 | 2 | Q80KC8 | 9ALPH | Q80kc8 | suid herpes | |
| 331 | 36 | 54.5 | 404 | 1 | PLEA1 | HUMAN | Q9hb21 | homo sapien | |
| 332 | 36 | 54.5 | 404 | 2 | Q92290 | 9ALPH | Q92290 | suid herpes | |
| 333 | 36 | 54.5 | 427 | 2 | Q6K255 | PICHTO | Q6k255 | microphilus | |
| 334 | 36 | 54.5 | 429 | 2 | Q52000 | PSEPU | Q52000 | pseudomonas | |
| 335 | 36 | 54.5 | 429 | 2 | Q9WW22 | PSEPU | Q9ww22 | pseudomonas | |
| 336 | 36 | 54.5 | 429 | 2 | Q8BN38 | PSEPK | Q8bn38 | pseudomonas | |
| 337 | 36 | 54.5 | 432 | 2 | Q834V2 | ENTFA | Q834v2 | enterococcu | |
| 338 | 36 | 54.5 | 436 | 1 | CBP22 | HORVU | P55748 | hordeum vul | |
| 339 | 36 | 54.5 | 438 | 2 | Q5LR41 | SILPO | Q5lr41 | silicibacte | |
| 340 | 36 | 54.5 | 448 | 2 | Q75CW7 | ASHGO | Q75cw7 | ashbya goss | |
| 341 | 36 | 54.5 | 448 | 2 | Q4KH32 | PSEFS | Q4kh32 | pseudomonas | |
| 342 | 36 | 54.5 | 461 | 2 | Q5QZY8 | IDILLO | Q5qzy8 | idiomarina | |
| 343 | 36 | 54.5 | 463 | 2 | Q4PSY2 | ARATH | Q4psy2 | arabidopsis | |
| 344 | 36 | 54.5 | 465 | 2 | Q04084 | ARATH | Q04084 | arabidopsis | |
| 345 | 36 | 54.5 | 470 | 2 | Q22732 | ARATH | Q22732 | arabidopsis | |
| 346 | 36 | 54.5 | 472 | 2 | Q4WW68 | ASPFU | Q4ww68 | aspergillus | |
| 347 | 36 | 54.5 | 472 | 2 | Q8MBU0 | VITVI | Q8mbu0 | vitis vinif | |
| 348 | 36 | 54.5 | 473 | 1 | SYN | TREDE | Q73p19 | treponema d | |
| 349 | 36 | 54.5 | 473 | 2 | Q9YEU4 | AERPE | Q9yeu4 | aeropyrum p | |
| 350 | 36 | 54.5 | 476 | 2 | Q5LC68 | CHLAE | Q5lc68 | chlamydophi | |
| 351 | 36 | 54.5 | 476 | 2 | Q8EVV4 | MYCPE | Q8evv4 | mycoplasma | |
| 352 | 36 | 54.5 | 478 | 2 | Q70KK4 | BACAM | Q70kk4 | bacillus am | |
| 353 | 36 | 54.5 | 480 | 2 | Q5ZAI9 | ORYSA | Q5za19 | oryza sativ | |
| 354 | 36 | 54.5 | 481 | 2 | Q9LYD5 | ARATH | Q9lyd5 | arabidopsis | |
| 355 | 36 | 54.5 | 482 | 1 | NF314 | NARFO | P42661 | naegleria f | |
| 356 | 36 | 54.5 | 482 | 2 | Q9VDT5 | DROME | Q9vdt5 | drosophila | |
| 357 | 36 | 54.5 | 482 | 2 | Q3W727 | ORYSA | Q3w727 | oryza sativ | |
| 358 | 36 | 54.5 | 482 | 2 | Q71VZ0 | LISMF | Q71vz0 | listeria mo | |
| 359 | 36 | 54.5 | 482 | 2 | Q8Y3R2 | LISMO | Q8y3r2 | listeria mo | |
| 360 | 36 | 54.5 | 485 | 2 | Q6H7I7 | ORYSA | Q6h7i7 | oryza sativ | |
| 361 | 36 | 54.5 | 488 | 2 | Q6CDV9 | YARLI | Q6cdv9 | yarrowia li | |
| 362 | 36 | 54.5 | 490 | 2 | Q6CYW8 | ERWCT | Q6cyw8 | erwinia car | |
| 363 | 36 | 54.5 | 494 | 2 | Q4IG89 | GIBZE | Q4ig89 | gibberella | |
| 364 | 36 | 54.5 | 499 | 2 | Q9FMX9 | ARATH | Q9fmx9 | arabidopsis | |
| 365 | 36 | 54.5 | 499 | 2 | Q8A923 | BACTN | Q8a923 | bacteroides | |
| 366 | 36 | 54.5 | 500 | 2 | Q5ZA26 | ORYSA | Q5za26 | oryza sativ | |
| 367 | 36 | 54.5 | 500 | 2 | Q5Z5A3 | ORYSA | Q5z5a3 | oryza sativ | |
| 368 | 36 | 54.5 | 502 | 2 | Q8SQK8 | ENCCU | Q8sqk8 | encephalito | |
| 369 | 36 | 54.5 | 505 | 1 | MATK | PHASI | Q5j2w2 | phaulotham | |
| 370 | 36 | 54.5 | 505 | 2 | Q5J2W3 | 9CARY | Q5j2w3 | achatocarpu | |
| 371 | 36 | 54.5 | 508 | 2 | Q507P7 | 9MAGN | Q507p7 | ranunculus | |
| 372 | 36 | 54.5 | 511 | 2 | Q8MEB8 | 9ARAE | Q8mee8 | amorphophal | |
| 373 | 36 | 54.5 | 511 | 2 | Q5LDE3 | BACFPN | Q5lde3 | bacteroides | |
| 374 | 36 | 54.5 | 511 | 2 | Q64UG8 | BACFR | Q64ug8 | bacteroides | |
| 375 | 36 | 54.5 | 516 | 2 | Q8MEF1 | 9ARAE | Q8mef1 | amorphophal | |
| 376 | 36 | 54.5 | 516 | 2 | Q8MEF7 | 9ARAE | Q8mef7 | amorphophal | |
| 377 | 36 | 54.5 | 516 | 2 | Q8MEF8 | 9ARAE | Q8mef8 | amorphophal | |
| 378 | 36 | 54.5 | 516 | 2 | Q9IW00 | PRVKA | Q9iw00 | pseudorabie | |
| 379 | 36 | 54.5 | 516 | 2 | Q7XU80 | ORYSA | Q7xu80 | oryza sativ | |
| 380 | 36 | 54.5 | 527 | 2 | Q5J6J0 | TRIRU | Q5j6j0 | trichophyto | |
| 381 | 36 | 54.5 | 536 | 2 | Q417B3 | GIBZE | Q417b3 | gibberella | |
| 382 | 36 | 54.5 | 540 | 2 | 1 | LNT | CHLPN | Q5vjg9 | aspergillus |
| 383 | 36 | 54.5 | 543 | 1 | Q5VJG9 | ASPFU | Q5vjg9 | aspergillus | |
| 384 | 36 | 54.5 | 543 | 2 | Q4WLH2 | ASPFU | Q4wlh2 | aspergillus | |
| 385 | 36 | 54.5 | 543 | 2 | Q4Y2J3 | PLACH | Q4y2j3 | plasmodium | |
| 386 | 36 | 54.5 | 548 | 2 | Q5AA10 | CANAL | Q5aa10 | candida alb | |
| 387 | 36 | 54.5 | 550 | 2 | Q5AA97 | CANAL | Q5aa97 | candida alb | |
| 388 | 36 | 54.5 | 552 | 2 | Q5B1Y8 | EMENI | Q5b1y8 | aspergillus | |
| 389 | 36 | 54.5 | 552 | 2 | Q96VC4 | EMENI | Q96vc4 | emeritella | |
| 390 | 36 | 54.5 | 552 | 2 | Q527M7 | MAGGR | Q527m7 | magnaporthe | |
| 391 | 36 | 54.5 | 552 | 2 | Q4IBQ6 | GIBZE | Q4ibq6 | gibberella | |
| 392 | 36 | 54.5 | 553 | 2 | Q6S6F1 | ORYSA | Q6s6f1 | oryza sativ | |
| 393 | 36 | 54.5 | 553 | 2 | Q6R7W8 | NEUCR | Q6r7w8 | neuropora | |
| 394 | 36 | 54.5 | 554 | 2 | Q6FTB1 | CANGA | Q6ftb1 | candida gla | |
| 395 | 36 | 54.5 | 567 | 2 | Q4P3P4 | USTWA | Q4p3p4 | ustilago ma | |
| 396 | 36 | 54.5 | 574 | 2 | | | | | |

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|-----|------|------|------|---|--------------|--------------------|-----|----|------|-----|---|---------------|---------------------|
| 397 | 36 | 54.5 | 589 | 2 | Q6CB63_YARLI | Q6cb63 yarrowia li | 470 | 35 | 53.0 | 106 | 2 | Q9QVP0_9MURI | Q9qvp0 mus sp. . c |
| 398 | 36 | 54.5 | 594 | 2 | Q9UJD6_HUMAN | Q9ujd6 homo sapien | 471 | 35 | 53.0 | 117 | 1 | HV12_MOUSE | P01756 mus musculus |
| 399 | 36 | 54.5 | 599 | 2 | Q4IN26_GIBZE | Q4in26 gibberella | 472 | 35 | 53.0 | 118 | 2 | Q4X750_PLACH | Q4x750 plasmodium |
| 400 | 36 | 54.5 | 616 | 2 | Q64FP0_9VIRU | Q64fp0 white clove | 473 | 35 | 53.0 | 119 | 2 | Q5FK70_LACAC | Q5fk70 lactobacill |
| 401 | 36 | 54.5 | 622 | 2 | Q95SK1_DROME | Q95sk1 drosophila | 474 | 35 | 53.0 | 120 | 2 | Q830H0_ENTFA | Q830h0 enterococcu |
| 402 | 36 | 54.5 | 626 | 2 | Q9V9U2_DROME | Q9v9u2 drosophila | 475 | 35 | 53.0 | 120 | 2 | Q74J77_LACJO | Q74j77 lactobacill |
| 403 | 36 | 54.5 | 630 | 2 | Q44545_CAEEL | Q44545 caenorhabdi | 476 | 35 | 53.0 | 134 | 2 | Q73Y48_CRYPV | Q73y48 cryptospori |
| 404 | 36 | 54.5 | 640 | 2 | Q86HP3_DICDI | Q86hp3 dictyosteli | 477 | 35 | 53.0 | 139 | 2 | Q8ISR0_PLAF7 | Q8isr0 plasmodium |
| 405 | 36 | 54.5 | 656 | 2 | Q9M576_ORYSA | Q9m576 oryza sativ | 478 | 35 | 53.0 | 141 | 2 | Q78E86_RAT | Q78e86 rattus norv |
| 406 | 36 | 54.5 | 657 | 2 | Q9LI55_ORYSA | Q9li55 oryza sativ | 479 | 35 | 53.0 | 142 | 2 | Q64724_RAT | Q64724 rattus norv |
| 407 | 36 | 54.5 | 657 | 2 | Q9SNF1_ORYSA | Q9snf1 oryza sativ | 480 | 35 | 53.0 | 173 | 2 | Q8KCU9_CHLTE | Q8kc9 chlorobium |
| 408 | 36 | 54.5 | 659 | 2 | Q725F5_LISMF | Q725f5 listeria mo | 481 | 35 | 53.0 | 176 | 2 | Q63V24_BURPA | Q63v24 burkholderi |
| 409 | 36 | 54.5 | 659 | 2 | Q8YAU9_LISMO | Q8yau9 listeria mo | 482 | 35 | 53.0 | 176 | 2 | Q62JM5_BURPA | Q62jm5 burkholderi |
| 410 | 36 | 54.5 | 659 | 2 | Q92FT9_LISIN | Q92ft9 listeria in | 483 | 35 | 53.0 | 177 | 2 | Q5H2W0_XANOR | Q5h2w0 xanthomonas |
| 411 | 36 | 54.5 | 664 | 2 | Q55AG3_DICDI | Q55ag3 dictyosteli | 484 | 35 | 53.0 | 182 | 2 | Q4X2A9_PLACH | Q4x2a9 plasmodium |
| 412 | 36 | 54.5 | 689 | 2 | Q7RNV4_PLAYO | Q7rnv4 plasmodium | 485 | 35 | 53.0 | 186 | 2 | Q6B869_9ACAR | Q6b869 ixodes paci |
| 413 | 36 | 54.5 | 733 | 2 | Q6PQ05_RAT | Q6pq05 rattus norv | 487 | 35 | 53.0 | 206 | 2 | Q8PKX9_METWA | Q8pkx9 methanosarc |
| 414 | 36 | 54.5 | 749 | 2 | Q56JK2_STECO | Q56jk2 stenella co | 487 | 35 | 53.0 | 208 | 2 | Q8THM0_METAC | Q8thm0 methanosarc |
| 415 | 36 | 54.5 | 750 | 2 | Q6C811_YARLI | Q6c811 yarrowia li | 488 | 35 | 53.0 | 211 | 2 | Q74AP5_GEOSL | Q74ap5 geobacter s |
| 416 | 36 | 54.5 | 751 | 1 | A4_SAIISC | Q95241 s amyloid b | 489 | 35 | 53.0 | 212 | 2 | Q9U8F1_SCHJA | Q9u8f1 schistosoma |
| 417 | 36 | 54.5 | 751 | 2 | Q6GSC0_HUMAN | Q6gsc0 homo sapien | 490 | 35 | 53.0 | 212 | 2 | Q8LIK7_ORYSA | Q8lik7 oryza sativ |
| 418 | 36 | 54.5 | 751 | 2 | Q6RH28_CANFA | Q6rh28 canis fami | 491 | 35 | 53.0 | 218 | 2 | Q4XBG2_PLACH | Q4xbg2 plasmodium |
| 419 | 36 | 54.5 | 751 | 2 | Q56JK5_CANFA | Q56jk5 canis fami | 492 | 35 | 53.0 | 223 | 2 | Q73NN8_TREDE | Q73nn8 treponema d |
| 420 | 36 | 54.5 | 751 | 2 | Q4R4R8_MACFA | Q4r4r8 macaca fasc | 493 | 35 | 53.0 | 224 | 2 | Q72TU7_LEPIC | Q72tu7 leptospira |
| 421 | 36 | 54.5 | 751 | 2 | Q94RG7_CHICK | Q94rg7 gallus gall | 494 | 35 | 53.0 | 224 | 2 | Q8FIC3_LEPIN | Q8fic3 leptonira |
| 422 | 36 | 54.5 | 753 | 2 | Q6TXG3_RAT | Q6txg3 rattus norv | 495 | 35 | 53.0 | 227 | 2 | Q9QM5_MYCPU | Q9qm5 mycoplasma |
| 423 | 36 | 54.5 | 770 | 1 | A4_HUMAN | P05057 h amyloid b | 496 | 35 | 53.0 | 236 | 2 | Q9XHV8_ORYSA | Q9xhv8 oryza sativ |
| 424 | 36 | 54.5 | 770 | 1 | A4_MACFA | P53601 m amyloid b | 497 | 35 | 53.0 | 236 | 2 | Q688U1_ORYSA | Q688u1 oryza sativ |
| 425 | 36 | 54.5 | 770 | 1 | A4_MOUSE | P12033 m amyloid b | 498 | 35 | 53.0 | 241 | 2 | Q511T0_ENTHI | Q511t0 entamoeba h |
| 426 | 36 | 54.5 | 770 | 1 | A4_PANTR | P51880 p amyloid b | 499 | 35 | 53.0 | 242 | 2 | Q8EH21_SHEON | Q8eh21 shewanella |
| 427 | 36 | 54.5 | 770 | 1 | A4_PIG | P79307 s amyloid b | 500 | 35 | 53.0 | 250 | 2 | Q51GH1_ENTHI | Q51gh1 entamoeba h |
| 428 | 36 | 54.5 | 770 | 1 | A4_RAT | P08592 r amyloid b | 501 | 35 | 53.0 | 252 | 2 | Q5BYS4_SCHJA | Q5bys4 schistosoma |
| 429 | 36 | 54.5 | 770 | 2 | Q6RH30_CANFA | Q6rh30 canis fami | 502 | 35 | 53.0 | 254 | 2 | Q5TPJ3_ANOGA | Q5tpj3 anopheles g |
| 430 | 36 | 54.5 | 770 | 2 | Q56JK6_CANFA | Q56jk6 canis fami | 503 | 35 | 53.0 | 254 | 2 | Q4H86_DICDI | Q4h86 dictyosteli |
| 431 | 36 | 54.5 | 770 | 2 | Q532T3_MOUSE | Q532t3 mus musculu | 504 | 35 | 53.0 | 255 | 2 | Q4HXT5_GIBZE | Q4hxt5 gibberella |
| 432 | 36 | 54.5 | 770 | 2 | Q547B7_RAT | Q547b7 rattus norv | 505 | 35 | 53.0 | 256 | 2 | Q4HR69_CAMUP | Q4hr69 campylobact |
| 433 | 36 | 54.5 | 826 | 2 | Q6NSG3_MOUSE | Q6nsg3 mus musculu | 506 | 35 | 53.0 | 261 | 2 | Q5HRT7_STAEP | Q5hrt7 staphylococ |
| 434 | 36 | 54.5 | 839 | 2 | Q6GQX3_MOUSE | Q6gqx3 mus musculu | 507 | 35 | 53.0 | 261 | 2 | Q8COT1_STAEP | Q8cot1 staphylococ |
| 435 | 36 | 54.5 | 845 | 2 | Q895B3_CLOTE | Q895b3 clostridium | 508 | 35 | 53.0 | 265 | 1 | CEAMA_MOUSE | CEAMA_MOUSE |
| 436 | 36 | 54.5 | 874 | 2 | Q7S180_EMENI | Q7s180 emericella | 509 | 35 | 53.0 | 265 | 2 | Q99LD6_MOUSE | Q99ld6 mus musculu |
| 437 | 36 | 54.5 | 880 | 2 | Q5B934_EMENI | Q5b934 aspergillus | 510 | 35 | 53.0 | 265 | 2 | Q9D329_MOUSE | Q9d329 mus musculu |
| 438 | 36 | 54.5 | 920 | 2 | Q4P912_USTWA | Q4p912 ustilago ma | 511 | 35 | 53.0 | 267 | 2 | Q522A6_MAGGR | Q522a6 magnaporthe |
| 439 | 36 | 54.5 | 957 | 2 | Q5LDC5_BACFN | Q5ldc5 bacteroides | 512 | 35 | 53.0 | 267 | 2 | Q9MG87_9STRA | Q9mg87 trypanoplas |
| 440 | 36 | 54.5 | 957 | 2 | Q64UE8_BACFR | Q64ue8 bacteroides | 513 | 35 | 53.0 | 270 | 2 | Q831L9_ENTFA | Q831l9 enterococcu |
| 441 | 36 | 54.5 | 978 | 2 | Q6XP55_YERPR | Q6xp55 yersinia fr | 514 | 35 | 53.0 | 275 | 2 | Q74SW8_YERPE | Q74sw8 yersinia pe |
| 442 | 36 | 54.5 | 1000 | 1 | PEX6_KLULA | Q6cpv1 kluyveromyc | 515 | 35 | 53.0 | 282 | 2 | Q82D66_YERPE | Q82d66 yersinia pe |
| 443 | 36 | 54.5 | 1028 | 1 | CNTN6_MOUSE | Q6jmb8 mus musculu | 516 | 35 | 53.0 | 282 | 2 | Q668T0_YERPS | Q668t0 yersinia ps |
| 444 | 36 | 54.5 | 1028 | 1 | CNTN6_RAT | P97528 rattus norv | 517 | 35 | 53.0 | 285 | 2 | Q7QBEN6_ANOGA | Q7qbn6 anopheles g |
| 445 | 36 | 54.5 | 1243 | 2 | Q69ZL6_MOUSE | Q69z16 mus musculu | 518 | 35 | 53.0 | 286 | 1 | COX3_TRYBO | Q37353 trypanoplas |
| 446 | 36 | 54.5 | 1255 | 2 | Q92604_9REOV | Q92604 rice ragged | 519 | 35 | 53.0 | 286 | 2 | Q4FS63_9GAMM | Q4f63 psychrobact |
| 447 | 36 | 54.5 | 1275 | 2 | Q00372_HUMAN | Q00372 homo sapien | 520 | 35 | 53.0 | 298 | 1 | ECTD_NGCPA | Q5yw75 nocardia fa |
| 448 | 36 | 54.5 | 1289 | 2 | Q34986_BACSU | Q34986 bacillus su | 521 | 35 | 53.0 | 303 | 2 | Q74432_SCHPO | Q74432 schizosacch |
| 449 | 36 | 54.5 | 1397 | 2 | Q551C5_DICDI | Q551c5 dictyosteli | 522 | 35 | 53.0 | 304 | 2 | Q6CU01_KLULA | Q6cu01 kluyveromyc |
| 450 | 36 | 54.5 | 1438 | 2 | Q9P2K9_HUMAN | Q9p2k9 homo sapien | 523 | 35 | 53.0 | 305 | 2 | Q7R849_PLAYO | Q7r849 plasmodium |
| 451 | 36 | 54.5 | 1438 | 2 | Q5VTU9_HUMAN | Q5vtu9 homo sapien | 524 | 35 | 53.0 | 308 | 2 | Q8YBY0_BRUME | Q8yby0 bruceella me |
| 452 | 36 | 54.5 | 1463 | 2 | Q55124_MOUSE | Q55124 mus musculu | 525 | 35 | 53.0 | 309 | 2 | Q4UJB8_RICFE | Q4ujb8 rickettsia |
| 453 | 36 | 54.5 | 1465 | 2 | Q811S4_PLAF7 | Q811s4 plasmodium | 526 | 35 | 53.0 | 310 | 1 | XTH33_ARATH | Q81c45 arabidopsis |
| 454 | 36 | 54.5 | 1760 | 2 | Q4RUJ7_TETNG | Q4ruj7 tetraodon n | 527 | 35 | 53.0 | 310 | 2 | Q6FLQ4_CANGA | Q6flq4 candida gla |
| 455 | 36 | 54.5 | 2525 | 2 | Q4Q184_LEIMA | Q4q184 leishmania | 528 | 35 | 53.0 | 313 | 2 | Q4LV92_9BURK | Q4lv92 burkholderi |
| 456 | 36 | 54.5 | 3920 | 2 | Q4UF61_THEAN | Q4uf61 theileria a | 529 | 35 | 53.0 | 318 | 2 | Q5FPF0_GLOOX | Q5fpf0 gluconobact |
| 457 | 36 | 54.5 | 3934 | 2 | Q4N4D7_THEPA | Q4n4d7 theileria p | 530 | 35 | 53.0 | 323 | 2 | Q4MFW4_BACCE | Q4mfw4 bacillus ce |
| 458 | 35.5 | 53.8 | 126 | 2 | Q7P509_FUSNV | Q7p509 fusobacteri | 531 | 35 | 53.0 | 329 | 2 | Q82IW2_STRAW | Q82iw2 streptomyce |
| 459 | 35.5 | 53.8 | 531 | 1 | PTM1_YEAST | P32857 saccharomyc | 532 | 35 | 53.0 | 330 | 2 | Q9BKN9_CABEL | Q9bkn9 caenorhabdi |
| 460 | 35.5 | 53.8 | 946 | 1 | YINT_YEAST | F40462 saccharomyc | 533 | 35 | 53.0 | 330 | 2 | Q8EUS9_MYCFE | Q8eus9 mycoplasma |
| 461 | 35 | 53.0 | 35 | 2 | Q56ZA0_ARATH | Q56za0 arabidopsis | 534 | 35 | 53.0 | 334 | 2 | Q5TTG2_ANOGA | Q5ttg2 anopheles g |
| 462 | 35 | 53.0 | 54 | 2 | Q7R9B0_PLAYO | Q7r9b0 plasmodium | 535 | 35 | 53.0 | 334 | 2 | Q5T7R12_TREDE | Q5t7r12 treponema d |
| 463 | 35 | 53.0 | 69 | 2 | Q9R661_9SYNC | Q9r661 synecocyst | 536 | 35 | 53.0 | 335 | 2 | Q81L86_PLAF7 | Q81l86 plasmodium |
| 464 | 35 | 53.0 | 73 | 1 | PSAE_SYNY3 | P12975 synecocyst | 537 | 35 | 53.0 | 341 | 2 | Q9JMK5_9MURI | Q9jmk5 rattus sp. |
| 465 | 35 | 53.0 | 86 | 2 | Q9HLC9_THEAC | Q9hlc9 thermoplasm | 538 | 35 | 53.0 | 347 | 2 | Q4KE60_PSEPE | Q4ke60 pseudomonas |
| 466 | 35 | 53.0 | 95 | 2 | Q4YF19_PLAEB | Q4yfi9 plasmodium | 539 | 35 | 53.0 | 348 | 2 | Q6UBL4_9FLAV | Q6ubl4 dengue viru |
| 467 | 35 | 53.0 | 96 | 2 | Q9U8C6_CAEEL | Q9u8c6 caenorhabdi | 540 | 35 | 53.0 | 348 | 2 | Q6UBL5_9FLAV | Q6ubl5 dengue viru |
| 468 | 35 | 53.0 | 96 | 2 | Q7UKB3_RHOBA | Q7ukb3 rhodopirell | 541 | 35 | 53.0 | 348 | 2 | Q6UBL6_9FLAV | Q6ubl6 dengue viru |
| 469 | 35 | 53.0 | 97 | 2 | Q5ZTR9_LEGPH | Q5ztr9 legionella | 542 | 35 | 53.0 | 348 | 2 | Q7TCM7_9FLAV | Q7tcm7 dengue viru |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|--------------|----------------------|-----|----|------|-----|---|---------------|--------------------|
| 543 | 35 | 53.0 | 348 | 2 | Q7TCM8_9FLAV | Q7tcm8 dengue viru | 616 | 35 | 53.0 | 483 | 2 | Q72X70_BACCI | Q72x70 bacillus ce |
| 544 | 35 | 53.0 | 348 | 2 | Q7TCM9_9FLAV | Q7tcm9 dengue viru | 617 | 35 | 53.0 | 483 | 2 | Q52L51_MOUSE | Q52l51 mus musculu |
| 545 | 35 | 53.0 | 348 | 2 | Q7TCN0_9FLAV | Q7tcn0 dengue viru | 618 | 35 | 53.0 | 487 | 2 | Q4UW1_XANCP | Q4uw1 xanthomonas |
| 546 | 35 | 53.0 | 348 | 2 | Q7TCN1_9FLAV | Q7tcn1 dengue viru | 619 | 35 | 53.0 | 487 | 2 | Q8P7P9_XANCP | Q8p7p9 xanthomonas |
| 547 | 35 | 53.0 | 348 | 2 | Q7TCN2_9FLAV | Q7tcn2 dengue viru | 620 | 35 | 53.0 | 488 | 2 | Q8P112_XANAC | Q8p112 xanthomonas |
| 548 | 35 | 53.0 | 348 | 2 | Q7TCN3_9FLAV | Q7tcn3 dengue viru | 621 | 35 | 53.0 | 489 | 2 | Q4IIT1_GIBZE | Q4iit1 gibberella |
| 549 | 35 | 53.0 | 348 | 2 | Q7TCN4_9FLAV | Q7tcn4 dengue viru | 622 | 35 | 53.0 | 491 | 2 | Q6CMT5_KLUJA | Q6cmt5 kluyveromyc |
| 550 | 35 | 53.0 | 348 | 2 | Q7TCN5_9FLAV | Q7tcn5 dengue viru | 623 | 35 | 53.0 | 493 | 2 | Q6CGJ3_YARLI | Q6cgj3 yarrowia li |
| 551 | 35 | 53.0 | 348 | 2 | Q7TCN6_9FLAV | Q7tcn6 dengue viru | 624 | 35 | 53.0 | 497 | 2 | Q4S2T8_TETNG | Q4s2t8 tetraodon n |
| 552 | 35 | 53.0 | 348 | 2 | Q7TCN7_9FLAV | Q7tcn7 dengue viru | 625 | 35 | 53.0 | 498 | 2 | Q695H2_PHYDV | Q695h2 phylloperth |
| 553 | 35 | 53.0 | 348 | 2 | Q7TCN8_9FLAV | Q7tcn8 dengue viru | 626 | 35 | 53.0 | 499 | 2 | Q5FV41_ARATH | Q5fv41 arabidopsis |
| 554 | 35 | 53.0 | 348 | 2 | Q7TCN9_9FLAV | Q7tcn9 dengue viru | 627 | 35 | 53.0 | 499 | 2 | Q84TU6_ARATH | Q84tu6 arabidopsis |
| 555 | 35 | 53.0 | 348 | 2 | Q7TCP0_9FLAV | Q7tcp0 dengue viru | 628 | 35 | 53.0 | 500 | 1 | XYNB_THESA | Q36906 thermoanaer |
| 556 | 35 | 53.0 | 348 | 2 | Q7TCP1_9FLAV | Q7tcp1 dengue viru | 629 | 35 | 53.0 | 503 | 2 | Q9LEV7_ARATH | Q9lev7 arabidopsis |
| 557 | 35 | 53.0 | 348 | 2 | Q7TCP2_9FLAV | Q7tcp2 dengue viru | 630 | 35 | 53.0 | 504 | 1 | XYNB_BACST | Q9zfm2 bacillus st |
| 558 | 35 | 53.0 | 348 | 2 | Q7TCP3_9FLAV | Q7tcp3 dengue viru | 631 | 35 | 53.0 | 508 | 1 | YBY9_YEAST | Q38109 saccharomyc |
| 559 | 35 | 53.0 | 348 | 2 | Q7TCP4_9FLAV | Q7tcp4 dengue viru | 632 | 35 | 53.0 | 510 | 2 | Q83144_TREPA | Q83144 treponema p |
| 560 | 35 | 53.0 | 348 | 2 | Q7TCP5_9FLAV | Q7tcp5 dengue viru | 633 | 35 | 53.0 | 513 | 2 | Q63289_RAT | Q63289 rattus norv |
| 561 | 35 | 53.0 | 348 | 2 | Q7TCP6_9FLAV | Q7tcp6 dengue viru | 634 | 35 | 53.0 | 514 | 2 | Q5GXP8_XANOR | Q5gxp8 xanthomonas |
| 562 | 35 | 53.0 | 348 | 2 | Q7TCP7_9FLAV | Q7tcp7 dengue viru | 635 | 35 | 53.0 | 517 | 2 | Q9LSW0_9BACT | Q9lsw0 prevotella |
| 563 | 35 | 53.0 | 348 | 2 | Q7TCP8_9FLAV | Q7tcp8 dengue viru | 636 | 35 | 53.0 | 517 | 2 | Q7N9R8_PHOLL | Q7n9r8 photorhabdu |
| 564 | 35 | 53.0 | 370 | 2 | Q6TUG6_RAT | Q6tug6 rattus norv | 637 | 35 | 53.0 | 519 | 1 | CEMI1_RAT | Q16573 rattus norv |
| 565 | 35 | 53.0 | 378 | 2 | Q4MGQ5_BACCE | Q4mgq5 bacillus ce | 638 | 35 | 53.0 | 523 | 1 | CBPY_PICPA | P52710 pichia past |
| 566 | 35 | 53.0 | 384 | 2 | Q7D6J3_MYCTU | Q7d6j3 mycobacteri | 639 | 35 | 53.0 | 523 | 2 | Q5LE91_BACFN | Q5le91 bacteroides |
| 567 | 35 | 53.0 | 384 | 2 | Q7I644_MYCTU | Q7i644 mycobacteri | 640 | 35 | 53.0 | 523 | 2 | Q64VD4_BACFR | Q64vd4 bacteroides |
| 568 | 35 | 53.0 | 384 | 2 | Q7TXX8_MYCBO | Q7txt8 mycobacteri | 641 | 35 | 53.0 | 524 | 2 | Q757J1_ASHGO | Q757j1 ashbya goss |
| 569 | 35 | 53.0 | 386 | 2 | Q4S2T0_TETNG | Q4s2t0 tetraodon n | 642 | 35 | 53.0 | 527 | 2 | O58750_PYRHO | O58750 pyrococcus |
| 570 | 35 | 53.0 | 387 | 2 | Q7QBV3_ANOGA | Q7qbv3 anopheles g | 643 | 35 | 53.0 | 527 | 2 | Q6FOT4_MESFL | Q6fot4 mesoplasma |
| 571 | 35 | 53.0 | 388 | 2 | Q8JG07_FUGRU | Q8jg07 fugu rubrip | 644 | 35 | 53.0 | 533 | 2 | Q4TEL0_TETNG | Q4tel0 tetraodon n |
| 572 | 35 | 53.0 | 394 | 2 | Q7U926_SYNPX | Q7u926 synechococc | 645 | 35 | 53.0 | 535 | 2 | Q6CXA3_KLUJA | Q6cxa3 kluyveromyc |
| 573 | 35 | 53.0 | 398 | 2 | Q4WV76_ASPFU | Q4wv76 aspergillus | 646 | 35 | 53.0 | 536 | 2 | Q6BT19_DEBHA | Q6bt19 debaryomyc |
| 574 | 35 | 53.0 | 405 | 2 | Q73CG4_BACCI | Q73cg4 bacillus ce | 647 | 35 | 53.0 | 536 | 2 | Q7UYF8_RHOBA | Q7uyf8 rhodopirell |
| 575 | 35 | 53.0 | 410 | 1 | QD02_BUCBP | Q89a16 buchera ap | 648 | 35 | 53.0 | 543 | 2 | Q4SNW9_TETNG | Q4snw9 tetraodon n |
| 576 | 35 | 53.0 | 414 | 2 | Q5MU61_MYCMS | Q5mu61 mycoplasma | 649 | 35 | 53.0 | 548 | 1 | SYNC_HUMAN | Q43776 homo sapien |
| 577 | 35 | 53.0 | 415 | 1 | FTSW_MESVI | Q8num4 mesostigma | 650 | 35 | 53.0 | 548 | 2 | Q6BU73_DEBHA | Q6bu73 debaryomyc |
| 578 | 35 | 53.0 | 418 | 2 | Q9KK74_BRELN | Q9kk74 brevivibacter | 651 | 35 | 53.0 | 548 | 2 | Q53G06_HUMAN | Q53g06 homo sapien |
| 579 | 35 | 53.0 | 419 | 2 | Q5QJF5_TYCR | Q5qjfe trypanosoma | 652 | 35 | 53.0 | 550 | 2 | Q8J0R1_NECHA | Q8j0r1 nectria hae |
| 580 | 35 | 53.0 | 423 | 2 | Q7SXN0_BRATT | Q7sxn0 brachydanio | 653 | 35 | 53.0 | 550 | 2 | O14419_NECTHA | O14419 nectria hae |
| 581 | 35 | 53.0 | 429 | 2 | Q5NFF9_PRATT | Q5nff9 francisella | 654 | 35 | 53.0 | 554 | 2 | Q6CG27_YARLI | Q6cg27 yarrowia li |
| 582 | 35 | 53.0 | 426 | 2 | Q6A609_PROAC | Q6a609 propionibac | 655 | 35 | 53.0 | 556 | 2 | Q63305_RAT | Q63305 rattus norv |
| 583 | 35 | 53.0 | 432 | 2 | Q7R714_PLAYO | Q7r714 plasmodium | 656 | 35 | 53.0 | 557 | 2 | Q6BTAS_DEBHA | Q6bta5 debaryomyc |
| 584 | 35 | 53.0 | 432 | 2 | Q7ZZX7_XENLA | Q7zzx7 xenopus lae | 657 | 35 | 53.0 | 559 | 2 | Q5ZK08_CHICK | Q5zk08 gallus gall |
| 585 | 35 | 53.0 | 432 | 2 | Q6GLT2_XENLA | Q6glrt2 xenopus lae | 658 | 35 | 53.0 | 559 | 2 | Q6DD18_XENLA | Q6dd18 xenopus lae |
| 586 | 35 | 53.0 | 432 | 2 | Q6NT12_XENLA | Q6ntl2 xenopus lae | 659 | 35 | 53.0 | 562 | 2 | Q4TEK9_TETNG | Q4tek9 tetraodon n |
| 587 | 35 | 53.0 | 432 | 2 | Q6DIJ6_XENTR | Q6dij6 xenopus tro | 660 | 35 | 53.0 | 563 | 2 | Q751M5_ASHGO | Q751m5 ashbya goss |
| 588 | 35 | 53.0 | 434 | 2 | Q6HAQ7_BACHK | Q6haq7 bacillus th | 661 | 35 | 53.0 | 565 | 2 | Q7PST8_ANOGA | Q7pst8 anopheles g |
| 589 | 35 | 53.0 | 434 | 2 | Q81212_BACCR | Q81212 bacillus ce | 662 | 35 | 53.0 | 573 | 2 | O16166_9DIPT | O16166 drosophila |
| 590 | 35 | 53.0 | 434 | 2 | Q81J52_BACAN | Q81j52 bacillus an | 663 | 35 | 53.0 | 574 | 2 | Q4WHE9_ORYSA | Q4whe9 aspergillus |
| 591 | 35 | 53.0 | 434 | 2 | Q630M2_BACCC | Q630m2 bacillus ce | 664 | 35 | 53.0 | 588 | 2 | Q7FAW5_ORYSA | Q7faw5 oryza sativ |
| 592 | 35 | 53.0 | 435 | 2 | Q92U62_ARATH | Q92u62 arabidopsis | 665 | 35 | 53.0 | 595 | 2 | O5ZZT8_MYCHV | O5zzt8 mycoplasma |
| 593 | 35 | 53.0 | 436 | 2 | Q30428_CALSA | Q30428 caldocellum | 666 | 35 | 53.0 | 595 | 2 | Q8JTV1_LSDV | Q8jtv1 lumpy skin |
| 594 | 35 | 53.0 | 440 | 2 | Q4K798_PSEF5 | Q4k798 pseudomonas | 667 | 35 | 53.0 | 596 | 2 | Q91MW7_LSDV | Q91mw7 lumpy skin |
| 595 | 35 | 53.0 | 441 | 2 | Q4ZP93_PSESM | Q4z993 pseudomonas | 668 | 35 | 53.0 | 603 | 1 | SYT_SINY3 | Q55806 synechocyst |
| 596 | 35 | 53.0 | 441 | 2 | Q87X92_PGESH | Q87x92 pseudomonas | 669 | 35 | 53.0 | 604 | 2 | Q9NDG9_CAEBR | Q9ndg9 caenorhabdi |
| 597 | 35 | 53.0 | 442 | 2 | Q9JHL7_RAT | Q9jhl7 rattus norv | 670 | 35 | 53.0 | 610 | 2 | Q620F2_CAEBR | Q620f2 caenorhabdi |
| 598 | 35 | 53.0 | 452 | 2 | Q6CSV8_KLUJA | Q6csv8 kluyveromyc | 671 | 35 | 53.0 | 616 | 2 | Q7TP71_RAT | Q7tp71 rattus norv |
| 599 | 35 | 53.0 | 452 | 2 | Q8NMH0_CORGL | Q8nmh0 corynebacte | 672 | 35 | 53.0 | 627 | 2 | Q7RAY6_PLAYO | Q7ray6 plasmodium |
| 600 | 35 | 53.0 | 453 | 2 | Q70S31_KLUJA | Q70s31 kluyveromyc | 673 | 35 | 53.0 | 629 | 2 | Q9F3Q6_STRCO | Q9f3q6 streptomyce |
| 601 | 35 | 53.0 | 454 | 2 | Q5D9C4_SCHJA | Q5d9c4 schistosoma | 674 | 35 | 53.0 | 631 | 2 | Q8A0R8_BACTN | Q8a0r8 bacteroides |
| 602 | 35 | 53.0 | 454 | 2 | Q637C8_BACCC | Q637c8 bacillus ce | 675 | 35 | 53.0 | 633 | 2 | Q6PA48_XENLA | Q6pa48 xenopus lae |
| 603 | 35 | 53.0 | 456 | 2 | Q7ULY7_RHOBA | Q7uly7 rhodopirell | 676 | 35 | 53.0 | 636 | 1 | SYT_GEOSL | Q74d04 geobacter s |
| 604 | 35 | 53.0 | 458 | 2 | Q6CAX2_YARLI | Q6cax2 yarrowia li | 677 | 35 | 53.0 | 645 | 2 | Q8RFB4_FUSNN | Q8rfb4 fusobacteri |
| 605 | 35 | 53.0 | 458 | 2 | Q63093_RAT | Q63093 rattus norv | 678 | 35 | 53.0 | 671 | 2 | Q6CGT2_YARLI | Q6cgt2 yarrowia li |
| 606 | 35 | 53.0 | 459 | 2 | Q9JHL6_RAT | Q9jhl6 rattus norv | 679 | 35 | 53.0 | 671 | 2 | Q6CBJ1_YARLI | Q6cbj1 yarrowia li |
| 607 | 35 | 53.0 | 460 | 2 | Q4TEU1_TETNG | Q4tel1 tetraodon n | 680 | 35 | 53.0 | 685 | 2 | Q63288_RAT | Q63288 rattus norv |
| 608 | 35 | 53.0 | 461 | 2 | Q6C9R1_YARLI | Q6c9r1 yarrowia li | 681 | 35 | 53.0 | 686 | 1 | GBRAL_DROME | Q24352 drosophila |
| 609 | 35 | 53.0 | 462 | 2 | Q7UES9_RHOBA | Q7ues9 rhodopirell | 682 | 35 | 53.0 | 691 | 2 | Q9KQW0_VIBCH | Q9kqw0 vibrio chol |
| 610 | 35 | 53.0 | 463 | 2 | Q9A413_CAUCR | Q9a413 caulobacter | 683 | 35 | 53.0 | 717 | 2 | Q7RYE3_NEUCH | Q7rye3 neurospora |
| 611 | 35 | 53.0 | 465 | 1 | ARBB_ERWCH | P6206 erwinia chr | 684 | 35 | 53.0 | 723 | 2 | Q6C7L9_YARLI | Q6c7l9 yarrowia li |
| 612 | 35 | 53.0 | 473 | 2 | Q7TQ81_RAT | Q7tq81 rattus norv | 685 | 35 | 53.0 | 730 | 2 | Q6FNC7_CANGA | Q6fnc7 candida gla |
| 613 | 35 | 53.0 | 477 | 2 | Q7R857_PLAYO | Q7r857 plasmodium | 686 | 35 | 53.0 | 754 | 2 | Q6QI12_RAT | Q6qil2 rattus norv |
| 614 | 35 | 53.0 | 481 | 2 | Q6M2N3_CORGL | Q6m2n3 corynebacte | 687 | 35 | 53.0 | 766 | 2 | Q4WVZ5_ASPFU | Q4wvz5 aspergillus |
| 615 | 35 | 53.0 | 481 | 2 | Q8D7X6_VIBVU | Q8d7x6 vibrio vuln | 688 | 35 | 53.0 | 785 | 2 | Q9CNO5_PASPU | Q9cno5 pasteurella |

| | | | | | | | | | | | | | | | |
|-----|----|------|------|---|--------------|--------|-------------|-----|------|------|------|---|--------------|--------|-------------|
| 689 | 35 | 53.0 | 845 | 2 | Q5F858_GLUOX | Q5f858 | gluconobact | 762 | 35 | 53.0 | 3392 | 2 | Q8B646_9FLAV | Q8b646 | dengue viru |
| 690 | 35 | 53.0 | 896 | 2 | Q6APC9_DESPS | Q6apc9 | desulfocale | 763 | 35 | 53.0 | 3392 | 2 | Q8B647_9FLAV | Q8b647 | dengue viru |
| 691 | 35 | 53.0 | 970 | 2 | Q4UTT8_XANCP | Q4utt8 | xanthomonas | 764 | 35 | 53.0 | 3392 | 2 | Q8B648_9FLAV | Q8b648 | dengue viru |
| 692 | 35 | 53.0 | 970 | 2 | Q8P9U8_XANCP | Q8p9u8 | xanthomonas | 765 | 35 | 53.0 | 3392 | 2 | Q8B665_9FLAV | Q8b665 | dengue viru |
| 693 | 35 | 53.0 | 978 | 2 | Q8PLM7_XANAC | Q8plm7 | xanthomonas | 766 | 35 | 53.0 | 3392 | 2 | Q8JQD9_9FLAV | Q8jqd9 | dengue viru |
| 694 | 35 | 53.0 | 1015 | 2 | Q7TMA9_RAT | Q7tma9 | rattus norv | 767 | 35 | 53.0 | 3392 | 2 | Q8JQE3_9FLAV | Q8jqe3 | dengue viru |
| 695 | 35 | 53.0 | 1028 | 1 | QNT16_HUMAN | Q9uq52 | homo sapien | 768 | 35 | 53.0 | 3392 | 2 | Q8JQF0_9FLAV | Q8jqf0 | dengue viru |
| 696 | 35 | 53.0 | 1028 | 1 | Q51BN5_ENTHI | Q5lbn5 | entamoeba h | 769 | 35 | 53.0 | 3392 | 2 | Q8JQF2_9FLAV | Q8jqf2 | dengue viru |
| 697 | 35 | 53.0 | 1028 | 2 | Q5R6D4_PONPY | Q5r6d4 | pongo pygma | 770 | 35 | 53.0 | 3392 | 2 | Q8VBS2_9FLAV | Q8vb52 | dengue viru |
| 698 | 35 | 53.0 | 1056 | 2 | Q4Z5X1_FLABE | Q4z5x1 | plasmodium | 771 | 35 | 53.0 | 3392 | 2 | Q8VBS3_9FLAV | Q8vb53 | dengue viru |
| 699 | 35 | 53.0 | 1073 | 2 | Q6Q157_RAT | Q6q157 | rattus norv | 772 | 35 | 53.0 | 3392 | 2 | Q91ND2_9FLAV | Q91nd2 | dengue viru |
| 700 | 35 | 53.0 | 1074 | 1 | EMBC_MYCSM | Q50393 | mycobacteri | 773 | 35 | 53.0 | 3392 | 2 | Q91NH1_9FLAV | Q91nh1 | dengue viru |
| 701 | 35 | 53.0 | 1104 | 2 | Q6TUH9_RAT | Q6tuh9 | rattus norv | 774 | 35 | 53.0 | 3392 | 2 | Q91NH2_9FLAV | Q91nh2 | dengue viru |
| 702 | 35 | 53.0 | 1119 | 2 | Q6TUF9_RAT | Q6tuf9 | rattus norv | 775 | 35 | 53.0 | 3392 | 2 | Q91I01_9FLAV | Q91i01 | dengue viru |
| 703 | 35 | 53.0 | 1120 | 2 | Q5B3P4_EMENI | Q5b3p4 | aspergillus | 776 | 35 | 53.0 | 3392 | 2 | Q91I02_9FLAV | Q91i02 | dengue viru |
| 704 | 35 | 53.0 | 1142 | 2 | Q6Q165_RAT | Q6q165 | rattus norv | 777 | 35 | 53.0 | 3392 | 2 | P89313_9FLAV | P89313 | dengue viru |
| 705 | 35 | 53.0 | 1159 | 1 | SORC2_HUMAN | Q96p90 | homo sapien | 778 | 35 | 53.0 | 3392 | 2 | P89314_9FLAV | P89314 | dengue viru |
| 706 | 35 | 53.0 | 1159 | 1 | SORC2_HUMAN | Q96p95 | mus musculu | 779 | 35 | 53.0 | 3392 | 2 | P89315_9FLAV | P89315 | dengue viru |
| 707 | 35 | 53.0 | 1163 | 2 | Q7REA4_PLAYO | Q7rea4 | plasmodium | 780 | 35 | 53.0 | 3392 | 2 | Q8B104_9FLAV | Q8b104 | dengue viru |
| 708 | 35 | 53.0 | 1185 | 2 | Q8CHA4_MOUSE | Q8cha4 | mus musculu | 781 | 35 | 53.0 | 3392 | 2 | Q8B105_9FLAV | Q8b105 | dengue viru |
| 709 | 35 | 53.0 | 1202 | 2 | Q4T884_TETNG | Q4t884 | tetraodon n | 782 | 35 | 53.0 | 3392 | 2 | Q8B106_9FLAV | Q8b106 | dengue viru |
| 710 | 35 | 53.0 | 1217 | 2 | Q6TUF6_RAT | Q6tuf6 | rattus norv | 783 | 35 | 53.0 | 3392 | 2 | Q98Y40_9FLAV | Q98y40 | dengue viru |
| 711 | 35 | 53.0 | 1219 | 2 | Q9QTM3_MOUSE | Q9qtm3 | mus musculu | 784 | 35 | 53.0 | 3392 | 2 | Q9J7C5_9FLAV | Q9j7c5 | dengue viru |
| 712 | 35 | 53.0 | 1252 | 2 | Q9QWY2_MOUSE | Q9qwY2 | mus musculu | 785 | 35 | 53.0 | 3392 | 2 | Q9J7C6_9FLAV | Q9j7c6 | dengue viru |
| 713 | 35 | 53.0 | 1263 | 2 | Q50SH1_ENTHI | Q50sh1 | entamoeba h | 786 | 35 | 53.0 | 3392 | 2 | Q5IK03_9FLAV | Q5ik03 | dengue viru |
| 714 | 35 | 53.0 | 1275 | 2 | Q4JFW1_RAT | Q4jfw1 | rattus norv | 787 | 35 | 53.0 | 3396 | 1 | POLG_DEN1S | P33478 | d genome po |
| 715 | 35 | 53.0 | 1275 | 2 | Q4JFW3_RAT | Q4jfw3 | rattus norv | 788 | 34.5 | 52.3 | 161 | 2 | Q12155_YEAST | Q12155 | saccharomyc |
| 716 | 35 | 53.0 | 1281 | 1 | POL2_MOUSE | P11369 | mus musculu | 789 | 34.5 | 52.3 | 190 | 2 | Q6SGG5_9BACT | Q6sgg5 | uncultured |
| 717 | 35 | 53.0 | 1281 | 2 | Q54850_MOUSE | Q54850 | mus musculu | 790 | 34.5 | 52.3 | 203 | 2 | Q6SET4_9BACT | Q6set4 | uncultured |
| 718 | 35 | 53.0 | 1281 | 2 | Q91288_MOUSE | Q91288 | mus musculu | 791 | 34.5 | 52.3 | 272 | 2 | Q5P9D6_ANAMM | Q5p9d6 | anaplasm m |
| 719 | 35 | 53.0 | 1281 | 2 | Q88913_MOUSE | Q88913 | mus musculu | 792 | 34.5 | 52.3 | 323 | 2 | Q8LJ47_ORYSA | Q8lj47 | oryza sativ |
| 720 | 35 | 53.0 | 1281 | 2 | Q91289_MOUSE | Q91289 | mus musculu | 793 | 34.5 | 52.3 | 323 | 2 | Q8HV96_9LILI | Q8hv96 | alpinia gal |
| 721 | 35 | 53.0 | 1281 | 2 | Q9QWY3_MOUSE | Q9qwY3 | mus musculu | 794 | 34.5 | 52.3 | 515 | 2 | Q8HV99_9LILI | Q8hv99 | alpinia con |
| 722 | 35 | 53.0 | 1281 | 2 | Q88914_MOUSE | Q88914 | mus musculu | 795 | 34.5 | 52.3 | 613 | 2 | Q8VCX7_MOUSE | Q8vcx7 | mus musculu |
| 723 | 35 | 53.0 | 1281 | 2 | Q9QWY0_MOUSE | Q9qwY0 | mus musculu | 796 | 34.5 | 52.3 | 802 | 2 | Q7VMP1_HABDU | Q7vmp1 | haemophilus |
| 724 | 35 | 53.0 | 1281 | 2 | Q88915_MOUSE | Q88915 | mus musculu | 797 | 34 | 51.5 | 33 | 2 | Q72EV9_DESVH | Q72ev9 | desulfovibr |
| 725 | 35 | 53.0 | 1281 | 2 | Q79219_MOUSE | Q79219 | mus musculu | 798 | 34 | 51.5 | 39 | 1 | SIP_HUMAN | P83897 | homo sapien |
| 726 | 35 | 53.0 | 1281 | 2 | Q9QUI2_MOUSE | Q9qui2 | mus musculu | 799 | 34 | 51.5 | 47 | 2 | Q4SZA2_TETNG | Q4sza2 | tetraodon n |
| 727 | 35 | 53.0 | 1300 | 2 | Q97692_RAT | P97692 | rattus norv | 800 | 34 | 51.5 | 53 | 2 | Q4H157_9ASPA | Q4h157 | doryanthas |
| 728 | 35 | 53.0 | 1300 | 2 | Q08906_MOUSE | Q08906 | mus musculu | 801 | 34 | 51.5 | 59 | 2 | Q7QVG6_GIALA | Q7qvg6 | giardia lam |
| 729 | 35 | 53.0 | 1300 | 2 | Q61785_MOUSE | Q61785 | mus musculu | 802 | 34 | 51.5 | 67 | 2 | Q973Z1_SUITO | Q973z1 | sulfolobus |
| 730 | 35 | 53.0 | 1356 | 2 | Q6Q176_RAT | Q6q176 | rattus norv | 803 | 34 | 51.5 | 73 | 2 | Q4H151_9ASPA | Q4h151 | paterosonia |
| 731 | 35 | 53.0 | 1366 | 2 | Q6Q158_RAT | Q6q158 | rattus norv | 804 | 34 | 51.5 | 74 | 2 | Q547A4_DICDI | Q547a4 | dictyosteli |
| 732 | 35 | 53.0 | 1451 | 2 | Q6Q173_RAT | Q6q173 | rattus norv | 805 | 34 | 51.5 | 76 | 2 | Q5BRP5_SCHJA | Q5brp5 | schistosoma |
| 733 | 35 | 53.0 | 1476 | 2 | Q75870_ASHGO | Q75b70 | ashbya goss | 806 | 34 | 51.5 | 88 | 2 | Q56196_STAXY | Q56196 | staphylococ |
| 734 | 35 | 53.0 | 1504 | 2 | Q54877_DICDI | Q54gr7 | dictyosteli | 807 | 34 | 51.5 | 92 | 2 | Q5LBA8_BACFN | Q5lba8 | bacteroides |
| 735 | 35 | 53.0 | 1575 | 2 | Q6TXJ1_RAT | Q6txj1 | rattus norv | 808 | 34 | 51.5 | 104 | 2 | Q5AQ94_EMENI | Q5aq94 | aspergillus |
| 736 | 35 | 53.0 | 1614 | 2 | Q560B3_CRYNE | Q560b3 | cryptococcu | 809 | 34 | 51.5 | 104 | 2 | Q60533_MESAU | Q60533 | mesocricetu |
| 737 | 35 | 53.0 | 1617 | 2 | Q5KPB6_CRYNE | Q5kpb6 | cryptococcu | 810 | 34 | 51.5 | 106 | 2 | Q7UMY5_RHOBA | Q7umy5 | rhodopirell |
| 738 | 35 | 53.0 | 1687 | 2 | Q6Q117_RAT | Q6q117 | rattus norv | 811 | 34 | 51.5 | 109 | 2 | Q51P52_MAGGR | Q51p52 | magnaporthe |
| 739 | 35 | 53.0 | 1710 | 2 | Q6Q114_RAT | Q6q114 | rattus norv | 812 | 34 | 51.5 | 110 | 2 | Q6BM76_DEBHA | Q6bm76 | debaromyce |
| 740 | 35 | 53.0 | 1714 | 2 | Q6Q178_RAT | Q6q178 | rattus norv | 813 | 34 | 51.5 | 112 | 2 | Q8BM65_MOUSE | Q8bm65 | mus musculu |
| 741 | 35 | 53.0 | 1987 | 2 | Q50XF4_ENTHI | Q50xf4 | entamoeba h | 814 | 34 | 51.5 | 114 | 2 | Q76YY1_9CAUD | Q76yy1 | bacterioph |
| 742 | 35 | 53.0 | 2040 | 2 | Q6QRQ1_BRARE | Q6qrq1 | brachydanio | 815 | 34 | 51.5 | 117 | 2 | Q73222_9HIV2 | Q73222 | human immun |
| 743 | 35 | 53.0 | 2064 | 2 | Q9PAT8_XYLFA | Q9pat8 | xyella fas | 816 | 34 | 51.5 | 119 | 2 | Q8A317_BACTN | Q8a317 | bacteroides |
| 744 | 35 | 53.0 | 2196 | 2 | Q93WZ7_PHAVU | Q93wz7 | phaseolus v | 817 | 34 | 51.5 | 122 | 1 | HV20_MOUSE | P01789 | mus musculu |
| 745 | 35 | 53.0 | 2297 | 2 | Q7QXW5_GIALA | Q7qxw5 | giardia lam | 818 | 34 | 51.5 | 130 | 2 | Q7V0B0_PROMP | Q7v0b0 | prochloroco |
| 746 | 35 | 53.0 | 2457 | 2 | Q51ZRL_9FLAV | Q51zrl | dengue viru | 819 | 34 | 51.5 | 133 | 2 | Q8MK56_BOVIN | Q8mk56 | bos taurus |
| 747 | 35 | 53.0 | 3078 | 2 | Q8IKH4_PLAF7 | Q8ikh4 | plasmodium | 820 | 34 | 51.5 | 133 | 2 | Q93D48_9BACT | Q93d48 | uncultured |
| 748 | 35 | 53.0 | 3152 | 2 | Q4SRE1_TETNG | Q4sre1 | tetraodon n | 821 | 34 | 51.5 | 136 | 2 | Q7P0E8_CHRVO | Q7p0e8 | chromobacte |
| 749 | 35 | 53.0 | 3198 | 2 | Q9UG88_MANSE | Q9ug88 | manduca sex | 822 | 34 | 51.5 | 137 | 2 | Q973P7_SUITO | Q973p7 | sulfolobus |
| 750 | 35 | 53.0 | 3311 | 2 | Q6UBL1_9FLAV | Q6ubl1 | dengue viru | 823 | 34 | 51.5 | 138 | 2 | Q63M85_BURPS | Q63m85 | burkholderi |
| 751 | 35 | 53.0 | 3311 | 2 | Q6U7P9_9FLAV | Q6u7p9 | dengue viru | 824 | 34 | 51.5 | 138 | 2 | Q62D48_BURMA | Q62d48 | burkholderi |
| 752 | 35 | 53.0 | 3392 | 2 | Q5R1T6_9FLAV | Q5r1t6 | dengue viru | 825 | 34 | 51.5 | 140 | 2 | Q6JIM3_9CAUD | Q6jim3 | bacterioph |
| 753 | 35 | 53.0 | 3392 | 2 | Q5UCB9_9FLAV | Q5ucb9 | dengue viru | 826 | 34 | 51.5 | 140 | 2 | Q8W6U1_9CAUD | Q8w6u1 | bacterioph |
| 754 | 35 | 53.0 | 3392 | 2 | Q689G2_9FLAV | Q689g2 | dengue viru | 827 | 34 | 51.5 | 145 | 2 | Q924R3_MOUSE | Q924r3 | mus musculu |
| 755 | 35 | 53.0 | 3392 | 2 | Q689G3_9FLAV | Q689g3 | dengue viru | 828 | 34 | 51.5 | 149 | 2 | Q7R8C6_PLAYO | Q7r8c6 | plasmodium |
| 756 | 35 | 53.0 | 3392 | 2 | Q6WP56_9FLAV | Q6wp56 | dengue viru | 829 | 34 | 51.5 | 150 | 2 | Q6D887_ERWCT | Q6d887 | erwinia car |
| 757 | 35 | 53.0 | 3392 | 2 | Q6WP57_9FLAV | Q6wp57 | dengue viru | 830 | 34 | 51.5 | 153 | 2 | Q4UWV4_XANCP | Q4uwv4 | xanthomonas |
| 758 | 35 | 53.0 | 3392 | 2 | Q6WP58_9FLAV | Q6wp58 | dengue viru | 831 | 34 | 51.5 | 153 | 2 | Q8P798_XANCP | Q8p798 | xanthomonas |
| 759 | 35 | 53.0 | 3392 | 2 | Q75N59_9FLAV | Q75n59 | dengue viru | 832 | 34 | 51.5 | 157 | 2 | Q88UK2_LACPL | Q88uk2 | lactobacill |
| 760 | 35 | 53.0 | 3392 | 2 | Q80KC7_9FLAV | Q80kc7 | dengue viru | 833 | 34 | 51.5 | 160 | 2 | Q6K1S0_MYCOW | Q6k1s0 | mycoplasma |
| 761 | 35 | 53.0 | 3392 | 2 | Q80RP0_9FLAV | Q80rp0 | dengue viru | 834 | 34 | 51.5 | 165 | 2 | Q8MWC8_PLAFA | Q8mwc8 | plasmodium |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|--------------|---------------------|-----|----|------|-----|---|---------------|--------------------|
| 835 | 34 | 51.5 | 165 | 2 | Q8MWC9_PLAFA | Q8mwc9 plasmodium | 908 | 34 | 51.5 | 241 | 2 | Q8IK72_PLAFA7 | Q8ik72 plasmodium |
| 836 | 34 | 51.5 | 166 | 2 | Q8MWC6_PLAFA | Q8mwc6 plasmodium | 909 | 34 | 51.5 | 244 | 2 | Q8KV82_VIBCH | Q8kv82 vibrio chol |
| 837 | 34 | 51.5 | 166 | 2 | Q8MWC7_PLAFA | Q8mwc7 plasmodium | 910 | 34 | 51.5 | 245 | 2 | Q6LW75_PHOPR | Q6lw75 photobacter |
| 838 | 34 | 51.5 | 166 | 2 | Q8MWD0_PLAFA | Q8mwd0 plasmodium | 911 | 34 | 51.5 | 245 | 2 | Q663R9_YERPS | Q663r9 yersinia ps |
| 839 | 34 | 51.5 | 166 | 2 | Q8MWD1_PLAFA | Q8mwd1 plasmodium | 912 | 34 | 51.5 | 245 | 2 | Q7N9U1_PHOLL | Q7n9u1 photorhabdu |
| 840 | 34 | 51.5 | 167 | 2 | Q8PQ67_UREPA | Q8pq67 ureaplasma | 913 | 34 | 51.5 | 245 | 2 | Q829T5_YERPE | Q829t5 yersinia pe |
| 841 | 34 | 51.5 | 168 | 2 | Q8VDC9_MOUSE | Q8vdc9 mus musculus | 914 | 34 | 51.5 | 247 | 2 | Q6CYN8_ERWCT | Q6cyn8 erwinia car |
| 842 | 34 | 51.5 | 171 | 2 | Q8MWC5_PLAFA | Q8mwc5 plasmodium | 915 | 34 | 51.5 | 248 | 2 | Q99251_PLABE | Q99251 plasmodium |
| 843 | 34 | 51.5 | 172 | 2 | Q8HUF9_CAMJR | Q8huf9 campylobact | 916 | 34 | 51.5 | 249 | 2 | Q99254_PLACH | Q99254 plasmodium |
| 844 | 34 | 51.5 | 172 | 2 | Q8PNT7_CAMJR | Q8pnt7 campylobact | 917 | 34 | 51.5 | 249 | 2 | Q63694_PLAVI | Q63694 plasmodium |
| 845 | 34 | 51.5 | 173 | 2 | Q8RVH2_PLAFA | Q8rvh2 plasmodium | 918 | 34 | 51.5 | 249 | 2 | Q53B25_PLAKN | Q53b25 plasmodium |
| 846 | 34 | 51.5 | 173 | 2 | Q4T3M7_TETNG | Q4t3m7 tetrarodon n | 919 | 34 | 51.5 | 249 | 2 | Q4G3R6_PLASI | Q4g3r6 plasmodium |
| 847 | 34 | 51.5 | 174 | 2 | Q89CS9_BRAJA | Q89cs9 bradyrhizob | 920 | 34 | 51.5 | 249 | 2 | Q4G3R3_PLAFR | Q4g3r3 plasmodium |
| 848 | 34 | 51.5 | 176 | 2 | Q51J85_MAGGR | Q51j85 magnaporthe | 921 | 34 | 51.5 | 250 | 2 | Q35441_PLAFA | Q35441 plasmodium |
| 849 | 34 | 51.5 | 176 | 2 | Q4LLM0_9BURK | Q4llm0 burkholderi | 922 | 34 | 51.5 | 250 | 2 | Q7YFB2_PLAFA | Q7yfe2 plasmodium |
| 850 | 34 | 51.5 | 179 | 2 | Q81972_PLAFA | Q81972 plasmodium | 923 | 34 | 51.5 | 250 | 2 | Q7YFE3_PLAFA | Q7yfe3 plasmodium |
| 851 | 34 | 51.5 | 181 | 1 | TXK35_CAEEL | Q93376 caenorhabdi | 924 | 34 | 51.5 | 250 | 2 | Q8SK24_PLAFA | Q8sk24 plasmodium |
| 852 | 34 | 51.5 | 181 | 2 | Q7N616_PHOLL | Q7n616 photorhabdu | 925 | 34 | 51.5 | 250 | 2 | Q6FZB4_BARQU | Q6fzb4 bartonella |
| 853 | 34 | 51.5 | 181 | 2 | Q983A1_RHILO | Q983a1 rhizobium l | 926 | 34 | 51.5 | 250 | 2 | Q6G2V7_BARHE | Q6g2v7 bartonella |
| 854 | 34 | 51.5 | 188 | 2 | Q60CP0_METCA | Q60cp0 methylococc | 927 | 34 | 51.5 | 251 | 2 | Q9ENN2_9PICO | Q9enn2 hepatitis a |
| 855 | 34 | 51.5 | 189 | 2 | Q8NSHO_HUMAN | Q8nsho homo sapien | 928 | 34 | 51.5 | 251 | 2 | Q9ENN3_9PICO | Q9enn3 hepatitis a |
| 856 | 34 | 51.5 | 189 | 2 | Q8MVV3_PLAFA | Q8mvv3 plasmodium | 929 | 34 | 51.5 | 251 | 2 | Q9ENN4_9PICO | Q9enn4 hepatitis a |
| 857 | 34 | 51.5 | 189 | 2 | Q8MVV5_PLAFA | Q8mvv5 plasmodium | 930 | 34 | 51.5 | 251 | 2 | Q9ENN5_9PICO | Q9enn5 hepatitis a |
| 858 | 34 | 51.5 | 189 | 2 | Q8MVV6_PLAFA | Q8mvv6 plasmodium | 931 | 34 | 51.5 | 251 | 2 | Q9ENN6_9PICO | Q9enn6 hepatitis a |
| 859 | 34 | 51.5 | 189 | 2 | Q8MVV9_PLAFA | Q8mvv9 plasmodium | 932 | 34 | 51.5 | 251 | 2 | Q9ENN8_9PICO | Q9enn8 hepatitis a |
| 860 | 34 | 51.5 | 189 | 2 | Q8MVW3_PLAFA | Q8mvw3 plasmodium | 933 | 34 | 51.5 | 251 | 2 | Q9ENN9_9PICO | Q9enn9 hepatitis a |
| 861 | 34 | 51.5 | 189 | 2 | Q767P6_9ACTO | Q767f6 actinoplane | 934 | 34 | 51.5 | 251 | 2 | Q9ENP0_9PICO | Q9enp0 hepatitis a |
| 862 | 34 | 51.5 | 192 | 2 | Q8T4L1_BRUMA | Q8t4l1 brugia mala | 935 | 34 | 51.5 | 251 | 2 | Q9ENP1_9PICO | Q9enp1 hepatitis a |
| 863 | 34 | 51.5 | 193 | 2 | Q73YD3_MYCPA | Q73y3d3 mycobacteri | 936 | 34 | 51.5 | 251 | 2 | Q9ENP2_9PICO | Q9enp2 hepatitis a |
| 864 | 34 | 51.5 | 196 | 1 | YFB3_LACIA | P42097 lactococcu | 937 | 34 | 51.5 | 251 | 2 | Q9ENP3_9PICO | Q9enp3 hepatitis a |
| 865 | 34 | 51.5 | 199 | 2 | Q6PAQ3_MOUSE | Q6paq3 mus musculu | 938 | 34 | 51.5 | 251 | 2 | Q9ENP4_9PICO | Q9enp4 hepatitis a |
| 866 | 34 | 51.5 | 200 | 2 | Q5WGR0_BACSK | Q5wgr0 bacillus cl | 939 | 34 | 51.5 | 251 | 2 | Q9ENP6_9PICO | Q9enp6 hepatitis a |
| 867 | 34 | 51.5 | 201 | 2 | Q88CR6_PSEPK | Q88cr6 pseudomonas | 940 | 34 | 51.5 | 251 | 2 | Q9ENP7_9PICO | Q9enp7 hepatitis a |
| 868 | 34 | 51.5 | 201 | 2 | Q5RFU3_PONPY | Q5rfu3 pongo pygma | 941 | 34 | 51.5 | 251 | 2 | Q9ENP8_9PICO | Q9enp8 hepatitis a |
| 869 | 34 | 51.5 | 201 | 2 | Q5L2H2_GROKA | Q5l2h2 geobacillus | 942 | 34 | 51.5 | 251 | 2 | Q9ENP9_9PICO | Q9enp9 hepatitis a |
| 870 | 34 | 51.5 | 202 | 1 | ADHR_DROER | P28485 drosophila | 943 | 34 | 51.5 | 251 | 2 | Q9ENQ0_9PICO | Q9enq0 hepatitis a |
| 871 | 34 | 51.5 | 202 | 2 | Q54CA3_DICDI | Q54ca3 dictyosteli | 944 | 34 | 51.5 | 251 | 2 | Q9ENQ1_9PICO | Q9enq1 hepatitis a |
| 872 | 34 | 51.5 | 202 | 2 | Q5DB14_SCHJA | Q5db14 schistosoma | 945 | 34 | 51.5 | 251 | 2 | Q9ENQ2_9PICO | Q9enq2 hepatitis a |
| 873 | 34 | 51.5 | 205 | 2 | Q8RB21_THETN | Q8rb21 thermoaer | 946 | 34 | 51.5 | 251 | 2 | Q9ENQ3_9PICO | Q9enq3 hepatitis a |
| 874 | 34 | 51.5 | 207 | 2 | Q8PTJ3_METMA | Q8ptj3 methanosarc | 947 | 34 | 51.5 | 251 | 2 | Q9ENQ4_9PICO | Q9enq4 hepatitis a |
| 875 | 34 | 51.5 | 207 | 2 | Q8PJK4_XANAC | Q8pj4k xanthomonas | 948 | 34 | 51.5 | 251 | 2 | Q9ENQ5_9PICO | Q9enq5 hepatitis a |
| 876 | 34 | 51.5 | 209 | 2 | Q9ZURO_ARATH | Q9zur0 arabidopsis | 949 | 34 | 51.5 | 251 | 2 | Q9ENQ6_9PICO | Q9enq6 hepatitis a |
| 877 | 34 | 51.5 | 209 | 2 | Q8Y043_RALSO | Q8y043 ralstonia s | 950 | 34 | 51.5 | 251 | 2 | Q9ENQ7_9PICO | Q9enq7 hepatitis a |
| 878 | 34 | 51.5 | 210 | 1 | ACUA_BACSU | P39065 bacillus su | 951 | 34 | 51.5 | 251 | 2 | Q9ENQ8_9PICO | Q9enq8 hepatitis a |
| 879 | 34 | 51.5 | 210 | 2 | Q4L778_STAHL | Q4l778 staphylococ | 952 | 34 | 51.5 | 251 | 2 | Q9ENQ9_9PICO | Q9enq9 hepatitis a |
| 880 | 34 | 51.5 | 210 | 2 | Q5KM44_GROKA | Q5kw44 geobacillus | 953 | 34 | 51.5 | 251 | 2 | Q9ENR0_9PICO | Q9enr0 hepatitis a |
| 881 | 34 | 51.5 | 210 | 2 | Q5WBB5_BACSK | Q5wbb5 bacillus cl | 954 | 34 | 51.5 | 251 | 2 | Q9ENR1_9PICO | Q9enr1 hepatitis a |
| 882 | 34 | 51.5 | 210 | 2 | Q8HCL6_BACHK | Q8hcl6 bacillus th | 955 | 34 | 51.5 | 252 | 1 | SPIT2_HUMAN | Q43291 homo sapien |
| 883 | 34 | 51.5 | 210 | 2 | Q81KS4_BACAN | Q81ks4 bacillus an | 956 | 34 | 51.5 | 252 | 2 | Q6LEU8_HUMAN | Q6leu8 homo sapien |
| 884 | 34 | 51.5 | 210 | 2 | Q6G8J3_STAAS | Q6g8j3 staphylococ | 957 | 34 | 51.5 | 256 | 2 | Q4HL37_CAMLA | Q4hl37 campylobact |
| 885 | 34 | 51.5 | 210 | 2 | Q6GFX4_STAAR | Q6gfx4 staphylococ | 958 | 34 | 51.5 | 257 | 2 | Q81112_WHEAT | Q81112 triticum ae |
| 886 | 34 | 51.5 | 210 | 2 | Q8HF40_STAAC | Q8hf40 staphylococ | 959 | 34 | 51.5 | 261 | 1 | Y1353_MGCTU | P67434 mycobacteri |
| 887 | 34 | 51.5 | 210 | 2 | Q7A534_STAAN | Q7a534 staphylococ | 960 | 34 | 51.5 | 261 | 1 | Y1388_MYCBO | P67435 mycobacteri |
| 888 | 34 | 51.5 | 210 | 2 | Q8NW35_STAAN | Q8nw35 staphylococ | 961 | 34 | 51.5 | 261 | 2 | Q95314_ECHGY | Q95314 echinosorex |
| 889 | 34 | 51.5 | 210 | 2 | Q89TD0_STAAM | Q89td0 staphylococ | 962 | 34 | 51.5 | 261 | 2 | Q710S9_JACJA | Q710s9 jaculis jac |
| 890 | 34 | 51.5 | 210 | 2 | Q9K7X3_BACHD | Q9k7x3 bacillus ha | 963 | 34 | 51.5 | 261 | 2 | Q94S84_PLABI | Q94s84 platichthys |
| 891 | 34 | 51.5 | 210 | 2 | Q65G33_BACLD | Q65g33 bacillus li | 964 | 34 | 51.5 | 263 | 1 | COX3_PLAVI | Q36675 plasmodium |
| 892 | 34 | 51.5 | 211 | 2 | Q73QD9_TREDE | Q73qd9 treponema d | 965 | 34 | 51.5 | 263 | 2 | Q9T4X8_PLAVI | Q9t4x8 plasmodium |
| 893 | 34 | 51.5 | 214 | 2 | Q4MVR1_BACCE | Q4mvr1 bacillus ce | 966 | 34 | 51.5 | 263 | 2 | Q7PCZ8_PLAYO | Q7pcz8 plasmodium |
| 894 | 34 | 51.5 | 214 | 2 | Q72Z67_BACCI | Q72z67 bacillus th | 967 | 34 | 51.5 | 263 | 2 | Q4XD06_PLACH | Q4xd06 plasmodium |
| 895 | 34 | 51.5 | 214 | 2 | Q81629_BACCR | Q81629 bacillus ce | 968 | 34 | 51.5 | 263 | 2 | Q5MJB2_9APIC | Q5mjb2 plasmodium |
| 896 | 34 | 51.5 | 214 | 2 | Q633C7_BACCC | Q633c7 bacillus ce | 969 | 34 | 51.5 | 263 | 2 | Q5MJB5_9APIC | Q5mjb5 plasmodium |
| 897 | 34 | 51.5 | 217 | 2 | Q8CX4A_OCEIH | Q8cxa4 oceanobacil | 970 | 34 | 51.5 | 263 | 2 | Q5MJB8_PLASI | Q5mjb8 plasmodium |
| 898 | 34 | 51.5 | 220 | 2 | Q60ZV9_CABER | Q60zv9 caenorhabdi | 971 | 34 | 51.5 | 263 | 2 | Q5MJC1_9APIC | Q5mjc1 plasmodium |
| 899 | 34 | 51.5 | 226 | 2 | Q931B2_STAAN | Q931b2 staphylococ | 972 | 34 | 51.5 | 263 | 2 | Q5MJC4_9APIC | Q5mjc4 plasmodium |
| 900 | 34 | 51.5 | 226 | 2 | Q51998_STAAN | Q51998 staphylococ | 973 | 34 | 51.5 | 263 | 2 | Q5S0B4_PLAVI | Q5s0b4 plasmodium |
| 901 | 34 | 51.5 | 226 | 2 | Q8CU53_STAEP | Q8cu53 staphylococ | 974 | 34 | 51.5 | 263 | 2 | Q5S0D2_PLAVI | Q5s0d2 plasmodium |
| 902 | 34 | 51.5 | 229 | 2 | Q7VF22_HELHP | Q7vf22 helicobacte | 975 | 34 | 51.5 | 263 | 2 | Q5S0S0_PLAVI | Q5s0s0 plasmodium |
| 903 | 34 | 51.5 | 231 | 2 | Q6TDN0_9VIRU | Q6tdn0 sulfolobus | 976 | 34 | 51.5 | 263 | 2 | Q5S0S3_PLAVI | Q5s0s3 plasmodium |
| 904 | 34 | 51.5 | 233 | 2 | Q8SWC1_HCMV | Q8swc1 human cytom | 977 | 34 | 51.5 | 263 | 2 | Q5S0V6_PLAVI | Q5s0v6 plasmodium |
| 905 | 34 | 51.5 | 237 | 2 | Q9VCB4_DROME | Q9vcb4 drosophila | 978 | 34 | 51.5 | 263 | 2 | Q5S176_PLAVI | Q5s176 plasmodium |
| 906 | 34 | 51.5 | 239 | 2 | Q03133_TROAR | Q03133 trochodendr | 979 | 34 | 51.5 | 263 | 2 | Q5S114_PLAVI | Q5s114 plasmodium |
| 907 | 34 | 51.5 | 240 | 2 | Q6WMX1_DROER | Q6wmx1 drosophila | 980 | 34 | 51.5 | 263 | 2 | Q5S1M0_PLAVI | Q5s1m0 plasmodium |

981 34 51.5 263 2 Q5S1N5 PLAVI
 982 34 51.5 263 2 Q5S0M5 PLAVI
 983 34 51.5 263 2 Q4G4V4 PLAVI
 984 34 51.5 263 2 Q4G4T6 PLAVI
 985 34 51.5 266 1 TRUA HALSA
 986 34 51.5 267 2 Q5KCY6 CRYNE
 987 34 51.5 267 2 Q8MVU4 PLAVA
 988 34 51.5 267 2 Q8MVU5 PLAVA
 989 34 51.5 267 2 Q8MVU6 PLAVA
 990 34 51.5 267 2 Q8MVU7 PLAVA
 991 34 51.5 267 2 Q8MVU8 PLAVA
 992 34 51.5 268 2 Q61SA9 CAEBR
 993 34 51.5 268 2 Q73XB5 MYCPA
 994 34 51.5 269 1 ADHR DROLE
 995 34 51.5 272 1 ADHR DROMA
 996 34 51.5 272 1 ADHR DROME
 997 34 51.5 272 1 ADHR DROTE
 998 34 51.5 272 2 Q6MMW4 9DIPT
 999 34 51.5 272 2 Q6MMW8 DROEU
 1000 34 51.5 272 2 Q6MMX0 DROOR

ALIGNMENTS

RESULT 1
 Q4IQ63_GIBZE
 ID Q4IQ63_GIBZE PRELIMINARY; PRT; 635 AA.
 AC Q4IQ63;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=FG00645.1;
 OS Gibberella zeae PH-1.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
 OX NCBI_TaxID=229533;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PH-1;
 RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
 RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
 RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
 RA Choepel J.S., Collymore A., Cook A., Cooke P., Corum B., DeArelano K.,
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
 RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
 RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
 RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
 RA Kalls C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
 RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
 RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
 RA Minova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
 RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
 RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
 RA Roman J., Schauer S., Schuback R., Seaman S., Severy P., Smirnov S.,
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
 RA Talanas J., Tesfaye S., Theodore J., Topham K., Travers M.,
 RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
 RA Lander E.;
 RT "Fusarium graminearum genome sequence.";
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC ENBL: AACW01000030; EAA68375.1; -; Genomic_DNA.
 DR EMBL: AACW01000030;
 KW Hypothetical protein.
 SQ SEQUENCE 635 AA; 72301 MW; 038C700441D151D6 CRC64;

Query Match 68.2%; Score 45; DB 2; Length 635;

Best Local Similarity 75.0%; Pred. No. 68;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 TVFYWYFD 10
 Db 543 TLFFWYFD 550
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RESULT 2
 Q6H0Z5_9CREN
 ID Q6H0Z5_9CREN PRELIMINARY; PRT; 108 AA.
 AC Q6H0Z5;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Sulfolobus tengchongensis.
 OG Plasmid pTC.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=207809;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Xiang X., Huang L.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY517480; AAT46501.1; -; Genomic_DNA.
 KW Hypothetical protein; Plasmid.
 SQ SEQUENCE 108 AA; 12360 MW; C12448875911B87F CRC64;

Query Match 66.7%; Score 44; DB 2; Length 108;
 Best Local Similarity 75.0%; Pred. No. 17;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 VFYWYFDV 11
 Db 53 IMYWYFDV 60
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RESULT 3
 Q4NJB2_9MICC
 ID Q4NJB2_9MICC PRELIMINARY; PRT; 197 AA.
 AC Q4NJB2;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=ArthCDRAFT_2925;
 OS Arthrobacter sp. FB24.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Micrococineae; Micrococcaceae; Arthrobacter.
 OX NCBI_TaxID=290399;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FB24;
 RG US DOE Joint Genome Institute (JGI-PGF);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
 RA Hammon N., Israni S., Pitluck S., Richardson P.,
 RA "Sequencing of the draft genome assembly of Arthrobacter sp. FB24.";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FB24;
 RG US DOE Joint Genome Institute (PGF-ORNL);
 RA Larimer F., Land M.;
 RT "Annotation of the draft genome assembly of Arthrobacter sp. FB24.";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL: AAHG01000003; EAL97058.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 197 AA; 22370 MW; 6A2F0A103C31FB7E CRC64;

Query Match 66.7%; Score 44; DB 2; Length 197;
 Best Local Similarity 50.0%; Pred. No. 31;
 Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 RETVFWYFD 10
 DB 132 RDSIFWYHFN 141
 |::|||::|
 132 RDSIFWYHFN 141

RESULT 4

Q030303_9VIRU PRELIMINARY; PRT; 222 AA.
 ID 09030303_9VIRU PRELIMINARY; PRT; 222 AA.
 AC 09030303_9VIRU PRELIMINARY; PRT; 222 AA.
 DT 01-NOV-1998 (TREMELrel. 08, Created)
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Rice tungro bacilliform virus.
 OC Viruses; Retroviral viruses; Caulimoviridae; Tungrovirus.
 OX NCBI_TaxID=10654;
 RN NCBI_TaxID=10654;
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Serdaang;
 RX MEDLINE=99119505; PubMed=9918890; DOI=10.1006/viro.1998.9519;
 RA Marney P., Bothner B., Jacquot E., de Kochko A., Ong C.A., Yot P.,
 RA Siuzdak G., Beachy R.N., Fauquet C.M.;
 RT "Rice tungro bacilliform virus open reading frame 3 encodes a single
 RT 37-kDa coat protein";
 RL Virology 253:319-326(1999).
 DR EMBL; AF076470; AAC27709.2; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 222 AA; 26460 MW; 95D805292B3760CA CRC64;

Query Match 65.2%; Score 43; DB 2; Length 222;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYWYFD 10
 DB 66 FYWYFD 71
 |||||
 66 FYWYFD 71

RESULT 5

Q8BV92_MOUSE PRELIMINARY; PRT; 244 AA.
 ID Q8BV92_MOUSE PRELIMINARY; PRT; 244 AA.
 AC Q8BV92_MOUSE PRELIMINARY; PRT; 244 AA.
 DT 01-MAR-2003 (TREMELrel. 23, Created)
 DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
 DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
 DE Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length
 DE enriched library, clone:9630050K02 product:weakly similar to
 DE HEPATOCELLULAR CARCINOMA-ASSOCIATED ANTIGEN 112.
 GN Name=061001104RIK;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN NCBI_TaxID=10090;
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 RN NCBI_TaxID=10090;
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staab F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Maehima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN NCBI_TaxID=10654;
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RA The FANTOM Consortium;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN NCBI_TaxID=10654;
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 RN NCBI_TaxID=10654;
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao K., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuaki T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN NCBI_TaxID=10654;
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao K., Sasaki N., Carninci P.,
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 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
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 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
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 RL Genome Res. 10:1757-1771(2000).
 RN NCBI_TaxID=10654;
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 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
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 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
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 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
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 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
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 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
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 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
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 RA Konno H., Akiyama J., Nishi K., Kitsuaki T., Tashiro H., Itoh M.,
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 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
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 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
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 RN NCBI_TaxID=10654;
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 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
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 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
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 RL Genome Res. 10:1757-1771(2000).
 RN NCBI_TaxID=10654;
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
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 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
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 RN NCBI_TaxID=10654;
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 RA Shibata K., Itoh M., Aizawa K., Nagao K., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuaki T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
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 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN NCBI_TaxID=10654;
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 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
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 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN NCBI_TaxID=10654;
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
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 RA Konno H., Akiyama J., Nishi K., Kitsuaki T., Tashiro H., Itoh M.,
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 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
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 RA Yoneda Y., Ishikawa T

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RETVFYWF 9
Db 145 RELNFWYF 153

RESULT 6

O9DCS1_MOUSE
ID O9DCS1_MOUSE PRELIMINARY; PRT: 244 AA.
AC O9DCS1; Q8K470;
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 31, Last annotation update)
DE Mus musculus adult male kidney cDNA, RIKEN full-length enriched
DE library, clone:0610011104 product:weakly similar to HEPATOCELLULAR
DE CARCINOMA-ASSOCIATED ANTIGEN 112 (0610011104RIK protein) (Kidney
DE Name:0610011104RIK; RIKEN cDNA 0610011104).
GN Mus musculus (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirai L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,
RA Hayashizaki Y.;
RL "Functional annotation of a full-length mouse cDNA collection."
RN Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
RN [5]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
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RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
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RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA Ebert L., Muenstermann E., Schatten R., Henze S., Bohn E.,
RA Mollenhauer J., Wiemann S., Schick M., Korn B.;
RT "Cloning of mouse full open reading frames in Gateway(R) system entry
RT vector (pDONR201)."
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6N; TISSUE=Kidney;
RA Nakajima H., Takenaka M., Kaimori J., Imai E., Hori M.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [9]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [10]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK002546; BAB22177.2; -; mRNA.
DR EMBL; CT010190; CAJ18398.1; -; mRNA.
DR EMBL; AB063313; BAB97230.1; -; mRNA.
DR EMBL; BC010831; AAH10831.2; -; mRNA.

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DR Ensembl; ENSMUSG00000023367; Mus musculus.
DR MGI; MGI:1913308; 0610011104Rik.
DR GO; GO:0016021; C: integral to membrane; TAS.
DR InterPro; IPR009281; LR8.
DR PANTHER; PTHR15756; LR8; 1.
DR Pfam; PF06077; LR8; 1.
SQ SEQUENCE 244 AA; 26596 MW; 515A3988A6243CCA CRC64;

Query Match      65.2%; Score 43; DB 2; Length 244;
Best Local Similarity 77.8%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RETVFWYF 9
||| |||||
Db 145 RELNFWYF 153

RESULT 7
Q9ENN7_9PICO
ID Q9ENN7_9PICO PRELIMINARY; PRT; 251 AA.
AC Q9ENN7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Polyprotein (fragment).
OS Hepatitis A virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Hepatovirus.
OX NCBI_TaxID=12092;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A712;
RA Fujiwara K.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB047676; BAB12184.1; -; Genomic_RNA.
KW Polyprotein.
FT NON_TER 1 1
SQ SEQUENCE 251 AA; 28785 MW; BPE79D3A26134F18 CRC64;

Query Match      63.6%; Score 42; DB 2; Length 251;
Best Local Similarity 77.8%; Pred. No. 83;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ETVFWYF 10
||| ||| |
Db 234 ETVFNWYD 242

RESULT 8
Q8XTN1_RALSO
ID Q8XTN1_RALSO PRELIMINARY; PRT; 437 AA.
AC Q8XTN1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PUTATIVE ALPHA-KETOGLUTARATE PERMEASE TRANSMEMBRANE PROTEIN.
GN Name=kgtP; OrderedLocusNames=RS0075; ORFNames=RS05546;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Plasmid megaplasmid.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GM11000;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cumac S., Demange N.,
RA Gapin C., Lavie M., Moisan R., Robert C., Saurin W., Schiex T.,
RA Sigquier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissensbach J., Boucher C.A.;

"Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; AL646076; CADI7226.1; -; Genomic_DNA.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0016020; C: membrane; IEA.
DR GO; GO:0005215; F: transporter activity; IEA.
DR GO; GO:0006810; P: transport; IEA.
DR InterPro; IPR004736; Cit_H_symport.
DR InterPro; IPR007114; MFS_1.
DR InterPro; IPR005828; Sub_transporter.
DR InterPro; IPR005829; Sug_transporter.
DR Pfam; PF00083; Sugar_tr; 1.
DR TIGRFAMs; TIGR00883; 2A0106; 1.
DR PROSITE; PS50850; MFS; 1.
DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
KW Complete proteome; Plasmid; Transmembrane.
SQ SEQUENCE 437 AA; 47326 MW; 619FD527C73A9C7D CRC64;

Query Match      63.6%; Score 42; DB 2; Length 437;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RETVFWY 8
||| |||||
Db 402 RESTFWY 409

RESULT 9
Q569B3_RAT
ID Q569B3_RAT PRELIMINARY; PRT; 617 AA.
AC Q569B3;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE LOC314521 protein.
GN Name=LOC314521;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC092586; AAH92586.1; -; mRNA.
DR GO; GO:0003823; F: antigen binding; IEA.
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DR Ensembl; ENSMUSG00000023367; Mus musculus.
DR MGI; MGI:1913308; 0610011104Rik.
DR GO; GO:0016021; C: integral to membrane; TAS.
DR InterPro; IPR009281; LR8.
DR PANTHER; PTHR15756; LR8; 1.
DR Pfam; PF06077; LR8; 1.
SQ SEQUENCE 244 AA; 26596 MW; 515A3988A6243CCA CRC64;

Query Match      65.2%; Score 43; DB 2; Length 244;
Best Local Similarity 77.8%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RETVFWYF 9
||| |||||
Db 145 RELNFWYF 153

RESULT 7
Q9ENN7_9PICO
ID Q9ENN7_9PICO PRELIMINARY; PRT; 251 AA.
AC Q9ENN7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Polyprotein (fragment).
OS Hepatitis A virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Hepatovirus.
OX NCBI_TaxID=12092;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A712;
RA Fujiwara K.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB047676; BAB12184.1; -; Genomic_RNA.
KW Polyprotein.
FT NON_TER 1 1
SQ SEQUENCE 251 AA; 28785 MW; BPE79D3A26134F18 CRC64;

Query Match      63.6%; Score 42; DB 2; Length 251;
Best Local Similarity 77.8%; Pred. No. 83;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ETVFWYF 10
||| ||| |
Db 234 ETVFNWYD 242

RESULT 8
Q8XTN1_RALSO
ID Q8XTN1_RALSO PRELIMINARY; PRT; 437 AA.
AC Q8XTN1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PUTATIVE ALPHA-KETOGLUTARATE PERMEASE TRANSMEMBRANE PROTEIN.
GN Name=kgtP; OrderedLocusNames=RS0075; ORFNames=RS05546;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Plasmid megaplasmid.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GM11000;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cumac S., Demange N.,
RA Gapin C., Lavie M., Moisan R., Robert C., Saurin W., Schiex T.,
RA Sigquier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissensbach J., Boucher C.A.;
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DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGG1; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 617 AA; 68362 MW; 5943B1AFDD14C460 CRC64;

Query Match 63.6%; Score 42; DB 2; Length 617;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TVFYWYFD 10
Db 122 TGYWYFD 129

RESULT 10
ID Q4XGUG_PLACH PRELIMINARY; PRT; 34 AA.
AC Q4XGUG;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PC401639.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Sidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; CAJ01006323; CAH83871.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 34 AA; 4233 MW; 5D6964BAE37D8AD2 CRC64;

Query Match 62.1%; Score 41; DB 2; Length 34;
Best Local Similarity 60.0%; Pred. No. 17;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 ETVFYWFYFDV 11
Db 17 KNVFYFYFDI 26

RESULT 11
ID Q7GHK8_9TRYP PRELIMINARY; PRT; 111 AA.
AC Q7GHK8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome c oxidase III (Fragment).
GN Name=COXIII;
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;

RN NUCLEOTIDE SEQUENCE.
RP STRAIN=BATRO 164;
RX MEDLINE=89003084; PubMed=2844415; DOI=10.1016/0092-8674(88)90049-9;
RA Abraham J.M., Feagin J.E., Stuart K.;
RT "Characterization of cytochrome c oxidase III transcripts that are
RT edited only in the 3' region.";
RL Cell 55:267-272(1988).
DR ENBL; M22662; AAA63544.1; -; mRNA.
FT NON_TER 1
SQ SEQUENCE 111 AA; 13581 MW; 21C3265699917280 CRC64;

Query Match 62.1%; Score 41; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VFYWFYF 9
Db 67 VFYWFYF 72

RESULT 12
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -1- MISCELLANEOUS: The sequences of 10 hybridoma proteins that also
CC bind dextran differ from that shown at 1-7 positions, many of
CC which occur in the D and J segments.
CC -1- MISCELLANEOUS: This protein binds dextran.
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC PIR; A26242; MHMSJ5.
DR HSSP; P01751; INOB.
DR SMR; P01757; 1-117.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 116 Ig-like.
FT DISULFID 22 96 By similarity.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13025 MW; 292E2AF4BE447E41 CRC64;

Query Match 62.1%; Score 41; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YWYFDV 11
Db 6 YWYFDV 11
```

```
Db 101 YWYFDV 106
RESULT 13
HV21_MOUSE
ID HV21_MOUSE STANDARD; PRT; 122 AA.
AC P01790;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region MS11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=81054880; PubMed=6776528;
RA Robinson E.A., Appella E.;
RT "Complete amino acid sequence of a mouse immunoglobulin alpha chain
(MOPC 511).";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4909-4913(1980).
CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that
binds phosphorylcholine.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
DR HSSP; P01789; IMCP.
DR SMR; P01790; 1-122.
DR Ensembl; ENSMUSG00000021155; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 114
FT NON TER 122 122 Ig-like.
SQ SEQUENCE 122 AA; 13652 MW; 9F4837731EA50207 CRC64;
Query Match 62.1%; Score 41; DB 1; Length 122;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 YWYFDV 11
Db 106 YWYFDV 111
RESULT 14
HV18_MOUSE
ID HV18_MOUSE STANDARD; PRT; 123 AA.
AC P01787;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Ig heavy chain V regions TPC 15/S107/HPCM1/HPCM2/HPCM3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE (TPC 15).
RX MEDLINE=76222762; PubMed=819932;
RA Rudikoff S., Potter M.;
RT "Size differences among immunoglobulin heavy chains from
phosphorylcholine-binding proteins.";
Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
[2]
RP NUCLEOTIDE SEQUENCE (H107).
RX MEDLINE=80199926; PubMed=6769593; DOI=10.1016/0092-8674(80)90089-6;
Early P., Huang H., Davis M., Calame K., Hood L.;
RA "An immunoglobulin heavy chain variable region gene is generated from
three segments of DNA: VH, D and JH.";
Cell 19:981-992(1980).
[3]
RP PROTEIN SEQUENCE (S107).
RX MEDLINE=76110488; PubMed=813561;
DOI=10.1146/annurev.ge.09.120175.001513;
Rudikoff S., Barstad P., Potter M., Hood L.;
RA Unpublished results, cited by:
Hood L., Campbell J.H., Elgin S.C.R.;
RL Annu. Rev. Genet. 9:305-353(1975).
[4]
RP PROTEIN SEQUENCE (HPCM1; HPCM2 AND HPCM3).
RX MEDLINE=81197602; PubMed=7231520;
Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
RA "IgG antibodies to phosphorylcholine exhibit more diversity than their
IGM counterparts.";
RL Nature 291:29-34(1981).
[5]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89035545; PubMed=3141511;
Claflin J.L., Barry J.;
RA "Genetics of the phosphocholine-specific antibody response to
Streptococcus pneumoniae. Germ-line but not mutated T15 antibodies are
dominantly selected.";
J. Immunol. 141:4012-4019(1988).
CC -!- MISCELLANEOUS: All those sequence appears to be identical.
CC -!- MISCELLANEOUS: These chains were isolated from myeloma and
hybridoma proteins that bind phosphorylcholine.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
DR PIR; A93804; AVMS75.
DR HSSP; P01789; IMCP.
DR SMR; P01787; 1-123.
DR Ensembl; ENSMUSG00000021155; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 114
FT NON TER 123 123 Ig-like.
SQ SEQUENCE 123 AA; 13777 MW; 9D58086DE12F7000 CRC64;
Query Match 62.1%; Score 41; DB 1; Length 123;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 YWYFDV 11
Db 107 YWYFDV 112
RESULT 15
HV19_MOUSE
ID HV19_MOUSE STANDARD; PRT; 123 AA.
AC P01788;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
```

DE Ig heavy chain V region H8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
RN NCB1_TaxID=10090;
RP [1]
RA PROTEIN SEQUENCE.
RA Barstad P.;
RL Thesis (1975). California Institute of Technology, United States.
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC binds phosphorylcholine.
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR HSSP; P01789; IMCP.
DR SNR; P01788; 1-123.
DR Ensembl; ENSMUSG000000021155; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 114
FT NON_TER 123 123 Ig-like.
SQ SEQUENCE 123 AA; 13805 MW; 9D581401912F7000 CRC64;

Query Match 62.1%; Score 41; DB 1; Length 123;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YWYFDV 11
| | | | |
DB 107 YWYFDV 112

RESULT 16
HV23 MOUSE
ID HV23_MOUSE STANDARD; PRT; 123 AA.
AC P01792;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region HPCG8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=81197602; PubMed=7231520;
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
RT "IgG antibodies to phosphorylcholine exhibit more diversity than their
RT IgM counterparts."
RL Nature 291:29-34(1981).
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC binds phosphorylcholine.
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; E93256; AVMSH8.
DR HSSP; P01789; IMCP.
DR SNR; P01793; 1-123.
DR Ensembl; ENSMUSG000000021155; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 114
FT NON_TER 123 123 Ig-like.
SQ SEQUENCE 123 AA; 13808 MW; 6599F256ECCDE50 CRC64;

Query Match 62.1%; Score 41; DB 1; Length 123;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YWYFDV 11
| | | | |
DB 107 YWYFDV 112

DR HSSP; P01789; IMCP.
DR SNR; P01792; 1-123.
DR Ensembl; ENSMUSG000000021155; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 114
FT NON_TER 123 123 Ig-like.
SQ SEQUENCE 123 AA; 13880 MW; 4559D3106CAF7D8D CRC64;

Query Match 62.1%; Score 41; DB 1; Length 123;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YWYFDV 11
| | | | |
DB 107 YWYFDV 112

RESULT 17
HV24 MOUSE
ID HV24_MOUSE STANDARD; PRT; 123 AA.
AC P01793;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region HPCG13.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=81197602; PubMed=7231520;
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
RT "IgG antibodies to phosphorylcholine exhibit more diversity than their
RT IgM counterparts."
RL Nature 291:29-34(1981).
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC binds phosphorylcholine.
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; F93256; AVMS13.
DR HSSP; P01789; IMCP.
DR SNR; P01793; 1-123.
DR Ensembl; ENSMUSG000000021155; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 114
FT NON_TER 123 123 Ig-like.
SQ SEQUENCE 123 AA; 13808 MW; 6599F256ECCDE50 CRC64;

Query Match 62.1%; Score 41; DB 1; Length 123;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YWYFDV 11
| | | | |
DB 107 YWYFDV 112

```

RESULT 18
Q924P5_MOUSE PRELIMINARY; PRT; 144 AA.
ID Q924P5_MOUSE
AC Q924P5_MOUSE
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VHI86.2-D-J-C mu protein (Fragment).
GN Name=VHI86.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Archontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CS7BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069920; BAB63936.1; -; mRNA.
DR PIR; PH1137; PH1137.
DR PIR; S26744; S26744.
DR HSP; P01751; IAGW.
DR SMR; Q924P5; 1-135.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00406; IGV; 1_v.
DR PROSITE; PS00406; IGV; 1_v.
DR PROSITE; PS00406; IGV; 1_v.
FT NON_TER 144 144
FT FT 144 144
SQ SEQUENCE 144 AA; 15865 MW; CD07BE97B95C1B27 CRC64;

Query Match 62.1%; Score 41; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YWYFDV 11
|||||
Db 103 YWYFDV 108

RESULT 19
ID Q4UB94_THEAN PRELIMINARY; PRT; 276 AA.
AC Q4UB94_THEAN
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORENAMES=TAL7745;
OS Theileria annulata.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC Theileria.
OX NCBI_TaxID=5874;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ankara isolate clone C9;
RA Pain A., Renaud H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
RA Hall N., Barrell B.G.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
RL "The chromosome 3 genome sequence of Theileria annulata."
DR EMBL; CR940352; CAI75907.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 276 AA; 32517 MW; EE4A54AF2118AE0E CRC64;

Query Match 62.1%; Score 41; DB 2; Length 276;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VFYWYF 9
|||||

RESULT 20
Q34935_LEITA PRELIMINARY; PRT; 284 AA.
ID Q34935_LEITA
AC Q34935_LEITA
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cytochrome c oxidase subunit 3 (EC 1.9.3.1) (Cytochrome c oxidase
DE polypeptide III).
OS Leishmania tarentolae (Saurleishmania tarentolae).
OC Leishmania tarentolae.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania;
OC Lizard Leishmania.
OX NCBI_TaxID=5689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=UC;
RA Shaw J.M., Feagin J.B., Stuart K.D., Simpson L.;
RL "Editing of kinetoplast mitochondrial mRNAs by uridine addition and
RT deletion generates conserved amino acid sequences and AUG initiation

Query Match 62.1%; Score 41; DB 1; Length 284;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VFYWYF 9
|||||
Db 135 VFYWYF 140

RESULT 21
Q34935_LEITA PRELIMINARY; PRT; 287 AA.
ID Q34935_LEITA
AC Q34935_LEITA
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cytochrome oxidase.
GN Name=COIII;
OS Leishmania tarentolae (Saurleishmania tarentolae).
OC Leishmania tarentolae.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania;
OC Lizard Leishmania.
OX NCBI_TaxID=5689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=UC;
RA Shaw J.M., Feagin J.B., Stuart K.D., Simpson L.;
RL "Editing of kinetoplast mitochondrial mRNAs by uridine addition and
RT deletion generates conserved amino acid sequences and AUG initiation

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RT codons.";
 RL Cell 53:401-411(1988).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=UC;
 RX MEDLINE=85079995; PubMed=6096360;
 RA de la Cruz V.F., Neckelmann N., Simpson L.;
 RT "Sequences of six genes and several open reading frames in the
 RT kinetoplast maxicircle DNA of *Leishmania tarentolae*.";
 RL J. Biol. Chem. 259:15136-15147(1984).
 DR EMBL; L07539; AAA31877.1; -; mRNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR000298; CytC_oxdse_III.
 DR PROSITE; PS50253; COX3; 1.
 SQ SEQUENCE 287 AA; 34174 MW; CC5F69B18DFB54C8 CRC64;

Query Match 62.1%; Score 41; DB 2; Length 287;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VFYWF 9
 |||||
 Db 138 VFYWF 143

RESULT 22

Q33549_9TRYP
 ID Q33549_9TRYP PRELIMINARY; PRT; 288 AA.
 AC Q33549;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Cytochrome C oxidase subunit III.
 GN Name=COIII;
 OS Blastocystidia culicis.
 OG Mitochondrion.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
 OC Blastocystidia.
 OX NCBI_TaxID=28005;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC30288;
 RX MEDLINE=9417338; PubMed=8127370; DOI=10.1038/368345a0;
 RA Maslov D.A., Avila H.A., Lake J.A., Simpson L.;
 RT "Evolution of RNA editing in kinetoplastid protozoa: pan-editing
 RT preceded 5'-editing.";
 RL Nature 368:345-348(1994).
 DR EMBL; U05814; AAA73419.1; -; Unassigned_DNA.
 DR PIR; S43289; S43289.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR000298; CytC_oxdse_III.
 DR PROSITE; PS50253; COX3; 1.
 SQ SEQUENCE 288 AA; 33994 MW; 3F670C5AE053D127 CRC64;

Query Match 62.1%; Score 41; DB 2; Length 288;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VFYWF 9
 |||||
 Db 139 VFYWF 144

RESULT 23
 Q35993_9TRYP
 ID Q35993_9TRYP PRELIMINARY; PRT; 288 AA.
 AC Q35993; Q26739;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Cytochrome c oxidase III.
 GN Name=COIII;
 OS Trypanosoma brucei.
 OG Mitochondrion.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5691;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BATRO 164;
 RX MEDLINE=88210466; PubMed=2452697; DOI=10.1016/0092-8674(88)90161-4;
 RA Feagin J.E., Abraham J.M., Stuart K.D.;
 RT "Extensive editing of the cytochrome c oxidase III transcript in
 RT Trypanosoma brucei.";
 RL Cell 53:413-422(1988).
 DR EMBL; M20379; AAA32122.1; -; mRNA.
 DR PIR; A28782; A28782.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR000298; CytC_oxdse_III.
 DR PROSITE; PS50253; COX3; 1.
 SQ SEQUENCE 288 AA; 34689 MW; 47CA8E3F88E5D6E8 CRC64;

Query Match 62.1%; Score 41; DB 2; Length 288;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VFYWF 9
 |||||
 Db 139 VFYWF 144

RESULT 24

Q5X2F2_LEGPA
 ID Q5X2F2_LEGPA PRELIMINARY; PRT; 305 AA.
 AC Q5X2F2;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=lp2441;
 OS Legionella pneumophila (strain Paris).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
 OC Legionellaceae; Legionella.
 OX NCBI_TaxID=297246;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15467720; DOI=10.1038/ngl1447;
 RA Cazalet C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
 RA Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,
 RA Etienne J., Glaser P., Buchrieser C.;
 RT "Evidence in the Legionella pneumophila genome for exploitation of
 RT host cell functions and high genome plasticity.";
 RL Nat. Genet. 36:1165-1173(2004).
 DR EMBL; CR628336; CAH13594.1; -; Genomic_DNA.
 DR LegiOList; lp2441; -.
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0009086; P:methionine biosynthesis; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR000847; HTH_Lyser.
 DR InterPro; IPR005119; LysR_subst.
 DR Pfam; PF00126; HTH 1; 1.
 DR Pfam; PF03466; LysR_substrate; 1.


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DR PROSITE; PS50931; HTH_LYSR; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 305 AA; 34885 MW; 4AD291961B9C9B94 CRC64;

Query Match 62.1%; Score 41; DB 2; Length 305;
Best Local Similarity 80.0%; Pred. NO. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RETVFWYFVD 10
Db 202 RETFPYNYFD 211

RESULT 25
Q5ZS20 LEGPH PRELIMINARY; PRT; 305 AA.
AC Q5ZS20_
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Transcriptional regulator, LysR family.
GN OrderedLocusNames=lgp2376;
OS Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 /
ATCC 33152).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=272624;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1548271; DOI=10.1126/science.1099776;
RA Chien M., Morozova I., Shi S., Sheng H., Chen J., Gomez S.M.,
RA Asamani G., Hill K., Nuara J., Feder M., Rineer J., Greenberg J.J.,
RA Steshenko V., Park S.H., Zhao B., Teplitekaya E., Edwards J.R.,
RA Pampou S., Georgiou A., Chou I.-C., Iannuccilli W., Ulz M.E.,
RA Kim D.H., Geringer-Sameth A., Goldsberry C., Morozov P., Fischer S.G.,
RA Segal G., Qu X., Rzhetsky A., Zhang P., Cayanis E., De Jong P.J.,
RA Ju J., Kalachikov S., Shuman H.A., Russo J.J.;
RT "The genomic sequence of the accidental pathogen Legionella
pneumophila.";
RL Science 305:1966-1968(2004).
DR EMBL; AE017354; AAU28437.1; -; Genomic_DNA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0009086; P:methionine biosynthesis; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000847; HTH_LysR.
DR InterPro; IPR005119; LysR_subst.
DR Pfam; PF00126; HTH_1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PROSITE; PS50931; HTH_LYSR; 1.
KW Complete proteome.
SQ SEQUENCE 305 AA; 34907 MW; 8CDA907F8DB2DEC CRC64;

Query Match 62.1%; Score 41; DB 2; Length 305;
Best Local Similarity 80.0%; Pred. NO. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RETVFWYFVD 10
Db 202 RETFPYNYFD 211

RESULT 26
SYN THEVO
ID SYN THEVO STANDARD; PRT; 429 AA.
AC Q979Y4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Asparaginyl-tRNA synthetase (EC 6.1.1.22) (Asparagine--tRNA ligase)
DE (AsnRS).
GN Name=asnS; OrderedLocusNames=TV1026; ORFNames=TVG1050051;
OS Thermoplasma volcanum.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;

Thermoplasmataceae; Thermoplasma.
NCBI_TaxID=50339;
[1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=GSS1 / DSM 4299 / JCM 9571;
MEDLINE=20570466; PubMed=11121031; DOI=10.1073/pnas.97.26.14257;
RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
RA Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
RA Nunohiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
RT "Archaeal adaptation to higher temperatures revealed by genomic
sequence of Thermoplasma volcanum.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
CC -!- CATALYTIC ACTIVITY: ATP + L-asparagine + tRNA (Asn) = AMP +
phosphate + L-asparaginyl-tRNA (Asn).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the class-II aminoacyl-tRNA synthetase
family.

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removed.
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EMBL; BA000011; BAB60168.1; -; Genomic_DNA.
HSSP; Q52428; 1B8A.
HAMAP; MF_00534; -; 1.
InterPro; IPR004522; AsnS.
InterPro; IPR004365; OB tRNA_NA_bd.
InterPro; IPR004364; tRNA-synt_2.
InterPro; IPR002312; tRNA-synt_asep.
InterPro; IPR006195; tRNA_ligase_II.
Pfam; PF00152; tRNA-synt_2; 1.
Pfam; PF01336; tRNA_anti_1.
PRINTS; PR01042; TRNASYNTHASP.
DR TIGRFAMs; TIGR00457; asnS; 1.
DR PROSITE; PS50862; AA tRNA_LIGASE II; 1.
KW Aminoacyl-tRNA synthetase; ATP-binding; Complete proteome; Ligase;
Nucleotide-binding; Protein biosynthesis.
SQ SEQUENCE 429 AA; 49893 MW; 92ACE28F75CEDE87 CRC64;

Query Match 62.1%; Score 41; DB 1; Length 429;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ETVFYWFVDV 11
Db 377 ESAYYWIIDL 386

RESULT 27
Q87F73_XYLFT PRELIMINARY; PRT; 435 AA.
AC Q87F73;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha-ketoglutarate permease symporter.
GN Name=kgtP; OrderedLocusNames=PD0064;
OS Xylella fastidiosa (strain Temecula / ATCC 700964).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=183190;
RN [1]
RP NUCLEOTIDE SEQUENCE.
MEDLINE=22421331; PubMed=12533478;
DOI=10.1128/JB.185.3.1018-1026.2003;
RA Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B., Moon D.H.,
RA Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., da Silva F.R.,
RA Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,
RA Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorri H., Tsai S.M.,
RA Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,
RA Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.E.,

```

RA Marino C.L., Gigliotti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,
 RA Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,
 RA da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,
 RA Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sasaki F.T., Sena J.A.D.,
 RA de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G.,
 RA Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
 RA Kitajima J.P.;
 RT "Comparative analyses of the complete genome sequences of Pierce's
 RT disease and citrus variegated chlorosis strains of Xylella
 RT fastidiosa."; 185:1018-1026(2003).
 RL J. Bacteriol. 185:1018-1026(2003).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 DR EMBL; AE012553; AAC02964.1; -; Genomic DNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0006100; C:membrane; IEA.
 DR GO; GO:0005215; P:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR GO; GO:0005215; P:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR007114; MPS.
 DR InterPro; IPR005828; Sub transporter.
 DR InterPro; IPR005829; Sug transporter.
 DR Pfam; PF00083; Sugar tr; 1.
 DR PROSITE; PS00850; MFS; 1.
 DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
 DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
 KW Complete proteome; Transmembrane.
 SQ SEQUENCE 435 AA; 47918 MW; 03181910C660E5B5 CRC64;
 Query Match 62.1%; Score 41; DB 2; Length 435;
 Best Local Similarity 85.7%; Pred. No. 2.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ETVFYWY 8
 Db 403 ETVFFWY 409
 RESULT 28
 Q9PH59_XYLFA
 ID Q9PH59_XYLFA PRELIMINARY; PRT; 435 AA.
 AC Q9PH59;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Alpha-ketoglutarate permease symporter.
 GN OrderedLocusNames=Xf0087;
 OS Xylella fastidiosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xylella.
 OX NCBI_TaxID=2371;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=945C;
 RX MEDLINE=20345717; PubMed=10910347; DOI=10.1038/35018003;
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
 RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Brites M.R.S.,
 RA Buono M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
 RA Colauto N.B., Colombo C., Costa F.P., Costa M.C.R., Costa-Neto C.M.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
 RA Pacinca A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
 RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 RA Krieger J.E., Kuranee E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
 RA Menck C.P.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
 RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,

RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
 RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
 RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
 RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
 RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
 RL Nature 406:151-159(2000).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 DR EMBL; AS003863; AAF82900.1; -; Genomic DNA.
 DR PIR; E82848; E82848.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005215; P:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR007114; MPS.
 DR InterPro; IPR005828; Sub transporter.
 DR InterPro; IPR005829; Sug transporter.
 DR Pfam; PF00083; Sugar tr; 1.
 DR PROSITE; PS00850; MFS; 1.
 DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
 KW Complete proteome; Transmembrane.
 SQ SEQUENCE 435 AA; 47987 MW; 2663EAD5B8454C1C CRC64;
 Query Match 62.1%; Score 41; DB 2; Length 435;
 Best Local Similarity 85.7%; Pred. No. 2.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ETVFYWY 8
 Db 403 ETVFFWY 409
 RESULT 29
 Q87JR8_VIBPA
 ID Q87JR8_VIBPA PRELIMINARY; PRT; 463 AA.
 AC Q87JR8;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Phospho-beta-glucosidase B.
 GN OrderedLocusNames=VPA0180;
 OS Vibrio parahaemolyticus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=570;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=RIMD 2210633 / Serotype O3:k6;
 RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
 RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
 RA Tajiima Y., Najiima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
 RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
 RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
 RT distinct from that of V. cholerae.";
 RL Lancet 361:743-749(2003).
 DR EMBL; BA000032; BAC61523.1; -; Genomic DNA.
 DR HSSP; P11546; IPBG.
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR001360; Glyco hydro_1.
 DR Pfam; PF00232; Glyco hydro_1; 1.
 DR PRINTS; PR00131; GLHYDRLASE1.
 DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; 1.
 DR PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2; 1.
 KW Complete proteome; Glycosidase; Hydrolase.
 SQ SEQUENCE 463 AA; 52993 MW; 4E39CFD9D23342A CRC64;
 Query Match 62.1%; Score 41; DB 2; Length 463;
 Best Local Similarity 63.6%; Pred. No. 2.2e+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RETVFWYFDV 11
 Db 1 RETVFWYFDV 11

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Db      443 RKSFYVYQDV 453

RESULT 30
Q9G9U3_LEIIN
ID Q9G9U3_LEIIN PRELIMINARY; PRT; 467 AA.
AC Q9G9U3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 6-phospho-beta-glucosidase-like protein.
GN Name=arabB;
OS Leishmania infantum.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5671;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Requena R.M., Perez-Pertejo Y., Balana-Fouce R., Ordonez-Escudero D.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF309637; AAG46031.1; -; Genomic_DNA.
DR HSSP; Q59976; 1GON.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001360; Glyco_hydro_1.
DR Pfam; PF00232; Glyco_hydro_1; 1.
DR PRINTS; PR00131; GLHYDRLASE1.
DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; UNKNOWN_1.
DR PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 467 AA; 53063 MW; E03D69A2EDF4F2EF CRC64;

Query Match 62.1%; Score 41; DB 2; Length 467;
Best Local Similarity 63.6%; Pred. No. 2.3e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 RETVFWYFDV 11
|: |||||
Db      445 RKSFYVYQDV 455

RESULT 31
Q4VK76_PECCE
ID Q4VK76_PECCE PRELIMINARY; PRT; 467 AA.
AC Q4VK76;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE CasB.
GN Name=CasB;
OS Pectobacterium carotovorum (subsp. carotovorum) (Erwinia carotovora
(subsp. carotovora)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=555;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=LV34;
RA An C.L., Lim W.J., Hong S.Y., Kim Y.K., An J.M., Choi B.R., Cho K.M.,
RA Kang J.M., Lee S.M., Yun H.D.;
RT "A Cryptic beta-glucosidase Gene, casB, of Pectobacterium carotovorum
subsp. carotovorum LV34."
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY866383; AAX57580.1; -; Genomic_DNA.
DR InterPro; IPR001360; Glyco_hydro_1.
DR Pfam; PF00232; Glyco_hydro_1; 1.
DR PRINTS; PR00131; GLHYDRLASE1.
DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; 1.
DR PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 467 AA; 53597 MW; 0BC94AF1A75C4248 CRC64;

Query Match 62.1%; Score 41; DB 2; Length 467;
Best Local Similarity 63.6%; Pred. No. 2.3e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 RETVFWYFDV 11
|: |||||
Db      445 RKSFYVYQDV 455

RESULT 32
Q6D9F4_ERWCT
ID Q6D9F4_ERWCT PRELIMINARY; PRT; 467 AA.
AC Q6D9F4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 6-phospho-beta-glucosidase (EC 3.2.1.86).
GN OrderedLocusNames=BCA0662;
OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SRI 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
RA Bell K.S., Sebahia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holleva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmund G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
RT "Genome sequence of the enterobacterial phytopathogen Erwinia
carotovora subsp. atroseptica and characterization of virulence
factors."
RT Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
DR EMBL; BX950851; CAG73576.1; -; Genomic DNA.
DR GO; GO:0008706; F:6-phospho-beta-glucosidase activity; IEA.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001360; Glyco_hydro_1.
DR Pfam; PF00232; Glyco_hydro_1; 1.
DR PRINTS; PR00131; GLHYDRLASE1.
DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; 1.
DR PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2; 1.
KW Complete proteome; Glycosidase; Hydrolase.
SQ SEQUENCE 467 AA; 53622 MW; 24FD49FF7BD37E26 CRC64;

Query Match 62.1%; Score 41; DB 2; Length 467;
Best Local Similarity 63.6%; Pred. No. 2.3e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 RETVFWYFDV 11
|: |||||
Db      449 RKSFYVYQDV 459

RESULT 33
Q6QGY5_PECCE
ID Q6QGY5_PECCE PRELIMINARY; PRT; 468 AA.
AC Q6QGY5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE BglB.
GN Name=bglB;
OS Pectobacterium carotovorum (subsp. carotovorum) (Erwinia carotovora
(subsp. carotovora)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=555;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15564664; DOI=10.1271/bbb.68.2270;
RA An C.L., Lim W.J., Hong S.Y., Kim E.J., Shin E.C., Kim M.K., Lee J.R.,

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Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 RETVFWYFDV 11
|: |||||
Db      449 RKSFYVYQDV 459

RESULT 32
Q6D9F4_ERWCT
ID Q6D9F4_ERWCT PRELIMINARY; PRT; 467 AA.
AC Q6D9F4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 6-phospho-beta-glucosidase (EC 3.2.1.86).
GN OrderedLocusNames=BCA0662;
OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SRI 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
RA Bell K.S., Sebahia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holleva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmund G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
RT "Genome sequence of the enterobacterial phytopathogen Erwinia
carotovora subsp. atroseptica and characterization of virulence
factors."
RT Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
DR EMBL; BX950851; CAG73576.1; -; Genomic DNA.
DR GO; GO:0008706; F:6-phospho-beta-glucosidase activity; IEA.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001360; Glyco_hydro_1.
DR Pfam; PF00232; Glyco_hydro_1; 1.
DR PRINTS; PR00131; GLHYDRLASE1.
DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; 1.
DR PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2; 1.
KW Complete proteome; Glycosidase; Hydrolase.
SQ SEQUENCE 467 AA; 53622 MW; 24FD49FF7BD37E26 CRC64;

Query Match 62.1%; Score 41; DB 2; Length 467;
Best Local Similarity 63.6%; Pred. No. 2.3e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 RETVFWYFDV 11
|: |||||
Db      449 RKSFYVYQDV 459

RESULT 33
Q6QGY5_PECCE
ID Q6QGY5_PECCE PRELIMINARY; PRT; 468 AA.
AC Q6QGY5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE BglB.
GN Name=bglB;
OS Pectobacterium carotovorum (subsp. carotovorum) (Erwinia carotovora
(subsp. carotovora)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=555;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15564664; DOI=10.1271/bbb.68.2270;
RA An C.L., Lim W.J., Hong S.Y., Kim E.J., Shin E.C., Kim M.K., Lee J.R.,

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RA Park S.R., Woo J.G., Lim Y.P., Yun H.D.;
RT "Analysis of bgl Operon Structure and Characterization of beta-
RT Glucosidase from Pectobacterium carotovorum subsp. carotovorum L134.";
RL Biosci. Biotechnol. Biochem. 68:2270-2278(2004).
DR EMBL; AY542524; AAS55459.1; -; Genomic DNA.
DR GO; GO:0004553; P:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001360; Glyco hydro 1.
DR Pfam; PF00232; Glyco hydro 1; 1.
DR PRINTS; PR00131; GLHYDRLASE1.
DR PROSITE; PS00572; GLYCOSYL HYDROL_F1_1; 1.
DR PROSITE; PS00653; GLYCOSYL HYDROL_F1_2; 1.
KW Glucosidase; Hydrolase.
SQ SEQUENCE 468 AA; 53494 MW; 4B08C2E31087293A CRC64;

Query Match 62.1%; Score 41; DB 2; Length 468;
Best Local Similarity 63.6%; Pred. No. 2.3e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RETVFYWFVDV 11
   : |||||
Db 445 RKKSFYWKDV 455

RESULT 34
Q7TMK1_MOUSE PRELIMINARY; PRT; 470 AA.
AC Q7TMK1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein A1324046.
GN Name=A1324046;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RX MEDLINE=22388257; Pubmed=124717932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055910; AAS55910.1; -; mRNA.
DR HSSP; P01865; 1KB5.

DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 470 AA; 51728 MW; 6D90E4DF896B090 CRC64;

Query Match 62.1%; Score 41; DB 2; Length 470;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WYFVDV 11
   : |||||
Db 124 WYFVDV 129

RESULT 35
Q6MZQ6_HUMAN PRELIMINARY; PRT; 475 AA.
AC Q6MZQ6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686G1190.
GN Name=DKFZp686G1190;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Esophagus tumor;
RC The German cDNA Consortium;
RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640947; CAE45972.1; -; mRNA.
DR HSSP; P01861; 1ADQ.
DR SNR; Q6MZQ6; 20-475.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGV; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match 62.1%; Score 41; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WYFVDV 11
   : |||||
Db 129 WYFVDV 134

RESULT 36
Q91XEL_MOUSE PRELIMINARY; PRT; 480 AA.
AC Q91XEL;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
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OC Burkholderiaceae; Burkholderia; pseudomallei group.
ON NCBI_TaxID=28450;
OX [1]
RC NUCLEOTIDE SEQUENCE.
RP STRAIN=K96243;
RX PubMed=15377794; DOI=10.1073/pnas.0403302101;
RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M.,
RA Atkins T., Crossman L.C., Pitt T., Church C., Mungall K.L.,
RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Crosett B., Davis P., Deshaizer D.,
RA Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA Songgivilai S., Stevens K., Tumapa S., Vesaratchaveit M.,
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT "Genomic plasticity of the causative agent of melioidosis,
RT Burkholderia pseudomallei";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
RM ENBL; BX571966; CAH38194.1; -, Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016759; F:cellulose synthase activity; IEA.
DR GO; GO:0016740; E:transferase activity; IEA.
DR GO; GO:0006011; F:UDP-glucose metabolism; IEA.
DR InterPro; IPRO003919; Cell_synth A.
DR InterPro; IPRO011173; Glyco trans 2.
DR Pfam; PF00535; Glycos transf 2; 1.
DR PRINTS; PR01439; CELLSENTHASEA.
KW Complete proteome; Transferase.
SQ SEQUENCE 655 AA; 72469 MW; 0961DFD6680B7826 CRC64;

Query Match 62.1%; Score 41; DB 2; Length 655;
Best Local Similarity 62.5%; Pred.No.3.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps
QY 4 VYWTFDV 11
 : |||||:
Db 393 LLYWTFDI 400

RESULT 38
Q6ZBC6_BURMA PRELIMINARY; PRT; 655 AA.
ID Q6ZBC6_BURMA
AC Q6ZBC6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative cellulose synthase.
GN OrderedLocusNames=BMAA1391;
OS Burkholderia mallei (Pseudomonas mallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=13373;
ON [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 23344;
RX PubMed=15377793; DOI=10.1073/pnas.0403306101;
RA Niernan W.C., Deshaizer D., Kim H.S., Tettelin H., Nelson K.E.,
RA Feidilyum T.V., Ulrich R.L., Renning C.M., Brinkac L.M.,
RA Daugherty S.C., Davidson T.D., DeBooy R.T., Dmitrov G., Dodson R.J.,
RA Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
RA Madupu R., Mohammed Y., Nelson W.C., Radune D., Romero C.M.,
RA Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
RA Zafar N., Zhou L., Fraser C.M.;
RT "Structural flexibility in the Burkholderia mallei genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
RM ENBL; CP000011; AAU46463.1; -, Genomic_DNA.
DR DR
DR TIGR; BMAA1391; -;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016759; F:cellulose synthase activity; IEA.
DR GO; GO:0006011; F:UDP-glucose metabolism; IEA.
DR InterPro; IPRO003919; Cell_synth A.
DR InterPro; IPRO011173; Glyco trans 2.

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DR Pfam; PF00535; Glycos transf 2; 1.
DR PRINTS; PR01439; CELLSINTHASEA.
KW Complete proteome.
SQ SEQUENCE 655 AA; 72457 MW; BF28DFD6680B7FC0 CRC64;

Query Match 62.1%; Score 41; DB 2; Length 655;
Best Local Similarity 62.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 VFVWYFVD 11
Db 393 LLYWYFDI 400

RESULT 39
Q6NND0 DROME
ID Q6NND0 DROME PRELIMINARY; PRT; 1240 AA.
AC Q6NND0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE R869185p.
GN Name=CG31004;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Strain=Berkley;
RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
RA Park S., Wan K., Yu C., Rubin G.M., Celniker S.;
RA Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BT011360; AAR96152.1; -; mRNA.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR005533; AMOP.
DR InterPro; IPR003886; NIDO.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF03782; AMOP; 1.
DR Pfam; PF06119; NIDO; 1.
DR Pfam; PF00084; Sushi; 1.
DR Pfam; PF00094; VWD; 1.
DR SMART; SM00723; AMOP; 1.
DR SMART; SM00032; CCP; 1.
DR SMART; SM00539; NIDO; 1.
DR SMART; SM00216; VWD; 1.
DR PROSITE; PS50856; AMOP; 1.
DR PROSITE; PS50923; SUSHI; 1.
SQ SEQUENCE 1240 AA; 141592 MW; 087A69CD17D9DCD3 CRC64;

Query Match 62.1%; Score 41; DB 2; Length 1240;
Best Local Similarity 60.0%; Pred. No. 5.9e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RETVFWYFVD 10
Db 162 RSNFMWYFVD 171

RESULT 40
Q9VA05 DROME
ID Q9VA05 DROME PRELIMINARY; PRT; 1431 AA.
AC Q9VA05;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG31004-PA, isoform A (CG31004-pb, isoform b).
GN Name=CG31004; ORFNames=CG31004;

OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flossler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glöck A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaiswal M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinart K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.B., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

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RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskaas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003777; AAF57123.2; -; Genomic DNA.
DR Ensembl; CG31004; Drosophila melanogaster.
DR FlyBase; FBgn051004; CG31004.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR005533; AMOP.
DR InterPro; IPR003886; NIDO.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF03782; AMOP; 1.
DR Pfam; PF06119; NIDO; 1.
DR Pfam; PF00084; Sushi; 1.
DR Pfam; PF00094; VWD; 1.
DR SMART; SM00723; AMOP; 1.
DR SMART; SM00032; CCP; 1.
DR SMART; SM00539; NIDO; 1.
DR SMART; SM00216; VWD; 1.
DR PROSITE; PS00856; AMOP; 1.
DR PROSITE; PS0923; SUSHI; 1.
SQ SEQUENCE 1431 AA; 162377 MW; 7C7P4C01CC052DFC CRC64;
Query Match 62.1%; Score 41; DB 2; Length 1431;
Best Local Similarity 60.0%; Pred. No. 6.9e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 RETVFYWFYD 10
Db 162 RSNFMYWFYD 171
RESULT 41
Q9EMR6 AMEPV
ID Q9EMR6 AMEPV PRELIMINARY; PRT; 287 AA.
AC Q9EMR6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE AMV133.
GN Name=AMV133;
OS Amsacta moorei entomopoxvirus (AmePV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
OC Betaentomopoxvirus.
OC Betaentomopoxvirus.
OX NCBI_TaxID=28321;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20396580; PubMed=10936094; DOI=10.1006/viro.2000.0449;
RA Bowden A.L., Glassberg K.J., Diggins J., Shaw R., Farmerie W.,
RA Moyer R.W.;
RT "Complete genomic sequence of the Amsacta moorei entomopoxvirus:
RT analysis and comparison with other poxviruses.";
RL Virology 274:120-139(2000).
DR EMBL; AF250284; AAG02839.1; -; Genomic DNA.

DR GO; GO:0004806; F:triacylglycerol lipase activity; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR InterPro; IPR002921; Lipase_3.
DR Pfam; PF01764; Lipase_3; 1.
SQ SEQUENCE 287 AA; 34119 MW; AC74943B9A5C42A9 CRC64;
Query Match 61.4%; Score 40.5; DB 2; Length 287;
Best Local Similarity 57.1%; Pred. No. 1.7e+02;
Matches 8; Conservative 1; Mismatches 0; Indels 5; Gaps 1;
Qy 3 TVFY-----WYFVDV 11
Db 248 TVYKIGKIWFYDV 261
RESULT 42
Q4XRH5 PLACH
ID Q4XRH5 PLACH PRELIMINARY; PRT; 62 AA.
AC Q4XRH5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PC107290.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Beriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAJ01003729; CAH80487.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 62 AA; 7636 MW; 435D6FD70CF780BD CRC64;
Query Match 60.6%; Score 40; DB 2; Length 62;
Best Local Similarity 77.8%; Pred. No. 44;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 3 TVFYWYFVD 11
Db 27 TVFYFHYDV 35
RESULT 43
Q59YX1 CANAL
ID Q59YX1 CANAL PRELIMINARY; PRT; 127 AA.
AC Q59YX1;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=CaO19.10707;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,

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RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of Candida albicans.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RA Dunagan J., Kuo A., Newport G., Ian C.-Y., Iijima C., Adegbola O.,
RA Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W.,
RA Jones T., Scherer S., Agabian N.;
RT "Annotatation of the Genome of Candida albicans.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AACQ01000097; EAK95700.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 127 AA; 15222 MW; B625A49643EF2BCC CRC64;
Query Match 60.6%; Score 40; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 TVFYWY 8
Db 95 TVFYWY 100
RESULT 44
QV07077 PROMP PRELIMINARY; PRT; 133 AA.
AC QV07077;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE HNH endonuclease:HNH nuclease.
GN OrderedLocusNames=PMW1403;
OS Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus
OX NCBI_TaxID=59919;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RL MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hees W.R.,
RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT niche differentiation.";
RL Nature 424:1042-1047(2003).
DR EMBL: BX572093; CAB19862.1; -; Genomic_DNA.
DR GO: GO:0004519; F:endonuclease activity; IEA.
DR GO: GO:0003676; F:nucleic acid binding; IEA.
DR InterPro: IPR002711; HNH.
DR InterPro: IPR003615; HNH_nuc.
DR Pfam: PF01844; HNH.
DR SMART: SM00507; HNHc; 1.
DR Complete proteome; Endonuclease.
SQ SEQUENCE 133 AA; 15449 MW; BDA7A95D647B2FC0 CRC64;
Query Match 60.6%; Score 40; DB 2; Length 133;
Best Local Similarity 85.7%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 ETVFYWY 8
Db 74 ENVFYWY 80
RESULT 45
YDYA_SCHPO
ID YDYA_SCHPO STANDARD; PRT; 162 AA.
Davis R.W., Scherer S.;
RT "The diploid genome sequence of Candida albicans.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RA Dunagan J., Kuo A., Newport G., Ian C.-Y., Iijima C., Adegbola O.,
RA Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W.,
RA Jones T., Scherer S., Agabian N.;
RT "Annotatation of the Genome of Candida albicans.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AACQ01000097; EAK95700.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 127 AA; 15222 MW; B625A49643EF2BCC CRC64;
Query Match 60.6%; Score 40; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 TVFYWY 8
Db 95 TVFYWY 100
RESULT 44
QV07077 PROMP PRELIMINARY; PRT; 133 AA.
AC QV07077;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE HNH endonuclease:HNH nuclease.
GN OrderedLocusNames=PMW1403;
OS Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus
OX NCBI_TaxID=59919;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RL MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hees W.R.,
RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT niche differentiation.";
RL Nature 424:1042-1047(2003).
DR EMBL: BX572093; CAB19862.1; -; Genomic_DNA.
DR GO: GO:0004519; F:endonuclease activity; IEA.
DR GO: GO:0003676; F:nucleic acid binding; IEA.
DR InterPro: IPR002711; HNH.
DR InterPro: IPR003615; HNH_nuc.
DR Pfam: PF01844; HNH.
DR SMART: SM00507; HNHc; 1.
DR Complete proteome; Endonuclease.
SQ SEQUENCE 133 AA; 15449 MW; BDA7A95D647B2FC0 CRC64;
Query Match 60.6%; Score 40; DB 2; Length 133;
Best Local Similarity 85.7%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 ETVFYWY 8
Db 74 ENVFYWY 80
RESULT 45
YDYA_SCHPO
ID YDYA_SCHPO STANDARD; PRT; 162 AA.
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AC OL13689;
DT 15-JUL-1998 (Rel. 36, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Hypothetical protein C11E3.10 in chromosome I.
GN ORFNames=SPAC11E3.10;
OS Schizosaccharomyces pombe (Fission Yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=972;
RL MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gwilliam R., Rajadream M.A., Lyne M.H., Lyne R., Stewart A.,
RA Sgouras J.G., Peat N., Hayles J., Baker S.G., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D.E., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K.D., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K.L., Murphy L.D., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K.M., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M.N., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J.R., Volkhardt G., Aert R., Robben J., Grymoprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Duesterhoeft A., Fritzc C., Holzer E., Moestl D.,
RA Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
DR EMBL: Z98595; CAB11189.2; -; Genomic_DNA.
DR PIR: T37538; T37538.
DR GeneDB Spombe; SPAC11E3.10; -.
DR InterPro: IPR006976; VanZ.
DR Pfam: PF04892; VanZ; 1.
KW Complete proteome; Hypothetical protein; Transmembrane.
FT TRANSMEM 15 35 Potential.
FT TRANSMEM 43 63 Potential.
FT TRANSMEM 70 90 Potential.
FT TRANSMEM 97 117 Potential.
SQ SEQUENCE 162 AA; 18481 MW; 6E10E58EF55131F CRC64;
Query Match 60.6%; Score 40; DB 1; Length 162;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 4 VFYWFYFDV 11
Db 55 VFYWFYFDL 62
RESULT 46
Q4KAS6_PSEFS
ID Q4KAS6_PSEFS PRELIMINARY; PRT; 213 AA.
```


Q4KAS6;
 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 Transcriptional regulator, TetR family.
 ORFNames=PFL_3534;
 OS Pseudomonas fluorescens (strain Pf-5).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 NCBI_TaxID=220664;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PF-5;
 RX PubMed=15980861; DOI=10.1038/nbt1110;
 RA Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S.,
 RA Mavroudis D., DeBoy R.T., Seahadri R., Ren Q., Madupu R., Dodson R.J.,
 RA Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M.,
 RA Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Iran K.,
 RA Khouri H.M., Pierson E., Pierson L. III, Thomashow L., Loper J.;
 RT "Complete genome sequence of the plant commensal Pseudomonas
 fluorescens Pf-5.";
 RL Nat. Biotechnol. 23: 873-878(2005).
 DR EMBL: CP000076; AA92821.1; -, Genomic DNA.
 SQ SEQUENCE 213 AA; 24433 MW; 9961C6935D9F8221 CRC64;
 Query Match 60.6%; Score 40; DB 2; Length 213;
 Best Local Similarity 85.7%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 TVFYWYF 9
 Db 49 TSFYWYF 55
 RESULT 47
 Q9MT27_9ASPA PRELIMINARY; PRT; 231 AA.
 AC Q9MT27;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Ribulose 1,5-bisphosphate carboxylase large subunit (Fragment).
 GN Name=rbcl;
 OS Apodolirion lanceolatum.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 -OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae;
 OC Apodolirion.
 NCBI_TaxID=112531;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=10487820.
 RA Meerow A.W., Fay M.F., Guy C.L., Li Q.-B., Zaman F.Q., Chase M.W.;
 RT "Systematics of Amaryllidaceae based on cladistic analysis of plastid
 rbcL and trnL-f sequences (1999)."
 RL Am. J. Bot. 86:1325-1345(1999).
 CC -1- FUNCTION: RuBisCO catalyzes two reactions: the carboxylation of D-
 ribulose 1,5-bisphosphate, the primary event in photosynthetic
 carbon dioxide fixation, as well as the oxidative fragmentation of
 the pentose substrate in the photorespiration process (By
 similarity).
 CC -1- FUNCTION: RuBisCO catalyzes two reactions: the carboxylation of D-
 ribulose 1,5-bisphosphate, the primary event in photosynthetic
 carbon dioxide fixation, as well as the oxidative fragmentation of
 the pentose substrate in the photorespiration process. Both
 reactions occur simultaneously and in competition at the same
 active site (By similarity).
 CC -1- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + CO(2) + H(2)O =
 2 3-phospho-D-glycerate.
 CC -1- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + O(2) = 3-
 phospho-D-glycerate + 2-phosphoglycolate.
 CC -1- SUBUNIT: 8 large chains + 8 small chains (By similarity).
 CC -1- SUBCELLULAR LOCATION: Chloroplast (By similarity).

CC -1- SIMILARITY: Belongs to the RuBisCO large chain family.
 DR EMBL: AF116944; AAP97638.1; -, Genomic DNA.
 DR SMR: Q9MT27; 9-229.
 DR GO: GO:0009507; C:chloroplast; IEA.
 DR GO: GO:0009573; C:ribulose biphosphate carboxylase complex (. . .); IEA.
 DR GO: GO:0016829; F:lyase activity; IEA.
 DR GO: GO:0004497; F:monooxygenase activity; IEA.
 DR GO: GO:0016984; F:ribulose-bisphosphate carboxylase activity; IEA.
 DR GO: GO:0015977; P:carbon utilization by fixation of carbon di. . .; IEA.
 DR GO: GO:0009853; P:photorespiration; IEA.
 DR GO: GO:0015979; P:photosynthesis; IEA.
 DR InterPro: IPR000685; RuBisCO large.
 DR Pfam: PF00016; RuBisCO large; 1.
 DR PROSITE: PS00157; RuBisCO large; 1.
 KW Carbon dioxide fixation; Chloroplast; Lyase; Monooxygenase;
 KW Oxidoreductase; Photorespiration; Photosynthesis.
 FT NON_TER 231 231
 FT NON_TER 1
 SQ SEQUENCE 231 AA; 26300 MW; 2794B15706B8A35F CRC64;
 Query Match 60.6%; Score 40; DB 2; Length 231;
 Best Local Similarity 71.4%; Pred. No. 1.6e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 VFYWYFD 10
 Db 47 IFYWYMD 53
 RESULT 48
 Q7NB50_MYCGA PRELIMINARY; PRT; 231 AA.
 ID Q7NB50 MYCGA PRELIMINARY; PRT; 231 AA.
 AC Q7NB50;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Unique hypothetical.
 GN OrderedLocNames=MYCGA4300; ORFNames=MGA_0082;
 OS Mycoplasma gallisepticum.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2096;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=R.
 RX MEDLINE=22830409; PubMed=12949158; DOI=10.1099/mic.0.26427-0;
 RA Papazisi L., Gorton T.S., Kutish G., Markham P.F., Browning G.F.,
 RA Nguyen D.K., Swartzell S., Madan A., Mahairas G., Geary S.J.;
 RT "The complete genome sequence of the avian pathogen Mycoplasma
 gallisepticum strain R(low).";
 RL Microbiology 149:2307-2316(2003).
 DR EMBL: AB016968; AAP56780.1; -, Genomic DNA.
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0003700; F:transcription factor activity; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 231 AA; 28093 MW; 2BB8ABD9846320C4 CRC64;
 Query Match 60.6%; Score 40; DB 2; Length 231;
 Best Local Similarity 54.5%; Pred. No. 1.6e+02;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 RETVYVYFDV 11
 Db 50 RQTIFNWFIV 60
 RESULT 49
 Q4WV37_ASPTU PRELIMINARY; PRT; 348 AA.
 ID Q4WV37_ASPTU PRELIMINARY; PRT; 348 AA.
 AC Q4WV37;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Afu5g10670;
OS Aspergillus fumigatus Af293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=330879;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Af293;
RA Nierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,
RA Arroya J., Berriman M., Abe K., Archer D.B., Bernejo C., Bennett J.,
RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
RA Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,
RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
RA Kellner N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
RA Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
RA Majors W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
RA Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
RA Penava M.A., Perlea N., Price C., Pritchard B.L., Quail M.A.,
RA Rabinowitz E., Rawlins N., Rajandream M.-A., Reichard U.,
RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA Renning C.M., Rutter S., Salzberg S.L., Sanchez M.,
RA Sanchez-Perrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
RA Machida M., Hall N., Barrell B., Denning D.W.;
RA "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT Aspergillus fumigatus";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC - CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHF01000003; EAL91539.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 348 AA; 41230 MW; 72310A91FEDD985B CRC64;

Query Match 60.6%; Score 40; DB 2; Length 348;
Best Local Similarity 55.6%; Pred. No. 2.4e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 TVFYWYFVDV 11
|||:|:|:
Db 24 TVFHWYFV 32

RESULT 50
Q8KKU1 RH1ET
ID Q8KKU1 RH1ET PRELIMINARY; PRT; 364 AA.
AC Q8KKU1
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein yp091.
GN Names-yp091:
OS Rhizobium etli.
OG Plasmid symbiotic plasmid p42d.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX NCBI_TaxID=29449;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CFN42;
RX MEDLINE=91193195; PubMed=2013564;
RA Girard M.L., Flores M., Brom S., Romero D., Palacios R., Davila G.;
RT "Structural complexity of the symbiotic plasmid of Rhizobium
leguminosarum bv. phaseoli";
RL J. Bacteriol. 173:2411-2419 (1991).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CFN42;

RX MEDLINE=97419521; PubMed=9274036;
RA Ramirez-Romero M.A., Bustos P., Girard L., Rodriguez O.,
RA Cevallos M.A., Davila G.;
RT "Sequence, localization and characteristics of the replicator region
of the symbiotic plasmid of Rhizobium etli.";
RL Microbiology 143:2825-2831 (1997).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CFN42;
RX MEDLINE=22309397; PubMed=12421308;
RA Quintero V., Cevallos M.A., Davila G.;
RT "A site-specific recombinase (sino) is required to exert
incompatibility towards the symbiotic plasmid of Rhizobium etli.";
RL Mol. Microbiol. 46:1023-1032 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CFN42;
RA Ramirez M.A., Bustos P., Girard L., Rodriguez O., Cevallos M.A.,
RA Davila G.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CFN42;
RA Quintero V., Bustos P., Davila G.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CFN42;
RA Gonzalez V., Bustos P., Medrano-Soto A., Ramirez-Romero M.A.,
RA Romero D., Salgado H., Hernandez-Gonzalez I., Hernandez-Celis J.C.,
RA Quintero V., Girard L., Rodriguez O., Flores M., Cevallos M.A.,
RA Collado-Vides J., Davila G.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CFN42;
RA Quintero V., Bustos P., Davila G.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U80928; AAM55039.1; -; Genomic_DNA.
DR InterPro; IPR009213; UCP031854.
DR PIRSF; PIRSF031854; UCP031854; 1.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 364 AA; 40120 MW; 20964670BB9D8F48 CRC64;

Query Match 60.6%; Score 40; DB 2; Length 364;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 YWYFV 11
|||:
Db 44 YWYFDI 49

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Job time : 125.769 secs